

XX	PS	Disclosure; Page 166-171; 285pp; English.
XX	CC	Human neuronal alpha 2 coding sequence (AAQ84664) transcript is
CC	CC	differentially processed in skeletal muscle, aorta, and CNS in
CC	CC	the region corresp. to nt 1595-1942 of AAQ84664 in each of the
CC	CC	tissues. Five alternatively spliced variant transcripts that differ
CC	CC	in the presence or absence of one to three different portions of
CC	CC	this region. There are three sequences involved (see AAQ84664.FT
CC	CC	and AAQ84665.FT), sequence 1, sequence 2 and sequence 3. The five
CC	CC	alpha 2 encoding transcripts from the different tissues include
CC	CC	different combinations of the three sequences, except for one of
CC	CC	the alpha 2 transcripts expressed in aorta which lacks all three
CC	CC	sequences. The five alpha 2 forms identified are (1) a form that
CC	CC	lacks sequence 3 called alpha 2a, expressed in skeletal muscle
CC	CC	(2) one that lacks sequence 1 called alpha 2b, expressed in CNS
CC	CC	(3) one that lacks sequences 1 and 2 called alpha 2c, expressed in
CC	CC	aorta (4) one that lacks sequences 1, 2 and 3 called alpha 2d,
CC	CC	expressed in aorta and (5) one that lacks sequences 1 and 3
CC	CC	called alpha 2e.
XX	CC	Sequence 1091 AA;
XX	QY	Query Match 100.0%; Score 5346; DB 16; Length 1091;
XX	QY	Best Local Similarity 100.0%; Pred. No. 0;
XX	QY	Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1	MAAGCLALTLTFLQSLIGPSSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNLVDI 60
DB	1	maagclaltltlflqslilgssseepfpaavtikswdkmqedlvtlaktasgvnqlvdi 60
QY	61	YKYQDLTYVEPNARQLVEIARDTEKLSNRSKALVSLALEAEKVAQAAHQWREFASN 120
DB	61	ykyqdltyvepnarqlveiaardteklslnrskalvslaleaekvqaahqwrdfasn 120
QY	121	EVVYNAKDDLPEKNDSEPGSORIKPVFTEDANFRQISQYHAAVHIPDIYEGSTIVL 180
DB	121	evvyinakddlpeknsepgsorkipvfteadanfrqisqyhavhipcdiyegstivl 180
QY	181	NELNWTALDEVFKNREEDPSLLWQVFGSATGLARYYPASPWVDNSRTPNKIDLDVRR 240
DB	181	nelnwtaldevfknreedsllwqvfgsatglaryypaspwvdnsrtpnkidldvrr 240
QY	241	RPWYIOGAASPKDMLILVDVSGVSGITLKLRTSVSEMLETSSDDDFVNVASFNSNAQD 300
DB	241	rpwyiogaaspkdmlilvdvsgsvsgitlklrtsvsemlletssdddfvnvasfnnaqd 300
QY	301	VSCFOHLVQANVRNKKVLDVANNITAKGTDYKGFSAFEOILLNYSRANCNKIIML 360
DB	301	vscfhlvqanvrnkkvldavnnitakgtdykgfafaefqllnynsrancnkliiml 360
QY	361	FTDGEERAQEIFNKYKRRVFRFVSQGHYVERGPIQWACENKGYIYEIPSGAIR 420
DB	361	ftdgeeraqeifnkykrrvfrfvsqghyvergpiqwmacenkgyyeipsigair 420
QY	421	INTQEYLDVLGRPMVLADGAKAQVQWNTNVLDALEGLVITGLPVPNITGQFENKTNLK 480
DB	421	intqeyldvlgrpmvladgkakqvwnvnlldaleglvitgltpvfnitgqfenktnlk 480
QY	481	NOLTLGVMGVDVSLDKRLTPRTLCPCNGYYPADPNQVYLLHPNLQPKNPKSQEPVTL 540
DB	481	nqltlgvmgvdvsledkrltprtlcpngyyfaidpnqyylvllhpnlpknpsqepvtl 540
QY	541	DFLDAELNDIKVEIRNMKIDGESGKFTFTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600
DB	541	dfldaelndikveirnmkidgesgkftftlvksqderydkgnrtytwtpvngtdysl 600
QY	601	ALVLPYTSFYIYKAKLBETITQARSKGKMKDSTLKPDPFESGYTFIAPRDYCNDLKI 660
DB	601	alvlpysfyiyaklaletitqarskkgmkdsetlkdndfesytfiaprdydcndlki 660
QY*	661	SDNTEFLNFNEIDRTPNPNSCNADLNRVLLDAGFTNELVQVWSKQKNIKGVKAR 720

DB	661	sdnteflnfnfdrktpnpscnadlnrvlldagftnelvqnywskgnikgvkar 720
QY	721	FVVTGGITRVYPKEAGENQWENPEYEDSFYKRSILDNDNYFTAPYFNKSGPGAYESGI 780
DB	721	fvvtgdgitrvypkeagenqwenpetyedsfykrsldndnyvftapyfnksgpgayesgi 780
QY	781	MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPACAGPYCDCKRNSDVMDCVI 840
DB	781	myskaveiyiqgkllkpvvgkldvnswnienftktsirdpcagpycdckrnsdvmdcvi 840
QY	841	LDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNSVYAFNKSVDYOSVCEPGAAPKQ 900
DB	841	lddggfllmanhddytngigrffgeidpslmrhlvnsyvyafnksydygsvcepgaapkq 900
QY	901	GAGHRSAYVPSVADILQIGWATAAASIILOQLLSLTPRLLAEVEMEDDDFTASLSKQ 960
DB	901	gaghraayvpsvadilqigwataaawslilqllsltprrlleavemedddftaslskq 960
QY	961	SCITEQTYFFDNDKSFSGVLDCGNCRIFHCHEKLMNTNLIIFIMVESKGTCPDCTRL 1018
DB	961	sciteqtqyffdnksfsfgvlcdgncsrifhgeklmntnliifimveskgtcpdctrl 1018
RESULT 2		
AAW63145		
ID	AAW63145 standard; Protein; 1091 AA.	
XX	AC AAW63145;	
XX	12-OCT-1998 (first entry)	
XX	Human calcium channel alpha-2 subunit.	
XX	Alpha-2 subunit; human; calcium channel; assay; detection;	
KW	characterisation; Lambert Eaton Syndrome; LES; diagnosis.	
XX	Homo sapiens.	
XX	US5792846-A.	
XX	11-AUG-1998.	
XX	31-MAY-1995; 95US-0455543.	
XX	04-APR-1994; 94US-0223305.	
PR	04-APR-1988; 88US-0176899.	
PR	04-APR-1989; 89US-0603751.	
PR	04-APR-1989; 89WO-US01408.	
PR	20-FEB-1990; 90US-0482384.	
PR	30-NOV-1990; 90US-0620250.	
PR	15-AUG-1991; 91US-0745206.	
PR	31-MAY-1995; 95US-0455543.	
XX	(SIBI-) SIBIA NEUROSCIENCES INC.	
XX	Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;	
PI	Williams ME;	
XX	WPI; 1998-456192/39.	
DR	N-PSDB; AAV42689.	
XX	DNA encoding human calcium channel alpha 1B subunit protein -	
PT	useful for recombinant production of the channel for screening of	
PT	its modulators, and diagnosis of Lambert Eaton Syndrome	
XX	Claim 4; Columns 283-288; 166pp; English.	
XX	The present sequence represents the alpha-2 subunit of a human calcium	
CC	channel. Calcium channels are membrane-spanning, multi-subunit proteins	
CC	that allow controlled entry of calcium ions into cells. This leads	
CC	to depolarisation events required for muscle contraction. The recombinant	
CC	subunit, when expressed with nucleic acids encoding the complete calcium	

CC described in the method of the invention.

XX
SQ sequence 1091 AA;

Query Match	100.0%;	Score 5346;	DB 21;	Length 1091;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1018;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

QY	1	MAAGCLLALTLTLFQSLILGPSEEPF	PSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI	60
Db	1	maagcllaltltlflqslilgpseepf	psavtikswdkmqedlvtlaktasgvnqlvdi	60
QY	61	YEKYQDLTYVEPNNAQOLVEIARDIEKLLSNRSKALVSLAEAKVQAAHQRDEFPASN	120	
Db	61	yekyqdltyvepnnaqlveiaardieklksnrskalsvslaeakvqaahqwrdefasn	120	
QY	121	EVVYVYNAKODDLDPKKNDSPGSGORIKPVFIEDANFGRQISYQHAAVHPTDIYEGSTIVL	180	
Db	121	evvyvynakddlpeknndsepgsgrikpvfiedanfgqisqhaavhptdiyegstivl	180	
QY	181	NELNWTSLADEVFKKREDDPSLLWQVFGSATGLARYYPASPWVDSNSTPKNIDLYDVR	240	
Db	181	nelnwtсалдеvfккнеедпсллwqvfgsatglaryypaspwvdsnstpknidlydvr	240	
QY	241	RPWYIOGAASPRDMLLTDVDSVSGSLTKLIRTSVSEMLFTLSDDDFWNVASFNSNAQD	300	
Db	241	rpwyiogaasprdmlltdvdsvsgsltklirtsvsemlftlsdddfwnvasfnsnaqd	300	
QY	301	VSCFOHLVQANVRNKKVLDAVNNITAKGIDTQYKGFSPAPQLLNYNVSRANCNKIITML	360	
Db	301	vscfqlhqlvanvrnkkvlдавnnitakgидтqyкgfспапqllnynvsrancnkiiмл	360	
QY	361	FTDGGERAQAEIFNKNYNDKKVYRFRFSVQGQINYERGPQIWMACENKGYEYBISGAIR	420	
Db	361	ftdggeraqaeifnknndkkyrvrfsyggqnyergpiqwmacenkgyyeypisgaир	420	
QY	421	INTQEYLDVLGRPMVLGAKQOVQWNTVYLDALGLVITGTLPVENITGOFENKTNLK	480	
Db	421	intqeyldvlgrpmvlgakqovqwnvyldaleglvitgtltpvenitgofenktnlk	480	
QY	481	NQILGVMGVDYSLEDIKRLTPRFTLCPNPGYFYADPNQSVLLHPLNLOPKNPKSQEPVTL	540	
Db	481	nqilgvmgvdysledikrltpfrftlcpnpgyfyaidpnqsvyllhplnlpknpkspqevtl	540	
QY	541	DFLDABLENDIKVEIRNKNMIDGSEKFTPTLVKQSDERYIDKGARTYTWTVPVNGTDYSL	600	
Db	541	dfldaelendikveirnkmidgesektftlvksgderyidkgartytwtvpvngtdysl	600	
QY	601	ALVLPYSFYIYKALEETITQARSKKGMKDSETLKPDPNFESGYTFTAPDYCNDLKI	660	
Db	601	alvlpysfyyiakleetitqarskkgmksdsetlkpdpnfesgytftapdycndlki	660	
QY	661	SDNTEFFLNFEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQYWSKOKNIKGVAR	720	
Db	661	sdntefflnfefidrktpnpnpscnadlinrvldagftnelvqywsqknikgvar	720	
QY	721	FVVTDGGLTRVYPKEAGENQWENPETYEDSFYKRSILDNDNDNYFTAPYKNKSGPGAYESGI	780	
Db	721	fvvtddggltrvypkeagenqwnpetyedsfykrsildndndnyftapyknksgpgayesgi	780	
QY	781	MYSKAVEIYIOQLKLKPAVVGKIKIDVNSWIENTFTKTSIRDPACAGPVCDCRNSDVMDCVI	840	
Db	781	myskaveiyioqllklkparvgvikidvnswnientftksirdpcagpvcckrnsdvmdcvi	840	
QY	841	LDDGGFLMANHDDVTNQIGRFFGEIDPSLMRHLVNIYSYAFNKSIDYQSVCEPGAAPKQ	900	
Db	841	lddggflmanhddvtnqigrffgeidpslmrhlvnisvafnksidyqsvcepgaapkq	900	
QY	901	GAGHSRAYPVSADILIQGWWATAAWSILQOFLLSLFLPRLLEAVEMEDDDFTASLSKQ	960	
Db	901	gaghsraypvsadilqgwwataaawsilqfllslflprlleavedddftaslskq	960	

QY	961	SCITEQTQYFFDNDKSFSGVLDGNCSEIFHGEKLMNTNLIFIMVESKGTCPCDTRL	1018
Db	961	sciteqtavffndndksfsqavldcncsrifhgeklmntnlifimveskgtcpcptrl	1018

RESULT 4

AAW37879
ID AAW37879 standard; Protein; 1091 AA.

XX
AC AAW37879;

XX
DT 28-AUG-1998 (first entry)

XX Human calcium channel $\alpha 2\delta$ subunit.
DE

XX
KW Calcium channel; human; central nervous system disorder;
KW Lambert-Eaton syndrome; diagnosis; therapy.

XX
OS Homo sapiens.

XX
PN WO9811131-A2.

XX
PD 19-MAR-1998.

XX
PF 11-SEP-1997; 97WO-US16146.

XX
PR 16-SEP-1996; 96US-0713118.

XX
PA (AMHP) AMERICAN HOME PROD CORP.

XX
PI
Chen ARS, Franco R, Shuey DJ;

XX
DR WPI; 1998-207325/18.

DR N-PSDB; AAV29060:
XX

PT DNA encoding human neuronal calcium channel subunit(s) - useful for
PT diagnosis of and treatment of central nervous system disorders, e.g.
PT Lambert-Eaton syndrome

XX
PS Disclosure: Fig 2: 89pp; English.

This polypeptide comprises the a2d subunit of the human neuronal calcium channel. cDNA clones (see AAV29059-61) encoding the a1b subunit (see AAW37878), the a2d subunit and a b3 subunit (see AAW37880) have been isolated. These have been inserted into expression vectors and are stably expressed in transformed cell lines. The transformed cells show omega-conotoxin GVIA binding activity, and omega-conotoxin GVIA toxin sensitive potassium-stimulated calcium uptake, indicating that the proteins expressed by the clones are capable of forming a functioning calcium channel. Nucleic acids encoding the 3 subunits, as well as vectors, host cells and methods of isolating nucleic acids encoding related calcium channels are disclosed. Fusion proteins incorporating the subunit proteins, antibodies, and assays for identifying agents that modulate calcium channel activity are also provided. Such agents can be used to treat certain central nervous system disorders by altering calcium channel activity. Methods of diagnosing diseases associated with particular calcium channels, such as Lambert-Eaton syndrome, are disclosed.

XX	Sequence	1091 AA;
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Query Match	99.9%	Score 5342;	DB 19;	Length 1091;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 1017;	Conservative	0;	Mismatches	1;
Indels	0;	Gaps	0;	

QY	1	MAAGCIIALTTLFQSLIGPSSEPPPSAVTIKSWDKMQEDVLTLAKTAGVNLVDI	60
Db	1	maagcIIalttlfqslIgpsseepfpsavtikswdkmqedvltlaktasvnlvdi	60
QY	61	YEKYQDLYTVEPNNAQJVEIARDDIEKLJLSNRSKALYSLEAEKVQAAHQWREDFASN	120


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Db 61 yekyqdytvepnnarqlveiaardleklslsrskalsvslaleaekvqaahqwfesfn 120
QY 121 EVYYNAKDDLDPEKNDSPGSRQIKPVFTEDANFGQISQYHAAVHIPTDIYEGSTIVL 180
Db 121 evyyynakddldpekndsepgsrqikpvfiedanfgqisyqhaavhiptdiyegstivl 180
QY 181 NELNWTSAIDVEFKKNEEDPSLLQVFGSATGLARYYPASPVWVNSRTPNKKIDLVDVRR 240
Db 181 nelnwtalsaidvefkknreedpsllwqvfsgsatglaryypaspvwvnsrtpnkidldvrr 240
QY 241 RPWYIOGAASPKDMLILVDVSGVSGITLKIRTSVSEMLETISDDDFVNVASFNSNAQD 300
Db 241 rpywiggaaspkdmllilvdvsgsvsgitklirtsvsemletisdddfvnvasfnsnaqd 300
QY 301 VSCFQHLVQANVRNKKVLDAVNNTAKGITYDKGFSFAFEOQLLNNVSRANCKIIML 360
Db 301 vscfqlhqvsnvrnkvlkdvannitakgitydkgfsfafeqllnnvsvranchkiiml 360
QY 361 FTDGGERAQEIPKNYKDKKVRFRFSGVGHNYERGPIOMACENKGGYYEIPSGAIR 420
Db 361 ftdggeeaeifknynkdkkvrfrfsvgqhnyergpiqwmacenkgyyeipsgair 420
QY 421 INTQEYLDVLGRPMVLGAKAKOVQNTNYLDALGLGLVITGTLPVFNITGQFENKTNLK 480
Db 421 intqeyldvlgrpmvlgakakovqntnyldaleglglvitgtlpvfnitgqfenktnlk 480
QY 481 NQILGVMGVDSLEDIKRLTPFTLCPNGYYPADPNGVLLHPNLQKNPKSQBPVTL 540
Db 481 nqilgvmgvdsleedikrltpftlcpngyyfapdnpgvllhpnlpknkpsqbpvltl 540
QY 541 DFLDALENDIKVEIRNMKIDGSGEKTFTLVKSDERYDKGNRTYTPVNGTDYSL 600
Db 541 dfldaelendikveirnmkldgsgektftllvksqderidkgnrtytvpvngtdysl 600
QY 601 ALVLPYSFYIYKAKLEETIQARSKGKMDSETLKPONFESEGYTFIAPRDCYNDLKI 660
Db 601 alvlpysfyiykakeetiqarskgkmdsetlkdndfeesgytfiaprdcndlki 660
QY 661 SDNTEFLNFEFIDRKTPNPNPCNADLNIRVLLDAGFTNELVQNYWSKQKNKGVKAR 720
Db 661 sdntefllnfeidrktpnpncnadlnirvllldagftnelvqnywskqknkgvkar 720
QY 721 FVYTDGGRVYPKKAGENQWENPEYEDSFYKRSLDNDNYFTAPYFNKSGPGAYESGI 780
Db 721 fvtydggtrvypkkagenqwenpeyedsfykrslndndnyftapyfnksgpgayesgi 780
QY 781 MVSKEVEIYIQGLLPVAVGVIKIDVNSWIENTFTKSIRDPACAGPVCDCKRNSDVMDCVI 840
Db 781 mvskaveiyiqgllpavvgvikidvnswnientftksirpdcagpvcdckrnsdvmdcvi 840
QY 841 LDDGGLMANHDDYTNQIGRFFGEIDPSLMRHLVNIYSYAFNKSXYDQSVCEPGAAPKQ 900
Db 841 lddggflmanhddytngigrffgeidpslmrhlvnisyafnksxydyqsvcepgaapkq 900
QY 901 GAGHSAVPVSADIIQIGWATAAASIIQOFLSLTTPRILEAVEMEDDDFTASLSKQ 960
Db 901 gadhsaaypvsadiiqigwataaasliqoqlsltpprileavemedddftaslskq 960
QY 961 SCITEQTYFFDNDKSFSGVLDCGNCRSIFHGEKLMNTNLIIFIMVESKGTCTPCDTRL 1018
Db 961 scitedqtyffndksfsgvlcgcncrsifhgeklnmntnliifimveskgtcpcdtrl 1018

RESULT 5
AAR33553
ID AAR33553 standard; Protein; 1091 AA.
XX
AC AAR33553;
XX
DT 30-JUN-1993 (first entry)
XX
DE Sequence of the alpha 2 human calcium channel subunit.
XX
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```
KW Human calcium channel subunit; diagnosis; agonist; antagonist;
KW Lambert Eaton syndrome.
OS Homo sapiens.
PN WO9304083-A.
XX
PD 04-MAR-1993.
XX
PF 14-AUG-1992; 92WO-US06903.
XX
PR 15-AUG-1991; 91US-0745206.
PR 10-APR-1992; 92US-0868354.
XX
PA (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
XX
PI Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;
PI Williams ME;
XX
DR WPI; 1993-093936/11.
DR N-PSDB; AAQ37821.
XX
PT DNA encoding specific human calcium channel sub-units - used for
PT identifying calcium channel agonists and antagonists and
PT diagnosing Lambert Eaton syndrome
XX
PS Disclosure; Page 134-138; 150pp; English.
XX
CC DNA encoding a human neuronal calcium channel alpha 2 subunit was
CC isolated from a human genomic DNA library probed under low and high
CC stringency conditions with a fragment of DNA encoding the rabbit
CC skeletal muscle calcium channel alpha 2 subunit. The fragment
CC included nucleotides having a sequence corresponding to the
CC nucleotide sequence between nucleotides 43 and 272 inclusive of
CC rabbit back skeletal muscle calcium channel alpha 2 subunit cDNA.
CC PCR analysis identified splice variants of the human calcium alpha
CC 2 subunit transcript. In particularly preferred embodiments, the
CC DNA encoding the alpha 2 subunit is produced by alternative
CC processing of a primary transcript that includes DNA encoding the
CC amino acids set forth in AAR33553 and the DNA of AAQ37823 inserted
CC between nucleotides 1624 and 1625 of AAQ37821.
XX
SQ Sequence 1091 AA;
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Query Match 99.9%; Score 5340; DB 14; Length 1091;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1017; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 MAAGCCLALTLTFLQSLIGPSSSEEPFPPSAVTIKSWDKMQEDLVTLAKTAGVNLVDI 60
Db 1 magcclaltltlflqsligpsseepfpsavtikswdkmqedlvtlaktasvnglvd 60
QY 61 YEKYQDYTVEPNNAQLVEIAARDIEKLNSKALVSLALEAEKVQAAHQRDPASN 120
Db 61 yekyqdytvepnnarqlveiaardieklslsrskalsvslaleaekvqaahqwfesfn 120
QY 121 EVYYNAKDDLDPEKNDSPGSRQIKPVFTEDANFGQISQYHAAVHIPTDIYEGSTIVL 180
Db 121 evyyynakddldpekndsepgsrqikpvfiedanfgqisyqhaavhiptdiyegstivl 180
QY 181 NELNWTSAIDVEFKKNEEDPSLLQVFGSATGLARYYPASPVWVNSRTPNKKIDLVDVRR 240
Db 181 nelnwtalsaidvefkknreedpsllwqvfsgsatglaryypaspvwvnsrtpnkidldvrr 240
QY 241 RPWYIOGAASPKDMLILVDVSGVSGITLKIRTSVSEMLETISDDDFVNVASFNSNAQD 300
Db 241 rpywiggaaspkdmllilvdvsgsvsgitklirtsvsemletisdddfvnvasfnsnaqd 300
QY 301 VSCFQHLVQANVRNKKVLDAVNNTAKGITYDKGFSFAFEOQLLNNVSRANCKIIML 360
Db 301 vscfqlhqvsnvrnkvlkdvannitakgitydkgfsfafeqllnnvsvranchkiiml 360
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QY 361 FTDGGERAEQELFNKYNKDKVVRERFSGOHNRYGPIQWACENKGYVEIPISGAI 420
Db 361 ftdggeeraqeelfnkynkdkkvrirfsvghnyergpiqwmacenkggyveipisgai 420
QY 421 INTQEYLDVLGRPMVLADKAKQVQWNTVYLDALGLVITGTLPVFNITGOFENKTNLK 480
Db 421 intqeyldvlgrpmvladkakqvqwtvnyldaleglvitgtlvpfnitgofenktlnk 480
QY 481 NQILIGVMGVDSLEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHNPKNPKSQEPVTL 540
Db 481 nqililgvmgvdvsledikrltprftlcpngyyfaidpnyvllhnpknpsqepvtl 540
QY 541 DFLDAELENDIKVEIRNKMIDGSEKFTPLVKSQDERYIDKGNRTYTWPVNGTDSL 600
Db 541 dfldaeelndikveirnmidgesekftplvksqderidkgnrtytwtpvngtdysl 600
QY 601 ALVLPYSFYIKAKLEETITQARSKGKMDSETLKPDNFESGYTFIAPRDYCNLKI 660
Db 601 alvlpysfyyikaleetitqarskkgmdsetlkdndfesytfiaprdydcndlki 660
QY 661 SONTEFLNFEIDRKTTPNPNNSCNADLINRVLLDAGFTNELVQYWSKQKNIGVKAR 720
Db 661 sdnteflnfneidrkttpnnpnsnadlinrvlldagftnelvqywsqknigkvar 720
QY 721 FVYTDGGITRVYPKEAGENQENPETYEDSFYKRSILDNDNVYFTAPYFNKSGPGAYESGI 780
Db 721 fvytdggitrvypkeagenqenpetyedsfyrksildndnyvftapyfnkspgayesgi 780
QY 781 MYSKAVEIYIOGLKLPVAVGKIDVNSHNIENFTKTSIRDPGAGVPCDCRNSDYMDCVI 840
Db 781 myskaveiyioqllkpvavgikidvnsnienftktsirdpgagpvcdcckrnsdymdcvi 840
QY 841 LDGGEFLMANHDDTYNQIGRFGEIDPSLMRHLVNSIVYAKNSYDYQSVCEPGAAPKQ 900
Db 841 ldggfllmanhddtyngigrfgeidpslmrhlvnsivyaknsydyqsvcepgaapkq 900
QY 901 GAGHSAYVPSVADIIQIGWATAAASWTLQOFLLSLTPRLLAEVEMEDDDFTASLSKQ 960
Db 901 gaghsayvpsvaddiiqgwataaawsllqgflsltprrlleavemedddftaslskq 960
QY 961 SCITEQTQYFFDNDKSKFSVGLDCGNCSTRIFRGEKIMNTNLNLFIMVESKGTGCPCTR 1018
Db 961 sciteqtqyffndkskfsvglcncstrifhgekimntnlfnimveskgtgcpctr 1018
RESULT 6
ID AAW63148
AC AAW63148;
XX AAW63148;
XX AAW63148;
DT 12-OCT-1998 (first entry)
XX Human calcium channel alpha-2 subunit.
DE Alpha-2 subunit; human; calcium channel; assay; detection;
KW characterisation; Lambert Eaton Syndrome; LES; diagnosis.
XX Homo sapiens.
XX US5792846-A.
XX 11-AUG-1998.
XX 31-MAY-1995; 95US-0455543.
XX 04-APR-1994; 94US-0223305.
XX 04-APR-1988; 88US-0176899.
XX 04-APR-1989; 89US-0603751.
XX 04-APR-1989; 89WO-US01408.
XX 20-FEB-1990; 90US-0482384.
XX 30-NOV-1990; 90US-0620250.
XX 15-AUG-1991; 91US-0745206.

PR 31-MAY-1995; 95US-0455543.
XX (SIBI-) SIBIA NEUROSCIENCES INC.
XX Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;
XX Williams ME;
XX WPI; 1998-456192/39.
XX N-PSDB; AAV42694.
XX DNA encoding human calcium channel alpha 1B subunit protein -
XX useful for recombinant production of the channel for screening of
XX its modulators, and diagnosis of Lambert Eaton Syndrome
XX Disclosure; Columns 131-138; 166pp; English.
XX The present sequence represents the alpha-2 subunit of a human calcium
XX channel. Calcium channels are membrane-spanning, multi-subunit proteins
XX that allow controlled entry of calcium ions into cells. This leads
XX to depolarisation events required for muscle contraction. The recombinant
XX subunit, when expressed with nucleic acids encoding the complete calcium
XX channel, can be used in assays for the detection and characterisation of
XX compounds that modulate the channel. The DNA encoding the subunits can
XX be alternatively spliced when transcribed, giving more than one form of
XX the protein from the same transcript, each having slightly different
XX properties. In addition, the reactivity of the alpha 1 subunit with IgG
XX molecules from the serum of an individual with Lambert Eaton Syndrome
XX (LES) can be used as a diagnostic for the disease.
XX Sequence 1110 AA;

Query Match 99.6%; Score 5326.5; DB 19; Length 1110;
Best Local Similarity 98.2%; Pred. NO. 0;
Matches 1018; Conservative 0; Mismatches 0; Indels 19; Gaps 1;
QY 1 MAAGCLLALTTLTFLFOSLIGPSSPEPEPSAVTIKSWDKMQEDVLTAKTAGSVNQLVDI 60
Db 1 maagcllalttlfloslilgspseepfpavtikswdkmqedvltaktasgvnqlvdi 60
QY 61 YEKYODLYTFEPNNAQLVEIAARDIEKLLSNRSLVSLALEAEKVQAAHQWREDFASN 120
Db 61 yekyodlytvepnnaqlveiaardieklslsrslvslaleaeekvqaahqwredfasn 120
QY 121 EVVYNAKDDLDPEKNSEPGSQRIKPVFIEDANFGRISSYOHAAVHIPTDIYEGSTIVL 180
Db 121 evvynakddldpeknsepgsqrikpvfiedanfgriysyqhaavhiptdiyegstivl 180
QY 181 NELNWTLSALDEVFKKNREEDPSLLHQVFGSATGLARYYPASVPWDSNRTPNKIDLYDVR 240
Db 181 nelnwtlsaldevfkknreedpsllhwvfgsatglaryypasvpwdsnrtpnkidlydvr 240
QY 241 RPWYIQGAASPKDMLILVDVSGSVSGLTLKLRISVSEMLETSDDDFVNVSFNSNAQD 300
Db 241 rpwyiqgaaspkdmlilvdvsgsvsgltlklrtvsemlletlsdddvnvsnasnaqd 300
QY 301 VSCFOHLYQAVNRNKKVLKDAVNNITAKGIDYKKGFSFAFQOLLNYSVRANCKNIIML 360
Db 301 vscfqlhlyqanvrnkvlkdavnnitakgidykkgfsfafqollnynvsrancknilml 360
QY 361 FTDGGERAEQELFNKYNKDKVVRERFSGOHNRYGPIQWACENKGYVEIPISGAI 420
Db 361 ftdggeeraqeelfnkynkdkkvrirfsvghnyergpiqwmacenkggyveipisgai 420
QY 421 INTQEYLDVLGRPMVLADKAKQVQWNTVYLDALGLVITGTLPVFNITGOFENKTNLK 480
Db 421 intqeyldvlgrpmvladkakqvqwtvnyldaleglvitgtlvpfnitgofenktlnk 480
QY 481 NQILIGVMGVDSLEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHNPKNPKSQEPVTL 530
Db 481 nqililgvmgvdvsledikrltprftlcpngyyfaidpnyvllhnpknpsqepvtin 540
QY 531 -----NPKSQEPVTLDFLDAELENDIKVEIRNKMIDGSEKFTPLVKSQDERYI 581

Db 541 lrkrprnqpkseqpvtldfdaelndkveirnmkmdgesgektfrtlvksqgeryl 600
 QY 582 DKGNNRYTWPVNGTYSIALVPTYSFYIYKAKLEETITQARSKRGKMDSETLKPDNF 641
 Db 601 dkgntytwpvngtysialvptysfyyikakleetitqarskkgkmdsetlkdndf 660
 QY 642 EESGYTFIAPRDYCNLDKISDNTTELLNFNEFIDRKTNNPSCNADLINRVLLDAGFTN 701
 Db 661 eesgytfiaprdyecnldkisdntteflnfnefidrktppnpscnadlinrvldagftn 720
 QY 702 ELVQNTWSQKNIKGVKARFVVDGIGITRVYPKEAGENQOENPETYEDSFYKRSLDNDY 761
 Db 721 elvqnywskgnikgkavrvvdgigitrpykkaegenqenpetyedsfyrksldndy 780
 QY 762 VFTAPFNKSGGAYESGIMVSKAVIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDP 821
 Db 781 vftapyfnksggayesgimvskaveiyiqgkllkpvavvgikidvnswiensfctksirp 840
 QY 822 CAGPVCCKRNSDVMDCVILDDGGFLMANHDDYTNOIGRFFGEIDPFLMRHLVNSIYVA 881
 Db 841 cagpvcckrnsdvmcvcvildggfflmanhddytngqirffgeidpflmrhlvnsiya 900
 QY 882 FNKSYDYQVCBPAGAPKQAGHRSAYVPSVADILQIGHWATAAASIILOQFLLSLTFPR 941
 Db 901 fnksydyqvcbpagapkgaghrsayvpsvadilqigwataaasliiqffllsiftpr 960
 QY 942 LLEAVEMEDDDFTASLSKQSCITEQTYFFDNDKSFSGVLDGNGSRIFHGEKLMNTNL 1001
 Db 961 lleavemedddftaslsksciteqtyffndksfsgvldcngsrifhgeklmntnl 1020
 QY 1002 IFIMVESKTCPCDRL 1018
 Db 1021 ifimvesktpcdtrl 1037

RESULT 7

ID AAR71013 standard; Protein; 1086 AA.
 XX AC AAR71013;
 XX DT 01-DEC-1995 (first entry)
 XX DE Human neuronal calcium channel subunit alpha 2c.
 XX KW Calcium channel subunit; antagonist; agonist; diagnosis;
 XX KW Lambert Eaton Syndrome.
 XX OS Homo sapiens.
 XX PN W09504822-A.
 XX PD 16-FEB-1995.
 XX PF 11-AUG-1994; 94WO-US09230.
 XX PR 11-AUG-1993; 93US-0105536.
 XX PR 05-NOV-1993; 93US-0149097.
 XX PA (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
 XX PI Ellis SB, Gillespie A, Harpold MM, McCue AF, Williams ME;
 XX WPI; 1995-090900/12.
 XX DR N-PSDB; AAQ84667.
 XX PT DNA encoding human calcium channel sub-unit(s) - used for
 XX PT developing prods. for studying calcium channels, e.g. for
 XX PT obtaining agonists and antagonists
 XX PS Disclosure; Page 237-242; 285pp; English.

CC Human neuronal alpha 2 coding sequence (AAQ84664) transcript is
 CC differentially processed in skeletal muscle, aorta, and CNS in
 CC the region corresp. to nt 1595-1942 of AAQ84664 in each of the
 CC tissues. Five alternatively spliced variant transcripts that differ
 CC in the presence or absence of one to three different portions of
 CC this region. There are three sequences involved (see AAQ84664 FT
 CC and AAQ84665 FT), sequence 1, sequence 2 and sequence 3. The five
 CC alpha 2 encoding transcripts from the different tissues include
 CC different combinations of the three sequences, except for one of
 CC the alpha 2 transcripts expressed in aorta which lacks all three
 CC sequences. The five alpha 2 forms identified are (1) a form that
 CC lacks sequence 3 called alpha 2a, expressed in skeletal muscle
 CC (2) one that lacks sequence 1 called alpha 2b, expressed in CNS
 CC (3) one that lacks sequences 1 and 2 called alpha 2c, expressed in
 CC aorta (4) one that lacks sequences 1, 2 and 3 called alpha 2d,
 CC expressed in aorta and (5) one that lacks sequences 1 and 3
 CC called alpha 2e. The DNA and AA sequences of alpha 2a - alpha 2e
 CC are set forth in AAQ84666-Q84669 and AAR71012-R71015 respectively.
 XX XX Sequence 1086 AA;
 SQ

Query Match 99.3%; Score 5306.5; DB 16; Length 1086;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 1013; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 1 MAAGCILLALTTLFQSLIGSPSEEPFSAVTIKSWDRMQEDLVTLAKTASGVNOLVDI 60
 Db 1 maagcillalttlfqslligspseepfpaavtikswdkmqedlvtlaktasgvnldi 60
 QY 61 YEKYQDLTYVEPNNAQVLEIAARDIEKLLSNRSKALVSLALEAEKVAQAAHQWREFASN 120
 Db 61 yekyqdltyvepnnarqlveiaardieklslrskalvslaleaeakvgaahqwfrefasn 120
 QY 121 EVVYVNAKDDLPEKNDSEPPGSRQIKPVFIEDANFGROISYQHAHVHPTDIYEGSTIVL 180
 Db 121 evvyynakddlpeknndseppgqrkpvfiedanfgriqsyqnaavhptdlyegstivl 180
 QY 181 NEINMTSALDVEYFKKNREEDPSLLMQVFGSATGLARYYPASPVDNRSRTPNKIDLYDVR 240
 Db 181 neinmtsaldvefkknreedpsllmqvfgsatglaryypaspvwnsrtpnkidlydvr 240
 QY 241 RPWYIGGAASPKDMLILVDVSGVSGLTILKLRITSVSEMLETISDDDFVNVASFNSNAOD 300
 Db 241 rpwyiggaaspkdmililvdsvsgsltlklirtsvsemletlssdddfnvafsnnaod 300
 QY 301 VSCFOHLYQANVRNKKVLKDAVNNITAKGIDYKKGFSFAFQOLLNYSRANCNKIIML 360
 Db 301 vscfghlyqanvrnkvlkdavnnitakgitykkgfsfafegllnynsvrancnkilm 360
 QY 361 FTDGGEERAQEIFKNYKDKKVRFRFSYQOHNYERGPQWMACENKGYEYIPISGAIR 420
 Db 361 ftdggeeraqeifknykdkkvrfrfsyqghnyergpqiwmacenkgyyeipsigair 420
 QY 421 INTQEYLDVLRPMVLGADKAKQOVNTNYYLDALLEGVITGTLTPVFNITGFENKTNLK 480
 Db 421 intqeyldvlgrpmvlgadkakqvntnvyldalelgvltgltltpvfnitgfenktnlk 480
 QY 481 NOLIILGVMGDVSLIEDIKELTPFTLCPNGYVFAIDPNGYVLLHNPLOPKNPKSQEPVTL 540
 Db 481 noliilgvmgdvsliedikeltpftlcpngyvfaidpnyvllhnplopknpsqepvltl 540
 QY 541 DFLDALELNDIKVEIRNKMIDGESGEKTFRTLVKSDERYIDKGNRTYTWTVPNGTDYSL 600
 Db 536 dfldaelndikveirnkmidgesgektfrtlvksqgeryidkgnrtytwtvpngtdysl 595
 QY 601 ALVLPYTFYFYIKAKLEETITQARSKGKMDSETLKPDNFESGYTFIAPRDYCNLDKI 660
 Db 596 alvlpysfyyikakleetitqarskkgkmdsetlkdndfeesgytfiaprdyecnldki 655
 QY 661 SDNNTTEFLNNEFIDRKTNNPSCNADLINRVLLDAGFTNELVQNYWSKQNKIKGVAR 720
 Db 656 sdnntteflnnnefidrktppnpscnadlinrvllldagftnelvqnywskqnkikgvkar 715

QY 721 FVTDGGITRVYKAEAGNENPETYEDSFYKRSLDNDNVETAPYFNKSGPAYESGI 780
Db 716 fvtvdggitrviykeagenwgenpetyedsfyrslndndnyvtapyfnksppayesgi 775
QY 781 MVSKEVEIYIOGKLLKPAVYGIKIDVNSWIENTFTKTSIRDPACAGPVCDCRNSDVMDCVI 840
Db 776 mvskaveiyyigkllkpvavvgikidvnswnientftktsiropcagpvcdcnrnsdvmdcvi 835
QY 841 LDGGFLLMANHDDYTNTQIGRFFGEIDPSLMRHLVNSVYAFNKSVDYQSVCEPGAAPKQ 900
Db 836 ldggfllmanhddytntqigrffgeidpslmrhlvnlsvyafnksydyqsvcepgaapkq 895
QY 901 GAGHRSAYVESVADILQIGHWATAAASIIQQFLSLSTFFPRLLLEAVEMEDDDFTASLSKQ 960
Db 896 gaghrsayvesvadilqigwataaasiiqqflslstffprlleavemedddftaslskq 955
QY 961 SCITEQYQYFFDNDKSFSGVLDCGNCGRIFHGEKLMNTNLIFIMVESKGTCPDTRL 1018
Db 956 sciteqyqyffndksfsgvldcgcncsrifhgeklmntnlifimveskgtcpdtrl 1013

RESULT 8

AAW63153 ID AAW63153 standard; Protein; 1086 AA.

AC AAW63153;

DT 12-OCT-1998 (first entry)

DE Human calcium channel alpha-2c subunit.

XX Alpha-2 subunit; human; calcium channel; assay; detection;
KW characterisation; Lambert Eaton Syndrome; LES; diagnosis.

XX Homo sapiens.

XX US5792846-A.

XX 11-AUG-1998.

XX 31-MAY-1995; 95US-0455543.

XX 04-APR-1994; 94US-0223305.

XX 04-APR-1988; 88US-0176899.

XX 04-APR-1989; 89US-0603751.

XX 20-FEB-1990; 89WO-US01408.

XX 30-NOV-1990; 90US-0482384.

XX 15-AUG-1991; 90US-0620250.

XX 31-MAY-1995; 91US-0745206.

XX (SIBI-) SIBIA NEUROSCIENCES INC.

XX Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;

XX Williams ME;

XX WPI; 1998-456192/39.

XX N-PSDB; AAV42702.

XX DNA encoding human calcium channel alpha 1B sub:unit protein -
XX useful for recombinant production of the channel for screening of
XX its modulators, and diagnosis of Lambert Eaton Syndrome

XX Claim 3; Columns 293-300; 166pp; English.

XX The present sequence represents the alpha-2c subunit of a human calcium
XX channel. Calcium channels are membrane-spanning, multi-subunit proteins
XX that allow controlled entry of calcium ions into cells. This leads
XX to depolarisation events required for muscle contraction. The recombinant
XX subunit, when expressed with nucleic acids encoding the complete calcium
XX channel, can be used in assays for the detection and characterisation of
XX compounds that modulate the channel. The DNA encoding the subunits can

CC be alternatively spliced when transcribed, giving more than one form of
CC the protein from the same transcript, each having slightly different
CC properties. In addition, the reactivity of the alpha 1 subunit with IgG
CC molecules from the serum of an individual with Lambert Eaton Syndrome
CC (LES) can be used as a diagnostic for the disease.

XX Sequence 1086 AA;

Query Match 99.3%; Score 5306.5; DB 19; Length 1086;
Best Local Similarity 99.5%; Pred. NO. 0;
Matches 1013; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 1 MAGCCLALTLTTLFOSLLIGPSSSEPEPSAVTTIKSWDKMQEDLVTLAKTAGSGVNLQVDI 60

Db 1 magcclalaltlittlfigsligpsseepfsvavtkswdkmqedlvtlaktagsgvnlqldi 60

QY 61 YEKYQDLTYVEPNNAQOLVEIAAARDIEKLSNRSKALVSLALEAEKVQAAHQWREDFASN 120

Db 61 yekyqdltyvepnnaqlveiaardieklisnrskalvslaleaeqvgaahqwrdfasn 120

QY 121 EYVYNAKDDLPEKNDSEPGSQRIKPVFIEDANFGRQISYQHAHVHPTDIYEGSTIVL 180

Db 121 evvyynakddldpekndsepgsqrikpvfiedanfgrqisyghaavhiptdiyegstivl 180

QY 181 NELNWTLSALDEVFKKNEEDPSSLWQVFGSATGLARYYPASPVWVNSRTPNKIDLYDVR 240

Db 181 nelnwtlsaldevfkknreedpsllwqvfgsatglaryypaspvwvnsrtpnkiidlydvr 240

QY 241 RPWYIOGAASPDKMLILVDVSGVSGLTLLKIRTSVSEMLETISDDDFNVVASFNSNAQD 300

Db 241 rpywiggaaspdkmllilvdvsgvsgltllkirtsvsemlletisdddfnvvasfnasnaqd 300

QY 301 VSCFQHLVQANVRNKKVLDVANNITAKGTDYKKGFSFAFQQLLNINVRANCKIIML 360

Db 301 vscfghlvqanvrnkvlkdavnnitakgtdykgfsfafeqllnynvrancknkiiml 360

QY 361 FTDGGERAQOEIENKYNKDKKVRFRFESVGOHNYERGIOWMACENKGYEIEISGAIR 420

Db 361 ftdggeeraoeienkynkdkkvrfrfsvqghnyerpiowmacenkgyyieipsigair 420

QY 421 INTQEYLDVLGRPMVLADGAKAQVQMTNVYLDALGLVITGTLPVFNITGQFENKYNLK 480

Db 421 intqeyldvlgrpmvlagdakqvqmntvyldalelgvitgtlpvfnitgqfenkntlk 480

QY 481 NQLILGVNGVDVSLIEDIKRLTPRTTLPNGYIFAIDPNGYVLLHPNLOPNKPSQEPVTL 540

Db 481 nqililgvngvdslesdikrltprftlcpngyifaidpngyvlhpnliqpk-----epvtl 535

QY 541 DFLLDAELENDIKVEIRNKMIDGESGKTFRTLVKSODERYIDKGNRYTWTVPVNGTDYSL 600

Db 536 dfldaeeleendikveirnmidgesgkftlrvksqgeryidkgnrytwtvpvngtdysl 595

QY 601 ALVLPYSFYIYKAKLETITQARSKGKMDSETLKPDPNFESGYTFIAPRDYCNLDKI 660

Db 596 alvlpysfyiyakleetitqarskkgkmdsetkphdnfeesgytfiaprdocndki 655

QY 661 SDNNTPELLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQNTWSKOKNKGVKAR 720

Db 656 sdntefllnfnefidrktppnpscnadlinrvlldagftnelvqnywsknkgvkar 715

QY 721 FVTDGGITRVYKAEAGNENPETYEDSFYKRSLDNDNVETAPYFNKSGPAYESGI 780

Db 716 fvtvdggitrviykeagenwgenpetyedsfyrslndndnyvtapyfnksppayesgi 775

QY 781 MVSKEVEIYIOGKLLKPAVYGIKIDVNSWIENTFTKTSIRDPACAGPVCDCRNSDVMDCVI 840

Db 776 mvskaveiyyigkllkpvavvgikidvnswnientftktsiropcagpvcdcnrnsdvmdcvi 835

QY 841 LDGGFLLMANHDDYTNTQIGRFFGEIDPSLMRHLVNSVYAFNKSVDYQSVCEPGAAPKQ 900

Db 836 ldggfllmanhddytntqigrffgeidpslmrhlvnlsvyafnksydyqsvcepgaapkq 895

QY 901 GAGHRSAYVPSVADILQIGWATAAASIILOQFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960
 Db |||||||
 QY 896 gaghrsayvpsvadilqigwataaawsilqqfllsltfprlleavemedddftaslskq 955
 Db |||||||
 QY 961 SCITEQTYFFDNDKSFSGVLDGNCGRIFPHGSKLMTNLIFITWESKGCPCDTRL 1018
 Db |||||||
 QY 956 sciteqtyffndksfsgvldcgnscrifhgeklmtnlfinveskgtcpcdtrl 1013

RESULT 9

AAAB10587
 ID AAB10587 standard; Protein; 1086 AA.

XX
 AC AAB10587;

XX 22-DEC-2000 (first entry)

XX Human calcium channel alpha-2c subunit protein.

KW Human; calcium channel; calcium channel subunit; diagnosis;
 KW Lambert Eaton Syndrome; calcium channel subunit alpha-2c.

XX Homo sapiens.

XX US6096514-A.

XX 01-AUG-2000.

XX 25-MAY-1995; 95US-0450562.

XX 04-APR-1988; 88US-0176899.

PR 02-FEB-1990; 90US-0482384.

PR 08-NOV-1990; 90US-0603751.

PR 30-NOV-1990; 90US-0620250.

PR 15-AUG-1991; 91US-0745206.

PR 10-APR-1992; 92US-0868354.

PR 13-JUL-1992; 92US-0914231.

PR 11-AUG-1993; 93US-0105536.

PR 07-FEB-1994; 94US-0193078.

PR 04-APR-1994; 94US-0223305.

PR 11-AUG-1994; 94US-0290012.

PR 23-SEP-1994; 94US-0311363.

PR 28-SEP-1994; 94US-0314083.

PR 07-NOV-1994; 94US-0336257.

PR 13-MAR-1995; 95US-0404950.

XX (SIBI-) SIBIA NEUROSCIENCES INC.

XX Ellis SB, Williams ME, McCue AF, Harpold MW;

XX WPI; 2000-548230/50.

XX N-PSDB; AAA71725.

XX Human calcium channel beta subunit polynucleotides, useful for
 PT producing recombinant eukaryotic cells and for diagnosing Lambert Eaton
 PT Syndrome -
 XX
 PS Disclosure; Column 237-244; 153pp; English.

XX This invention describes a novel isolated DNA molecule (I) comprising a
 CC sequence encoding a beta2-1 subunit of a human calcium channel.
 CC Nucleic acid probes comprising 14-30 contiguous nucleotides of
 CC beta.3 subunit encoding DNA are useful for isolation and cloning of
 CC calcium channel subunit-encoding DNA. Recombinant eukaryotic cells that
 CC express heterologous calcium channel are useful for identifying compounds
 CC that modulate calcium channel activity and in assays for identifying
 CC agonists and antagonists of calcium channel activity in humans. Human
 CC calcium channel subunit or eukaryotic cells expressing the channel are
 CC useful for diagnosing Lambert Eaton Syndrome (LES) in a human. This
 CC sequence represents the human calcium channel alpha-2c subunit which is
 CC described in the method of the invention.

SQ Sequence 1086 AA;
 Query Match 99.3%; Score 5306.5; DB 21; Length 1086;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 1013; Conservative 0; Mismatches 0; Indels 5; Gaps 1;
 QY 1 MAAGCLLALTLTFLQSLIGSSSEPPPSAVTIKSWDKMQEDLVTLAKTAGSNQLVDI 60
 Db |||||||
 QY 1 maagcllaltltlfgslilgssseepfpsavtikswdkmqedlvltaktasgqnvlvd1 60
 Db |||||||
 QY 61 YEKYQDLTYVEPNNAARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAHQWEDFASN 120
 Db |||||||
 QY 61 yekyqdltyvepnnaarqlveiaardiellksnrskalvslaleaekvqaahqwedfasn 120
 Db |||||||
 QY 121 EVVYINAKDDLDPEKNDSEPGSQRIKPVFIEDANFGQISYQHAHVHPTDIYEGSTVL 180
 Db |||||||
 QY 121 evvynakddldpekndsepgsqrikpvfiedanfgqisqyqhaavhlpdiyegstvl 180
 Db |||||||
 QY 181 NELNWTSAIDDEVFKKREEDPSLLWQVFGSATGLARYYPASWPVDNSRTPNKIDLYDVR 240
 Db |||||||
 QY 181 nelnwtalsaldevfkknreedpsllwqvfgsatglaryypaswpvdnsrtpnkidlvdvr 240
 Db |||||||
 QY 241 RPWYIQGAASPDKMLILVDYSGVSGTLKLIKRTSVSEMLETSDDDDFVNVASNSNAQD 300
 Db |||||||
 QY 241 rpwyiqgaaspdkmlilvdsvsgvsgtlklirtsvsemlletisdddfvnavasnsnaqd 300
 Db |||||||
 QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGSFAFEQLLNYSRANCKIIML 360
 Db |||||||
 QY 301 vscfqhlvqanvrnkklvdavnnitakgitydkkgsfafefeqllnynsrancnkiml 360
 Db |||||||
 QY 361 FTDGGEERAQEIFNKYKDKKVRVFRFSVQHNYERGPIONMACENKGYEYFISGAIR 420
 Db |||||||
 QY 361 ftdggeeraqeifnkykdkkvrfrfsvqghnyerpiqwmacenkgyyeyfispigair 420
 Db |||||||
 QY 421 INTOEYLDVLGRPMVLAGDKAKOVQWTVNLDLELGLVITGTLPVNTIGOFENKLNK 480
 Db |||||||
 QY 421 intoeyldvlgrpmvlagdkakqvqwcvtvnyldalelglvitgtlpvntigqfenknlk 480
 Db |||||||
 QY 481 NQLTLGVMGVDVSLIEDIKRLTPRETLCPNGYFAIDPNGYVLLHPNLPKNPKSQEPVTL 540
 Db |||||||
 QY 481 nqltlgvmgvdsleedikrltpretpcngyfaidpnyvllhpnlpknpksepevtl 540
 Db |||||||
 QY 541 DFLDAELENDIKVEIRNKMIDGSEKFTFLVKSQDERYIDKGNRTYTTPVNGTDYSL 600
 Db |||||||
 QY 536 dfldaeldendikveirnkmidgesektflvksqderiydkgnrtytvtpvngtdysl 595
 Db |||||||
 QY 601 ALVLPYTSFYIIRAKLEETITQARSKKGMKDSSETLKPDPNFEEGSGYTFIAPRDYCNLKI 660
 Db |||||||
 QY 596 alvlpysfyiirakleetitqarskkgmkdsetlkdnpnfesgytflaprdycndlki 655
 Db |||||||
 QY 661 SDNNTPELLNFEFIDRKTNNPNSCNADLNVRLLDAGFTNELVQYWSKQNKIKGVKAR 720
 Db |||||||
 QY 656 sdntefllnfnfeidrktnnpnsnadlnrvlldagfnelvqywsqknikgvkar 715
 Db |||||||
 QY 721 FVYTDGGRITRVYKREAGENQENPETYEDSFYKSLDNDNYFTAPYFNKSGPGAYESGI 780
 Db |||||||
 QY 716 fvytdgggritrvykragenqenpetyedsfykslndndnyvftapyfnksgpgayesgi 775
 Db |||||||
 QY 781 MVSKAVEIYIQGLKLPVAVGKIDVNSWIENFTKTSIRDPACAGPVCDCRNSDVMDCVI 840
 Db |||||||
 QY 776 mvskaveiyiqgkllkpavvgikidvnswieftktsirpcagpvcdcrnsdvmdcvi 835
 Db |||||||
 QY 841 LDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI SVYAFNKS DYQSVQCEPGAAPKQ 900
 Db |||||||
 QY 836 ldggfllmanhddytngqirffgeidpslmrhlvnsvyafnksdyqsvcepgaapqk 895
 Db |||||||
 QY 901 GAGHRSAYVPSVADILQIGWATAAASIILOQFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960
 Db |||||||
 QY 896 gaghrsayvpsvadilqigwataaawsilqqfllsltfprlleavemedddftaslskq 955
 Db |||||||
 QY 961 SCITEQTYFFDNDKSFSGVLDGNCGRIFHGEKLMNTNLIFITWESKGCPCDTRL 1018
 Db |||||||

Db 956 sciteqtqyffndsksfsgvldcgnscsrfhgeklmtnlifimveskgtcpcdtrl 1013

RESULT 10
AAR71015
ID AAR71015 standard; Protein; 1084 AA.

AC AAR71015;
XX
DT 01-DEC-1995 (first entry)
XX
DE Human neuronal calcium channel subunit alpha 2e.
XX
KW Calcium channel subunit; antagonist; agonist; diagnosis;
RW Lambert Eaton Syndrome.
XX
OS Homo sapiens.
XX
FN W09504822-A.
XX
PD 16-FEB-1995.
XX
XX 11-AUG-1994; 94WO-US09230.
XX
PF 11-AUG-1993; 93US-0105536.
PR 05-NOV-1993; 93US-0149097.
XX
XX (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.

XX Ellis SB, Gillespie A, Harpold MM, Mccue AF, Williams ME;
XX
XX WPI; 1995-090900/12.
DR N-PSDB; AAQ84669.
XX
XX DNA encoding human calcium channel sub-unit(s) - used for
PT developing prods. for studying calcium channels, e.g. for
PT obtaining agonists and antagonists
XX
XX Disclosure; Page 248-253; 285pp; English.
XX
XX Human neuronal alpha 2 coding sequence (AAQ84664) transcript is
CC differentially processed in skeletal muscle, aorta, and CNS in
CC the region corresp. to nt 1595-1942 of AAQ84664 in each of the
CC tissues. Five alternatively spliced variant transcripts that differ
CC in the presence or absence of one to three different portions of
CC this region. There are three sequences involved (see AAQ84664 FT
CC and AAQ84665 FT), sequence 1, sequence 2 and sequence 3. The five
CC alpha 2 encoding transcripts from the different tissues include
CC different combinations of the three sequences, except for one of
CC the alpha 2 transcripts expressed in aorta which lacks all three
CC sequences. The five alpha 2 forms identified are (1) a form that
CC lacks sequence 3 called alpha 2a, expressed in skeletal muscle
CC (2) one that lacks sequence 1 called alpha 2b, expressed in CNS
CC (3) one that lacks sequences 1 and 2 called alpha 2c, expressed in
CC aorta (4) one that lacks sequences 1, 2 and 3 called alpha 2d,
CC expressed in aorta and (5) one that lacks sequences 1 and 3
CC called alpha 2e. The DNA and AA sequences of alpha 2a - alpha 2e
CC are set forth in AAQ84666-084669 and AAR71012-R71015 respectively.
XX
XX Sequence 1084 AA;

Query Match 98.9%; Score 5289.5; DB 16; Length 1084;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1010; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY 1 MAAGCLLALTTLFOSLLIGSPSSPEPPSAVTIKSVDKMQEDLVTLAKTAGVGNQLYDI 60
DB 1 maagcllaltlcfllgspsspeppsaavtiksvdkmqedlvltlaktasgvnqlvdi 60
QY 61 YEKYODLYTVEPNARQLVEAARDIEKLLSNRSKALVSLALEAEKVQAAHOWREDFASN 120
DB 61 yekyodlytvepnarqlveaardieklslsnrskalvslaleaekvqaahwredfasn 120

QY 121 EVVYNAKDDLDPEKNDSEPSQSRIKPVFIETDANFGRQISYQHAHVHIPTDIYEGSTIVL 180
DB 121 evvynakddldpekdndsepsqsrirkpvfiedanfgriqsyhaavhiptdiyegstivl 180
QY 181 NELNWTSALEDEVFKKNEEDPSLLMQVFGSATGLARYYPASPWWNSRTPNKIDLYDVR 240
DB 181 nelnwtosaldevfkknreedpsllmqvfgsatglaryypaspwwnsrtpnkidlydvr 240
QY 241 RPWYIOGAASPKDMLILVDVSGSVSGLTTLKIRTSVSEMLETSLDDDFVNVASNSNAQD 300
DB 241 rpwyiggaaspkdmlilvdvsgsvsglttlkirtsvsemletsldddfvnvasnnaqd 300
QY 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGTDYKKGSEFAEQLLNYSRANCKIIML 360
DB 301 vscfhlvqanvrnkkvldkavnnitakgtdykgkgsfafaqllnysranckiml 360
QY 361 FTGGEERAQEIFNKYNKDKKRVFRFSVGOHNYERGIOMACENKGYIYEIPISGAIR 420
DB 361 ftggeeraqeifnkynkdkkrrvfrfsvgghnyergiqwmacenkgyyiyeipsigair 420
QY 421 INTQEYLDVLGRPMVLADGKAKQVQWNTNVLDALEGLVITGTLPVFNITQCFENKTNLK 480
DB 421 intqeyldvlgrpmvlagdkakqvgwntnvldalelgltvitgtlvpfnitqcfenknlk 480
QY 481 NQLILGVMGVDSLEDIKRLTPRETLCPNGYFPAIDPNGYVLLHPNLQPKNPKSQEPVTL 540
DB 481 nqlilgvmgvdsledikrltpretlcpngyypaidpngyvvllhpnlpknkpsqepvtl 540
QY 541 DFLDAELENDIKVEIRNMIDGESGKTFRTLVKSQDERYIDKGNRTYTTPVNGTDYSL 600
DB 541 dfldaelendikveirnmidgesgktrftlvksqderydkgntytwtvtpvngtdysl 600
QY 601 ALVLPYTSFYIYKAKLEETITQARSKKGMKDSITLKPDPNFEESGYTFIAPRDYCNDLKI 660
DB 601 alvlpysfyiykakleetitqary-----setlkpdpnfeesgytftiaprdocndlki 653
QY 661 SDNTEFLNFEEDIRKTPNPNPCNADLINRVLLDAGFTNELVQNYWSKQKNIKGVKAR 720
DB 654 sdnteflnfnefidrktppnpscnadlinrvlldagftnelvqnywskknkgvkar 713
QY 721 FVVTDDGTRVYRKEAGENWQENPETYEDSFYKRSLDNDNYFTTAPYFNKSGPGAYESGI 780
DB 714 fvtddgtrvypkeagenwqenpetyedsfyrslndndnyfttapyfnksgpgayesgi 773
QY 781 MVSXAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPGAGVCDCKNSDVMDCVI 840
DB 774 mvskavelyioqgkllkpavvgikdvnswieftktsirdpcagvcdcknsdvmdcvi 833
QY 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNIISVYAFNKSVDYQSVCEPAAAPKQ 900
DB 834 lddggflmanhddytnoigrffgeidpslmrhlvniisvafnksydyqsvcepgaaapk 893
QY 901 GAGHSRAYSVPVADILQIGMWATAAAMSILQOFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960
DB 894 gahrsraysvpvadilqigwataaawsilqgflsltfprlleavemedddftaslskq 953
QY 961 SCITEQTYQTFDNDKSFSGVLDGNCNCSRFHGEKLMNTNLIIFIMVESKGTCPDTRL 1018
DB 954 sciteqtqyffndsksfsgvldcgnscsrfhgeklmtnlifimveskgtcpcdtrl 1011

RESULT 11
AAW63155
ID AAW63155 standard; Protein; 1084 AA.
XX
AC AAW63155;
XX
DT 12-OCT-1998 (first entry)
XX
DE Human calcium channel alpha-2e subunit.
XX
KW Alpha-2 subunit; human; calcium channel; assay; detection;

characterisation; Lambert Eaton Syndrome; LES; diagnosis.

KW XX OS XX PN XX PD XX PF XX PR XX PR XX PR XX PR XX PR XX PR XX
 Homo sapiens.
 US5792846-A.
 11-AUG-1998.
 31-MAY-1995; 95US-0455543.
 04-APR-1994; 94US-0223305.
 04-APR-1988; 88US-0176899.
 04-APR-1989; 89US-0603751.
 04-APR-1989; 89WO-0501408.
 20-FEB-1990; 90US-0482384.
 30-NOV-1990; 90US-0620250.
 15-AUG-1991; 91US-0745206.
 31-MAY-1995; 95US-0455543.
 (SIBI-) SIBIA NEUROSCIENCES INC.
 Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;
 Williams ME;
 WPI: 1998-456192/39.
 N-PSDB; AAV42704.
 DNA encoding human calcium channel alpha 1B subunit protein -
 useful for recombinant production of the channel for screening of
 its modulators, and diagnosis of Lambert Eaton Syndrome
 Claim 3; Columns 305-310; 166pp; English.
 The present sequence represents the alpha-2e subunit of a human calcium
 channel. Calcium channels are membrane-spanning, multi-subunit proteins
 that allow controlled entry of calcium ions into cells. This leads
 to depolarisation events required for muscle contraction. The recombinant
 subunit, when expressed with nucleic acids encoding the complete calcium
 channel, can be used in assays for the detection and characterisation of
 compounds that modulate the channel. The DNA encoding the subunits can
 be alternatively spliced when transcribed, giving more than one form of
 the protein from the same transcript, each having slightly different
 properties. In addition, the reactivity of the alpha 1 subunit with IgG
 molecules from the serum of an individual with Lambert Eaton Syndrome
 (LES) can be used as a diagnostic for the disease.
 Sequence 1084 AA;
 Query Match 98.9%; Score 5289.5; DB 19; Length 1084;
 Best Local Similarity 99.2%; Pred. No. 0;
 Matches 1010; Conservative 0; Mismatches 1; Indels 7; Gaps 1;
 QY 1 MAAGCILLALTILFQSLIGPSEPPFSAVTKSWDKMQEDLVTLAKTAGVNLVDI 60
 DB 1 maagcillaaltlfigsligpseepfsvavtkswdkmqedlvtlaktasgvnqlvdi 60
 QY 61 YEKYQDLYTVEPNNAQOLVEIAARDIEKLLSNRKSALVSLALEAEKVQAAHQRDFASN 120
 DB 61 yekyqdylytvepnnarqlvelaardieklslsrksalvslaleaeakvqaahqrdfasn 120
 QY 121 EVVYNAKDDLPKNDSEPGSQRIKPVFIEDANFGRIQSYQHAAPHITDIYEGSTIVL 180
 DB 121 evvyynakddldpekndsepgsqrikpvfiedanfgriqsyqhaaphitdiyegstivl 180
 QY 181 NELNWTLSALDEVFKKNREDDPSLLNQVGSATGLARYTPASPWVNSRTPNPKIDLYDVR 240
 DB 181 nelnwtlsaldevfkknreedpsllnqvgsatglarytpaspwvnsrtpnknidlydvr 240
 QY 241 RPWYIQGAASPKMDLILVDVSGVSGSLTKLIRTSVSEMLETSLSDDDFVNVASFNSNAQD 300
 DB 241 rpwyiqgaaspkmdlilvdvsgsvsgsltklirtsvsemletlsdddfvnvasfnnaqd 300

QY 301 VSCFQHLVQANVRNKKVYLKDAVNNTAGITDYKKGFSAFQELLNYSRANCKIIML 360
 DB 301 vscfqlhvqanvrnkkvylkdavnnitakgltidykkgfsafeqllnysrancnkiiiml 360
 QY 361 FTDGGERRAQEIENKYNKDKKRVFRFSGQHNTERPIQWACENKGYIETPSIGAIR 420
 DB 361 ftdggeeraqeieinfnkynkdkkvrfrfsvgqghnyerpgiqwacenkgyyieipsigair 420
 QY 421 INTQEYLDVLGRPMVLADKAKOVQWNTNVYLDALGLVITGTLPVFNITGQFENKTNLK 480
 DB 421 intqeyldvlgrpmvlagdakakqvcwcnvyldalelgvltgtlplvfnitgqfenkcnlk 480
 QY 481 NQLILGYMGVDVSLIEDIKRLTPRFTLCPCNGYIFAIDPNGYVLLHPNLQPNKPSQEPVTL 540
 DB 481 nqlilgvmgvdvsledikrltpftlcpngyyfaidpngyvlhpnlpknpsqepvtl 540
 QY 541 DFLDAELENDIKVEIRNKMIDGESGEKTFRTLKSDQERIDKGNRTYTWTPVNGTDYSL 600
 DB 541 dfldaelendikveirnkmidgesgektftrlvksqderidkgnrtytwtpvngtdysl 600
 QY 601 ALVLPYTFYIIRAKLEETITQARSKKGMKMDSETLKPDMFEESGYTFIAPROYCNDLKI 660
 DB 601 alvlpysfyiirakleetitqary-----setlkpdmfeesgytfiaproycndiki 660
 QY 661 SDNTEFLNFEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQNTWSKQNKIKGYKAR 720
 DB 661 sdntefllnfeefidrktpnnpncnadlinrvlldagftnelvqnywskqknikgykar 720
 QY 721 FVYTDGGIRVYKPEAGENQENPEYEDSFYKRSLDNDNYFTAPYFNKSGGAYESGI 780
 DB 721 fvytdggirvykpeagenqenpeyedsfykrslndndnyftapyfnksggayesgi 780
 QY 781 MYSKAVEIYIQGLKLPVAVVGIKIDVNSWIENTFTKSIRDPACAGPCDCRNSDVMDCVI 840
 DB 781 myskaveiyiqglklpavvgiikidvnswnientftksirpdcagpdcdrnsdvmdcvi 840
 QY 841 LDGGLLMAHDDYTNQIGRFFGEIDPSLMRHLVNIISVYAFNKSXDYQVCEPFGAAPKQ 900
 DB 841 ldggllmahddytnqigrffgeidpslmrhlvnisvyafnksxdyqvccepfgaapkq 900
 QY 901 GAGHSAVYPSVADIIQGWATAAAWSILQQLLSLTTPRLLAEVEMEDDDFTASLSKQ 960
 DB 901 gaghsavypsavadiiqgwataaawsilqqllslsttprlleavemedddftaslskq 960
 QY 961 SCITEQTYFFDNDKSFSGVLDGNCSTRIFHGKELMNTNLIIFIMVESKGTCPCDTRL 1018
 DB 961 sciteqtyffndksfsfsgvldcncstrifhgekmlntnliifimveskgtcpcdtrl 1018
 QY 954 sciteqtyffndksfsfsgvldcncstrifhgekmlntnliifimveskgtcpcdtrl 1011

RESULT 12

AAB10589

ID AAB10589 standard; Protein; 1084 AA.

XX

AC AAB10589;

XX

DT 22-DEC-2000 (first entry)

XX

DE Human calcium channel alpha-2e subunit protein.

XX

KW Human; calcium channel; calcium channel subunit; diagnosis;
 Lambert Eaton Syndrome; calcium channel subunit alpha-2e.

XX

OS Homo sapiens.

XX

PN US6096514-A.

XX

PD 01-AUG-2000.

XX

PF 25-MAY-1995; 95US-0450562.

XX

PR 04-APR-1988; 88US-0176899.

XX

PR 02-FEB-1990; 90US-0482384.

XX

PR 08-NOV-1990; 90US-0603751.

PR 30-NOV-1990; 90US-0620250.
PR 15-AUG-1991; 91US-0745206.
PR 10-APR-1992; 92US-0868354.
PR 13-JUL-1992; 92US-0914231.
PR 11-AUG-1993; 93US-0105536.
PR 05-NOV-1993; 93US-0149097.
PR 07-FEB-1994; 94US-0193078.
PR 04-APR-1994; 94US-0223305.
PR 11-AUG-1994; 94US-0290012.
PR 23-SEP-1994; 94US-0311363.
PR 28-SEP-1994; 94US-0314083.
PR 07-NOV-1994; 94US-0336257.
PR 13-MAR-1995; 95US-0404950.
XX (SIBI-) SIBIA NEUROSCIENCES INC.
PA Ellis SB, Williams ME, McCue AF, Harpold MM;
XX
XX
XX
DR WPI; 2000-548230/50.
DR N-PSDB; AAR71727.
XX
PT Human calcium channel beta subunit polynucleotides, useful for
PT producing recombinant eukaryotic cells and for diagnosing Lambert Eaton
PT Syndrome.
XX
XX
PS Disclosure; Column 253-260; 153pp; English.
XX
XX This invention describes a novel isolated DNA molecule (I) comprising a
CC sequence encoding a beta3-1 subunit of a human calcium channel.
CC Nucleic acid probes comprising 14-30 contiguous nucleotides of
CC beta-3 subunit encoding DNA are useful for isolation and cloning of
CC calcium channel subunit-encoding DNA. Recombinant eukaryotic cells that
CC express heterologous calcium channel are useful for identifying compounds
CC that modulate calcium channel activity and in assays for identifying
CC agonists and antagonists of calcium channel activity in humans. Human
CC calcium channel subunit or eukaryotic cells expressing the channel are
CC useful for diagnosing Lambert Eaton Syndrome (LES) in a human. This
CC sequence represents the human calcium channel alpha-2e subunit which is
CC described in the method of the invention.
XX
XX Sequence 1084 AA;
XX
Query Match 98.9%; Score 5289.5; DB 21; Length 1084;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1010; Conservative 0; Mismatches 1; Indels 7; Gaps 1;
Qy 1 MAAGCLLALTTLFQSLIGPSSSEPPSPSAVTIKSWDKMOEDLVTLAKTAGVGNQLYDI 60
Db 1 maagcllaltltlfgsligpsseppfsavtikawdkmqedltlaktasgvnqlvdi 60
Qy 61 YEKYQDLTYVEPNNAARQVEIAARDIEKLLNSRKALVSLALEAEKVQAAHQWRDFASN 120
Db 61 yekyqdltyvepnnaarqveiaardieklslsrkalvslaleaeqvaaahqwrdfasn 120
Qy 121 EVVYNNAKDDLPEKNDSEPSQRIKPFIEDANGROISVQHAHVHPTDIYEGSTIVL 180
Db 121 evvyynnakddlpeknsepsqrikpfiedanfgroisvqhaahvhtptdiyegstivi 180
Qy 181 NELNWTSDLDVEFFKNRREDPSLLWQVFGSATGLARYYPASVPWDSNRTPNKKIDLYDVR 240
Db 181 nelnwtaldveffknreepdpsllwqvfgsatglaryypasvpwdsnrtpnkkidlydvr 240
Qy 241 RPWYIQGAASPKDMLILVDVSGVSGGLTKLIRTSVSEMLEFTLSDDDFNVASFNSNAQD 300
Db 241 rpwyiqgaaspkdmlilvdvsgvsgltklirtsvsemlftlsdddfnvasfnasnaqd 300
Qy 301 VSCFOHLVQANVRNKKYLKDVANNITAKGIDYKGFSAFEPQLLNNVSRANCNIIML 360
Db 301 vscfghlvqanvrnkylkdavnnitakgidykgfsgafepqllnnvsvrancnkilm 360
Qy 361 FTDGGERAQEIFNKNYDKKVRFRFVSQHNRYERGPIQWMACENKGYIYIPSGAIR 420
Db 361 ftdggeeraqeifnknynkdkkvrfrfvsqghnyergpiqwmacenkgyyiypsgair 420

Db 361 ftdggeeraqeifnknynkdkkvrfrfvsqghnyergpiqwmacenkgyyiypsgair 420
Qy 421 INTQEYLDVLGRPMVLAGDKAKQVQWTVNVIDALELGLVITGTLPVENITGQFENKTNLK 480
Db 421 intqeyldvlgpmvlagdkakqvqwvnyvidalelglvigtltlpvniitgqfennktnlk 480
Qy 481 NOLITGVMGVDVSLIEDIKRLTPRETTCPNGYFFAIDPNGYVLLHPNLQPKNPKSQEPVTL 540
Db 481 nolitgvmgvdvsliedikrltprettlcpngyffaidpnyvllhpnlpknpkseqeptl 540
Qy 541 DFLDAELNDIKVEIRNMIDGESGKTEFTLVKSQDERYIDKGNRYTWTVPVNGTYSL 600
Db 541 dfldaeelndikveirnmidgesgktrftlvksqderydkgnrtywtvpvngtdysl 600
Qy 601 ALVLPYTSFYIYKAKLEETITQARSKKGMKDSLETLPDNEESGYTFIARPDVCNDLKI 660
Db 601 alvlpysfyiykakleetitqary-----setlpxdnfeesgytftiarpdvcndlki 653
Qy 661 SDNTEFLNFEIDRKTPNNPCNADLINRVLLDAGFTNELVQNYWSKOKNKGVKAR 720
Db 661 sdnteflnfeidrktpnnpcsnadlinrvlldagftnelvqnywskknkgvkar 713
Qy 721 FVWTDGGITRVYPKEAGENWOENPETYEDSFYKRSLDNDNVYFTAPYFNKSGPGAYESGI 780
Db 721 fvtddggitrvypkeagenwqenpetyedsfyrslndnnyvftapyfnksgpgayesgi 773
Qy 781 MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPCAGPVCDCCKNSDVMDCVI 840
Db 774 mvskaveiyioqkllkpaavgikidvnswieftktsirldpcagpvccknsdvmdcvi 833
Qy 841 LDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLNIVSYAFNKSIDYQSVCEPGAAPKQ 900
Db 834 lddggfllmanhddytngiqgrffgeidpslmrhlvnsyafnksydyqsvcepgaapq 893
Qy 901 GAGHSAYVPSVADILQIGWATAAANSILOQFLSLTFPRLLEAVENEDDDFTASLSKQ 960
Db 894 gaghsayvpsvadilqigwataaawsilqgflsltfprlleavemedddftaslskq 953
Qy 961 SCITEQTOYFFDNDKSPSGVLDGNCGRIPFGKLMNTLIFIMVESKGTCPDTRL 1018
Db 954 sciteqtqyffndsksfsgvldcncsrifhgekmlntlifimveskgtcpcdtrl 1011
RESULT 13
AAR71012
ID AAR71012 standard; Protein; 1103 AA.
XX
AC AAR71012;
XX AC
XX AC
DF 01-DEC-1995 (first entry)
XX
DE Human neuronal calcium channel subunit alpha 2a.
XX
XX Calcium channel subunit; antagonist; agonist; diagnosis;
KW Lambert Eaton Syndrome.
XX
XX Homo sapiens.
OS
XX
XX WO9504822-A.
XX
XX 16-FEB-1995.
XX
XX 11-AUG-1994; 94WO-US09230.
XX
XX 11-AUG-1993; 93US-0105536.
PR 05-NOV-1993; 93US-0149097.
XX
XX (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
PA Ellis SB, Gillespie A, Harpold MM, McCue AF, Williams ME;
XX
XX WPI; 1995-090900/12.
DR N-PSDB; AAQ84666.

XX DNA encoding human calcium channel sub-unit(s) - used for
 PT developing prods. for studying calcium channels, e.g. for
 PT obtaining agonists and antagonists

XX Disclosure; Page 231-236; 285pp; English.

XX Human neuronal alpha 2 coding sequence (AAQ84664) transcript is
 CC differentially processed in skeletal muscle, aorta, and CNS in
 CC the region corresp. to nt 1595-1942 of AAQ84664 in each of the
 CC tissues. Five alternatively spliced variant transcripts that differ
 CC in the presence or absence of one to three different portions of
 CC this region. There are three sequences involved (see AAQ84664 FT
 CC and AAQ84665 FT), sequence 1, sequence 2 and sequence 3. The five
 CC alpha 2 encoding transcripts from the different tissues include
 CC different combinations of the three sequences, except for one of
 CC the alpha 2 transcripts expressed in aorta which lacks all three
 CC sequences. The five alpha 2 forms identified are (1) a form that
 CC lacks sequence 3 called alpha 2a, expressed in skeletal muscle
 CC (2) one that lacks sequence 1 called alpha 2b, expressed in CNS
 CC (3) one that lacks sequences 1 and 2 called alpha 2c, expressed in
 CC aorta (4) one that lacks sequences 1, 2 and 3 called alpha 2d,
 CC expressed in aorta and (5) one that lacks sequences 1 and 3
 CC called alpha 2e. The DNA and AA sequences of alpha 2a - alpha 2e
 CC are set forth in AAQ84666-84669 and AAR1012-R1015 respectively.

XX Sequence 1103 AA;

Query Match 98.6%; Score 5270; DB 16; Length 1103;
 Best Local Similarity 97.4%; Pred. No. 0;
 Matches 1010; Conservative 0; Mismatches 1; Indels 26; Gaps 2;

QY 1 MAAGCILLALTILFQSLGSPSEEPFPAVTKSWDKMQEDLVTLAKTAGVGNOLVDI 60
 Db 1 maagcillaaltlftqslgspseepfpavtkswdkmqedlvltlaktasynglvldi 60
 QY 61 YEKYQDLVTEPNNAQVLEIAARDIEKLNSKALVSLALEAEKVQAHOHREDFASN 120
 Db 61 yekyqdlvtepnnaqlveiaardieklnsrkalvslaleaeekvqaahwredfasn 120
 QY 121 EVVYNAKDDLPKNDSPGSGRIKPVIEDANFGROISYQHAAYHIPTDIYEGSTIVL 180
 Db 121 evvynakddlpkndspgsgrikpviedanfgroisqyhaayhiptdiyegstivl 180
 QY 181 NELNWTSAIDVFKKNEEDPSLLQVFGSATGLARYYPASVWDNSRTPNKKIDLYDVR 240
 Db 181 nelnwtaldevfkknreedpsllwqvfgsatglaryypasvwdnsrtpnkkidlydvr 240
 QY 241 RPWYIQAASPKDMLILVDVSGVSGLTLLKIRTSVSEMLETSLDDDFVNVASFNSAQD 300
 Db 241 rpwyiqgaaspkdmlilvdvsgvsgltllkirtsvesmletlsdddfvnvasfnsaqd 300
 QY 301 VSCFOHLVQANVRNKKVLDAVNNITAKGIDYKKGFSFAFQOLLNYSRANCNIIML 360
 Db 301 vscfqlvqanvrnkvldavnnitakgldykkgfsfafqollnysrancnkiml 360
 QY 361 FTDGGEERAQEIFKNYKDKVRFRFSVQHNRYERGPIQWACENKGYIYETPSIGAIR 420
 Db 361 ftdggeeraqeifknkdkvrfrfsvqhnryergpqlwacenkgyiypsigair 420
 QY 421 INTQEYDLVGRPVLGAKQAKOVQNTVYLDALLEGVLITGTPVFNITGOFENKTNLK 480
 Db 421 intqeydlvgrpvmvgakqkvqntvnyldalelgvlitgtlvpfnitgofenknk 480
 QY 481 NOLILGVMGVDSLEDIKRLTFRFTLCPNGYFYADPNPGYVLLHPNLQPK----- 530
 Db 481 nolilgvmgvdsledikrltfrftlcpngyfyadpnpgyvlhpnlpqkpgvgiptin 540
 QY 531 -----NPKSQEPVTLDFDAELNDIKVEIRNKMIDGESGEKTFRTLVKSQDERYI 581
 Db 541 lkrkpnqpkspqevptldfdaelndikveirnkmidgesgektftrtlvksqderyi 600

QY 582 DKGNRTYTWTPVNGTDYSALVLPTYSFYIKAKLETITQARSKKGMKDSKTLKPDNF 641
 Db 601 dkgnrtytwtpvngtdysalvlptysfyikakleetitgar-----setlkpndf 653
 QY 642 EESGYTFIAPRDYCNLDKISDNNTEFLNENETDRKTPNPNPCNADLINRVLLDAGFTN 701
 Db 654 eesgytfiaprdycndlkisdnnntefllnnefdrktpnpsncnadlinrvlldagftn 713
 QY 702 ELYQNTWSKQNKIKYKAREVWTDGGITRYYPKEAGENWQENPETYEDSYKRSLDNDNY 761
 Db 714 elqnywskqknlkgykarfvtdggitryypkeagenwqenpetyedsfkrslndny 773
 QY 762 VFTAPFNKSGPCAYESGIMVSRVAVELIYQGLLKPAVVGKIDVNSWIENFTKTSIRDP 821
 Db 774 vftapyfnkspgayesgimvskavelylqgklkpvavvgikidvnswieenftktsirdp 833
 QY 822 CAGPVCDCRNSDVMDCVILDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNSVYA 881
 Db 834 cagpvcdcrnsdvmcdvillddggfllmanhddytnoigrfgeidpslmrhlvnsvya 893
 QY 882 FNKSYDQSYCEPGAAPKQAGHRSAYVPSVADILQIGWWTATAAASILQOFLSLTFPR 941
 Db 894 fnksydyqsvcepgaapkgaghrsayvpsvadilqigwwataaawilqflsltfpr 953
 QY 942 LLEAVEMEDDDFTASLSKSCITEQTYFPDNDKSKFSFSGVLDGCGNCSRIHPHGEKLMNTNL 1001
 Db 954 lleavemedddftaslsksciteqtyffndndsksfsgvldcgcncsrifhgekmlmntl 1013
 QY 1002 IFIMVESKGTCTPCDTRL 1018
 Db 1014 ifimveskgtcpdtrl 1030
 RESULT 14
 ID AAW63151 standard; Protein; 1103 AA.
 AC AAW63151;
 DT 12-OCT-1998 (first entry)
 DE Human calcium channel alpha-2a subunit.
 KW Alpha-2 subunit; human; calcium channel; assay; detection;
 OS Homo sapiens.
 PN US5792846-A.
 PD 11-AUG-1998.
 PF 31-MAY-1995; 95US-0455543.
 PR 04-APR-1994; 94US-0223305.
 PR 04-APR-1988; 88US-0176899.
 PR 04-APR-1989; 89US-0603751.
 PR 04-APR-1989; 89WO-US01408.
 PR 20-FEB-1990; 90US-0482384.
 PR 30-NOV-1990; 90US-0620250.
 PR 15-AUG-1991; 91US-0745206.
 PR 31-MAY-1995; 95US-0455543.
 PA (SIBI-) SIBIA NEUROSCIENCES INC.
 PI Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;
 PI Williams ME;
 DR WPI; 1998-456192/39.
 DR N-PSDB; AAV42700.
 PT DNA encoding human calcium channel alpha 1B subunit protein -
 PT useful for recombinant production of the channel for screening of

its modulators, and diagnosis of Lambert Eaton Syndrome

Claim 3: Columns 287-294; 166pp; English.

The present sequence represents the alpha-2a subunit of a human calcium channel. Calcium channels are membrane-spanning, multi-subunit proteins that allow controlled entry of calcium ions into cells. This leads to depolarisation events required for muscle contraction. The recombinant subunit, when expressed with nucleic acids encoding the complete calcium channel, can be used in assays for the detection and characterisation of compounds that modulate the channel. The DNA encoding the subunits can be alternatively spliced when transcribed, giving more than one form of the protein from the same transcript, each having slightly different properties. In addition, the reactivity of the alpha 1 subunit with IgG molecules from the serum of an individual with Lambert Eaton Syndrome (LES) can be used as a diagnostic for the disease.

Sequence 1103 AA;

Query Match 98.6%; Score 5270; DB 19; Length 1103;

Best Local Similarity 97.4%; Pred. No. 0;

Matches 1010; Conservative 0; Mismatches 1; Indels 26; Gaps 2;

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DB 1 maagcllaltltflfoslilgspseppfsavtikswdkmqedlvtlaktasgvnqlvdi 60
QY 61 YEKYQDLYTVEPNNAQRLVEIARIEKLLSNRSKALVSLALEAEKVQAQHWREDFASN 120
DB 61 yekyqdytvepnnaqlveiaardiekllsnrskalvslaleaeekvqaahqwedfasn 120
QY 121 EVVYNAKDLDPKNDSPGSGQRKPVFIEDANGRQISYQHAHVHPTDIYEGSTIVL 180
DB 121 evvynakddlpeknndspgsgqrkpvfiedanfrqisyqhaavhptdiyegstivl 180
QY 181 NELNWTSAIDVEFKKREDEPSLLMQVFGSATGLARYYPASPWVDNRRTPNKIDLYDVR 240
DB 181 nelnwtasaidvfkknredpsllmqvfgsatglaryypaspwvdnrrtpnkidlydvrr 240
QY 241 RPYIQAASPKDMLILVDVSGVSGLTLLKLRISYSEMLETISDDDFYNVASFNSNAQD 300
DB 241 rpyiqgaaspkdmililvdvsgvsgltllklrtsvsemlletisdddfynvasfnsgad 300
QY 301 VSCFQHLVQANVRNKKVLKDVANNITAKITDYKGFSAFQOLLNYNVSRANCNKIML 360
DB 301 vscfqlhvdanvrnkkvlkdavnnitakitdykkgfsafaeqllnynvsrancnki1ml 360
QY 361 FTDGGERAQEIFNKYKDKKVRVFRFSVGOHNYERGPQWACENKGYEYIPTSIGAIR 420
DB 361 ftdggeeraqeifnkykdkkvrfrfsvgohnyergpiqwmacenkgyyeipsgair 420
QY 421 INTQEYLDVLRPMVLGAKAKQVQNTVYLDALGLVITGTPVFNITGQFENKTNLK 480
DB 421 intqeyldvlgrpmvlgakakqvqntvyldaleglvitgtplvfnitgqfenktnlk 480
QY 481 NQILGVMGVDVSLDIKRLTPRFTLCPCNGYFPAIDPNGYVLLHPNLQPK----- 530
DB 481 nqilgvmgvdsleldikrltpftlcpngyfpaidpnyvllhpnlpk----- 530
QY 531 -----NPKSQEPVTLDFDLAELENDIKVEIRNKMIDGESGEKTFRTLVKSQDERVI 581
DB 531 -----npskqepvtldfldaelendikveirnkmidgesgektftrtlvksqdervi 581
QY 582 DKGNRVYTPVNGTDYSLALVLPYTSFYIYAKLEETITOARSKKGMKDSSETLKPONF 641
DB 582 dkgnrvtvpngtdyslalvlpptysfyiyakleetitotarskkgmkdsetlkdponf 641
QY 601 dkgnrvtvpngtdyslalvlpptysfyiyakleetitqary-----setlkpndf 653
DB 601 dkgnrvtvpngtdyslalvlpptysfyiyakleetitqary-----setlkpndf 653
QY 642 EESGYTFIAPRDYCNLDKISDNNTEFLNFEIDRKTNNPNSCNADLINRVLLDAGFTN 701
DB 642 eesgytfiaprdydcnldkisdnnnteflnfneidrktnpnpscnadlinrvlldagftn 701
QY 702 ELVQNWSKQKNIKVKARVVDGDTITRVYPKEAGENQENPETYEDSFYKSLDNDNY 761
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DB 774 vftapyfnksgpgayesgimvskaveilyggkllkpvavvgikidvnswenftktsird 833
QY 822 CAGPYCDCKRNSDVMDCVLDDGGFLLMANHDDYTNQIGRFFGEIDPSSLRHLVNI SYVA 881
DB 834 cagpycdckrnsdvmdcvlddggfllmanhddytngqgrffgeidpslmlrlhvnisyva 893
QY 882 FNKSYDYOSVCEPGAAPKOGAGHRSAYVPSVADILOIGWATAAAMSIIQQFLLSLTFPR 941
DB 894 fnksydyosvcepgaapkgaghrsayvpsvadiilqigwwataaawsilqgflsltfpr 953
QY 942 LLEAVEMEDDDFTASLSKOSCITEQYFEEDNDSKFSGLDCGNCSTRIFHGEKLMNTNL 1001
DB 954 lleavemedddftaslsksciteqyffndnksfsgvldcgcncsrifhgeklmntnl 1013
QY 1002 IFIMVESKGTCTPCDTRL 1018
DB 1014 ifimveskgtcpcdtrl 1030
RESULT 15
AAB10586
ID AAB10586 standard; Protein; 1103 AA.
XX
AC AAB10586;
XX
DT 22-DEC-2000 (first entry)
XX
DE Human calcium channel alpha-2a subunit protein.
XX
KW Human; calcium channel; calcium channel subunit; diagnosis; Lambert Eaton Syndrome; calcium channel subunit alpha-2a.
XX
OS Homo sapiens.
XX
PN US06096514-A.
XX
PD 01-AUG-2000.
XX
PF 25-MAY-1995; 95US-0450562.
XX
PR 04-APR-1988; 88US-0176899.
PR 02-FEB-1990; 90US-0482384.
PR 08-NOV-1990; 90US-0603751.
PR 30-NOV-1990; 90US-0620250.
PR 15-AUG-1991; 91US-0745206.
PR 10-APR-1992; 92US-0868354.
PR 13-JUL-1992; 92US-0914231.
PR 11-AUG-1993; 93US-0105536.
PR 05-NOV-1993; 93US-0149097.
PR 07-FEB-1994; 94US-0193078.
PR 04-APR-1994; 94US-0223305.
PR 11-AUG-1994; 94US-0290012.
PR 23-SEP-1994; 94US-0311363.
PR 28-SEP-1994; 94US-0314083.
PR 07-NOV-1994; 94US-0336257.
PR 13-MAR-1995; 95US-0404950.
XX
PA (SIBI-) SIBIA NEUROSCIENCES INC.
XX
PI Ellis SB, Williams ME, McCue AF, Harpold MM;
XX
DR WPI: 2000-548230/50.
XX
DR N-PSDB; AAA71724.
XX
PT Human calcium channel beta subunit polynucleotides, useful for producing recombinant eukaryotic cells and for diagnosing Lambert Eaton Syndrome
XX
```

PS Disclosure; Column 229-236; 153pp; English.

XX This invention describes a novel isolated DNA molecule (I) comprising a
CC sequence encoding a beta3-1 subunit of a human calcium channel.
CC Nucleic acid probes comprising 14-30 contiguous nucleotides of
CC beta3 subunit encoding DNA are useful for isolation and cloning of
CC calcium channel subunit-encoding DNA. Recombinant eukaryotic cells that
CC express heterologous calcium channel and in assays for identifying compounds
CC that modulate calcium channel activity and in assays for identifying
CC agonists and antagonists of calcium channel activity in humans. Human
CC calcium channel subunit or eukaryotic cells expressing the channel are
CC useful for diagnosing Lambert Eaton Syndrome (LES) in a human. This
CC sequence represents the human calcium channel alpha-2a subunit which is
CC described in the method of the invention.

XX Sequence 1103 AA;

Query Match 98.6%; Score 5270; DB 21; Length 1103;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 1010; Conservative 0; Mismatches 1; Indels 26; Gaps 2;

QY	1	MAAGCLLALTTLFOSLLIGPSEEPFSAVTKSWDKMQEDLVTLAKTAGVNLVDI	60
Db	1	maagcllaltltlfgslllgpseepfpaavtkswdkmqedlvltaktasgvnldvi	60
QY	61	YEKYQDLYTVEPNNAQOLVEIAARDIEKLNSRKALVSLALEAEKVAQAHHQWREDFASN	120
Db	61	yekyqdltyvepnnaarqlveiaardieklnsrkalvslaleaeakvqaahqwedfasn	120
QY	121	EVVYVNAKDDLPKNDSEPGSQRIKPVIEDANFGRQISYQHAHVHPTDIYEGSTIVL	180
Db	121	evvyvnaakddlpeknndsepgsqrikpviedanfgrqisyqhaahvhiptdiyegstivl	180
QY	181	NELNWTALDEYFKNREDDPSLLWQVFGSATGLARYYPASPWVDNSRTPNKTDLVDVRR	240
Db	181	nelnwtaldevfknnreedpsllwqvfgsatglaryypaspwvdnsrtpnktldlydvrr	240
QY	241	RPWYIGGAASPDKMLILVDVSGSVSLTKLIRTSVSEMLETLSDDDFVNVASFNSNAQD	300
Db	241	rpwyiggaaspdkmlilvdvsgsvsgltklirtsvsemletlsdddffnvvasfnasqd	300
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QY	361	FTDGGERAQEIFNKYNKDKVVRPFVSQHNRYERGPIQWACENKGYIYEIPSGAIR	420
Db	361	fdggereaqeifnknkdkvrvrpfvsqhnryergpiqwmacenkgyyeipsgair	420
QY	421	INTQEYLDVLRPMVLGADKAKQVQWNTYLDALGLVITGTLPVFNITGOFENKTNLK	480
Db	421	intqeyldvlgrpmvlagdkakqvqwnvtyldaleglvitgtlpvfnitgofenktnlk	480
QY	481	NQLILGMGVDSVLEDIKRLTPFTLCPNGYFAIDPNCYVLLHPNLQPK-----	530
Db	481	nqliilgmvgdvsledikrltpftlcpngyffaidpncyvllhpnlpqpkigvgiptin	540
QY	531	-----NPKSOEPTVLDLDAELENDIKVEIRNKMIDGESGEKFTFLVKQSODERYI	581
Db	541	lkrkrrpnlgpkqsqepvtldfdaelendikveirnmkldgesgektftlvksqgeryi	600
QY	582	DKGNRTYTWTPVNGDYSIALVLPYISFYIYKAKLEETITQARSKKGMKMDSETLKPDNF	641
Db	601	dkgnrttytwtpvngtdysialvlpysfyiykakeetitqarskkgmkmkmdsetlcpdnf	653
QY	642	ESGTYFIAPROYCNDLKIISDNTPELLNFNEIDRKTNNPSCNADLINRVLLDAGFTN	701
Db	654	eesgytifiaprdycndlkisdnntefllnfneidrktnpnpscnaadlinrvlldagftn	713
QY	702	ELVONYWSKQNKIKGVKARFVVTGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNY	761
Db	714	elvonywsqknikgvkarfvvtddgitrvyypkeagenqenpetyedsfykrslndndny	773

QY	762	VFTAPYFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTSIRD	821
Db	774	vftapyfnksgpgayesgimvskaveiyiqgkllkpavvgikidvnswieenftktsird	833
QY	822	CAGPVCDCCKRNSDVMDCVILDDGGFTLLMANHDDYTNOIGRFFGCEIDPSSLMRHLVNI	881
Db	834	cagpvcddckrnsdvmdcvilddggfllmanhddytngirffgeidpslmrhlvnisvya	893
QY	882	FNKSVDYQSVCEPGAAPKOGAGHRSAYVPSVADILQIGMWATAAAWSILQQFLLSLT	941
Db	894	fnksydyqsvcepgaapkgaghrsayvpsvadilqigwataaawsilqqfillsltfpr	953
QY	942	LLEAVEMEDDDFTASLSKOSCIETEQTQYFFDNDKSKFSFVLDGCGNCSRIFHGEKLM	1001
Db	954	lleavemedddftaslsksciteqtqyffdnksksfsgvldcgncsrifhgeklmntl	1013
QY	1002	IFIMVESKGTGCPDTRL	1018
Db	1014	ifimveskgtcpcodtrl	1030

Search completed: July 23, 2001, 07:36:25
Job time: 466 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 23, 2001, 07:38:26 ; Search time 37.55 seconds
(without alignments)
546.132 Million cell updates/sec

Title: US-09-397-548-15

Perfect score: 5346

Sequence: 1 MAAGCLLALTFLFQSLIG.....TNLIFTWESKGTCPDTRL 1018

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
- 1: /cgml_7/ptodata/1/iaa/5A_COMB.pap:*
 - 2: /cgml_7/ptodata/1/iaa/5B_COMB.pap:*
 - 3: /cgml_7/ptodata/1/iaa/6A_COMB.pap:*
 - 4: /cgml_7/ptodata/1/iaa/6B_COMB.pap:*
 - 5: /cgml_7/ptodata/1/iaa/PCTUS_COMB.pap:*
 - 6: /cgml_7/ptodata/1/iaa/backfiles1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	5346	100.0	1091	1	US-08-455-543A-52
3	5346	100.0	1091	2	US-08-223-305C-52
4	5346	100.0	1091	2	US-08-311-363-25
5	5342	99.9	1091	3	US-08-713-118-4
6	5342	99.9	1091	4	US-09-452-007-4
7	5306.5	99.3	1086	1	US-08-455-543A-54
8	5306.5	99.3	1086	2	US-08-223-305C-54
9	5289.5	98.9	1084	1	US-08-455-543A-56
10	5289.5	98.9	1084	2	US-08-223-305C-56
11	5270	98.6	1103	1	US-08-455-543A-53
12	5270	98.6	1103	2	US-08-223-305C-53
13	5250	98.2	1079	1	US-08-455-543A-55
14	5250	98.2	1079	2	US-08-223-305C-55
15	5137.5	96.1	1106	1	US-08-435-675B-5
16	5119.5	95.8	1106	1	US-08-336-257A-8
17	4913	91.9	1086	6	5386025-8
18	2581.5	48.3	508	1	US-08-435-675B-6
19	182	3.4	885	3	US-09-074-579-5
20	182	3.4	885	4	US-09-388-774-5
21	159.5	3.0	946	3	US-09-074-579-3
22	159.5	3.0	946	4	US-09-388-774-3
23	154	2.9	903	1	US-08-021-601-12
24	154	2.9	903	1	US-08-082-849B-12
25	154	2.9	903	5	PCT-US94-01624-12
26	152.5	2.9	789	1	US-08-471-033-32
27	152.5	2.9	789	2	US-08-471-044-32

28 152.5 2.9 789 2 US-08-463-483A-32 Sequence 32, Appl
29 152.5 2.9 789 2 US-08-471-046A-32 Sequence 32, Appl
30 152.5 2.9 789 2 US-08-470-566B-32 Sequence 32, Appl
31 152.5 2.9 789 2 US-08-838-219B-4 Sequence 4, Appl
32 152.5 2.9 789 2 US-08-469-334-32 Sequence 32, Appl
33 152.5 2.9 789 3 US-09-300-529-32 Sequence 4, Appl
34 152.5 2.9 789 4 US-09-233-336A-4 Sequence 4, Appl
35 152.5 2.9 789 4 US-09-233-752A-4 Sequence 6, Appl
36 150.5 2.8 789 4 US-08-960-780-6 Sequence 6, Appl
37 150.5 2.8 789 4 US-09-073-898-6 Sequence 4, Appl
38 148.5 2.8 790 4 US-08-960-780-4 Sequence 4, Appl
39 148.5 2.8 790 4 US-09-073-898-4 Sequence 4, Appl
40 147.5 2.8 746 2 US-08-838-219B-6 Sequence 6, Appl
41 147.5 2.8 746 3 US-09-233-336A-6 Sequence 6, Appl
42 147.5 2.8 746 4 US-09-233-752A-6 Sequence 6, Appl
43 145.5 2.7 790 4 US-08-960-780-8 Sequence 8, Appl
44 145.5 2.7 790 4 US-09-073-898-8 Sequence 8, Appl
45 141.5 2.6 789 1 US-08-471-033-29 Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-07-745-206A-25
; Sequence 25, Application US/07745206A
; Patent No. 5429921
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: McCue, Ann
; APPLICANT: Feldman, Daniel
; TITLE OF INVENTION: Human Calcium Channel Compositions and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitch, Even, Tabin & Flannery
; STREET: 135 S. LaSalle
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07745,206A
; FILING DATE: 19910815
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Feder, Scott B
; REFERENCE/DOCKET NUMBER: 51504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-372-7842
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1091 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-745-206A-25

Query Match 100.0%; Score 5346; DB 1; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAGCLLALTFLFQSLIGPSSEFPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
|||||
DB 1 MAAGCLLALTFLFQSLIGPSSEFPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
|||||

QY 61 YEKYODLYTVEPNARQLVEIARDEIKLSNRKALVSLALEAEKVAHQHREDFASN 120
DB 61 YEKYODLYTVEPNARQLVEIARDEIKLSNRKALVSLALEAEKVAHQHREDFASN 120
QY 121 EYVYNKADDDPEKNDSEPSQRIKPVFIEDANFGQISQHAHVHPTDIYEGSIYL 180
DB 121 EYVYNKADDDPEKNDSEPSQRIKPVFIEDANFGQISQHAHVHPTDIYEGSIYL 180
QY 181 NELNWTSSALDEVFKNREDDPSLLQVFGSGLTGLARYYPASPDWNSRTPNKIDLYDVR 240
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QY 301 VSCFOHLYQVAVNRKVKLVKDAVNNTAKGIDYKKGFSFAFEQLLNYSRANGKNIIML 360
DB 301 VSCFOHLYQVAVNRKVKLVKDAVNNTAKGIDYKKGFSFAFEQLLNYSRANGKNIIML 360
QY 361 FTDGGEERAQEIFNKYNDKVRFRFSGVGHNYERGPIOMACENKGYIYEIPSIGAIR 420
DB 361 FTDGGEERAQEIFNKYNDKVRFRFSGVGHNYERGPIOMACENKGYIYEIPSIGAIR 420
QY 421 INTQYLDVLRPMVLAGDKAQVQWNTVYLDALGLVITGTLVPVFNITQGFENKTNLK 480
DB 421 INTQYLDVLRPMVLAGDKAQVQWNTVYLDALGLVITGTLVPVFNITQGFENKTNLK 480
QY 481 NOLILGVNGVDVSLDIKRLPRFTLCNGYFAIDPNGYVLLHPNLPKPKSOEPTVL 540
DB 481 NOLILGVNGVDVSLDIKRLPRFTLCNGYFAIDPNGYVLLHPNLPKPKSOEPTVL 540
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DB 541 DFLDAELNDIKVEIRNMKIDGSEKFTLVKSDQERYIDKGNRTYTWTVPVNGTDYSL 600
QY 601 ALVLPYTFYIYKAKLEETITQARSKKGMKDSEPLKPDNFEESGYTTIAPRDYCNLDKI 660
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QY 661 SDNNTFELLNFNEFTDRTPNPNPCNADLINRVLLDAGFTNELVQVYWSKOKNKGVAR 720
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DB 841 LDGGLFLLMANHDDYTNOIGRFGFIDPSLMRHLNYSIYAFNKSIDYQSVCEPAAAPKQ 900
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DB 901 GAGHSAYVPSVADILQIGWATAAASWSTLOQFLLSLFPRLLEAVENEDDDFTASLSQK 960
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DB 961 SCITEQTYFFNDKSKFSVGLDCGNCRIHFHGEKLMNTNLIFIMVESKGTGCPDCTRL 1018

RESULT 2

US-08-455-543A-52
; Sequence 52, Application US/08455543A
; Patent No. 5792846
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven

APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,543A
FILING DATE: May 31, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-455-543A-52

Query Match 100.0%; Score 5346; DB 1; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTTLTFLQSLTIGPSSEPPFSAVTIKSWDKMQEDLVTLAKTAGVNLVDI 60
DB 1 MAAGCLLALTTLTFLQSLTIGPSSEPPFSAVTIKSWDKMQEDLVTLAKTAGVNLVDI 60
QY 61 YEKYODLYTVEPNARQLVEIARDEIKLSNRKALVSLALEAEKVAHQHREDFASN 120

Db 61 YEKYQDLYTVEPNARQLVETARDIEKLLSNRSKALVSLALEAEKVAQAAHQWREDFASN 120
QY 121 EVVYNAKDDLDPEKNDSEPGSQRKIPVFTEDANFGQISYQHAHVHIPTDIYEGSTIVL 180
Db 121 EVVYNAKDDLDPEKNDSEPGSQRKIPVFTEDANFGQISYQHAHVHIPTDIYEGSTIVL 180
QY 181 NELNWTSDALDEVKKNKEEDPSLLMQVFGSATGLARYYPASPPVDNSRTNPKIDLYDVR 240
Db 181 NELNWTSDALDEVKKNKEEDPSLLMQVFGSATGLARYYPASPPVDNSRTNPKIDLYDVR 240
QY 241 RPWYIOGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETISDDDFVNVASFNSNAQD 300
Db 241 RPWYIOGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETISDDDFVNVASFNSNAQD 300
QY 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGTDYKGFSAFQOLLNYSRANCNKIIML 360
Db 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGTDYKGFSAFQOLLNYSRANCNKIIML 360
QY 361 FTDGGEERAQEIFKNYKNDKKVFRFVSVOHNVGPIOMACENKGYIYIETPSIGAIR 420
Db 361 FTDGGEERAQEIFKNYKNDKKVFRFVSVOHNVGPIOMACENKGYIYIETPSIGAIR 420
QY 421 INTQEVLDVLRPNVLAGKAKOVQNTNVDLDELGLVITGTPVFNITQGFENKTNL 480
Db 421 INTQEVLDVLRPNVLAGKAKOVQNTNVDLDELGLVITGTPVFNITQGFENKTNL 480
QY 481 NQILGVMGVDSLEDKRLTPFTLCNPGYFAIDPNGVYLLHPNLPKNPKSQBPVTL 540
Db 481 NQILGVMGVDSLEDKRLTPFTLCNPGYFAIDPNGVYLLHPNLPKNPKSQBPVTL 540
QY 541 DFLDAELNDIKVEIRKMKIDGESGKFTLVKSDERYIDKGNRTYTPVNGTDYSL 600
Db 541 DFLDAELNDIKVEIRKMKIDGESGKFTLVKSDERYIDKGNRTYTPVNGTDYSL 600
QY 601 ALVLPYSYIYKAKLEETITQARSKKGMKDSSETLKPDNFEESGYTFIAPRDYCNLDKI 660
Db 601 ALVLPYSYIYKAKLEETITQARSKKGMKDSSETLKPDNFEESGYTFIAPRDYCNLDKI 660
QY 661 SDNNTFELNFEEDIRKTPNPNPCNADLINRVLLDAGFTNELVQYNSKQKNKGVKAR 720
Db 661 SDNNTFELNFEEDIRKTPNPNPCNADLINRVLLDAGFTNELVQYNSKQKNKGVKAR 720
QY 721 FVYTDGGITRVPKAGENQWNPETEDSFYKRSLDNDNYFTAPYFNKSGPGAYESGI 780
Db 721 FVYTDGGITRVPKAGENQWNPETEDSFYKRSLDNDNYFTAPYFNKSGPGAYESGI 780
QY 781 MYSKAVEIYIQGLKLPVAVGKIDVNSWNIENFTKTSIRDPCAGPVCDCKRNSDVMDCVI 840
Db 781 MYSKAVEIYIQGLKLPVAVGKIDVNSWNIENFTKTSIRDPCAGPVCDCKRNSDVMDCVI 840
QY 841 LDGGFLLMANHDDYTNOIGRFFGIDPSLMRHLVNIYSVAFNKSVDYQSVCEPGAAPKQ 900
Db 841 LDGGFLLMANHDDYTNOIGRFFGIDPSLMRHLVNIYSVAFNKSVDYQSVCEPGAAPKQ 900
QY 901 GAGHSAYVPSVADILQIGWATAAASWSTLOQFLLSFPRLLEAVEMEDDDFTASLSKQ 960
Db 901 GAGHSAYVPSVADILQIGWATAAASWSTLOQFLLSFPRLLEAVEMEDDDFTASLSKQ 960
QY 961 SCITQTOYFFDNDKSPGVLDCNCSRIHFGEKLMNTNLIIMVESKGTGCPDTRL 1018
Db 961 SCITQTOYFFDNDKSPGVLDCNCSRIHFGEKLMNTNLIIMVESKGTGCPDTRL 1018

RESULT 3

US-08-223-305C-52
; Sequence 52, Application US/08223305C
; Patent No. 5851824
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel

; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/223,305C
; FILING DATE: April 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,250
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 52516 (P519739)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1091 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-223-305C-52

Query Match 100.0%; Score 5346; DB 2; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTTLFQSLIGPSSEPPFSAVTIKSWDKMQEDLVTLAKTAGSVNQLVDI 60
Db 1 MAAGCLLALTTLFQSLIGPSSEPPFSAVTIKSWDKMQEDLVTLAKTAGSVNQLVDI 60
QY 61 YEKYQDLYTVEPNARQLVETARDIEKLLSNRSKALVSLALEAEKVAQAAHQWREDFASN 120
Db 61 YEKYQDLYTVEPNARQLVETARDIEKLLSNRSKALVSLALEAEKVAQAAHQWREDFASN 120
QY 121 EVVYNAKDDLDPEKNDSEPGSQRKIPVFTEDANFGQISYQHAHVHIPTDIYEGSTIVL 180
Db 121 EVVYNAKDDLDPEKNDSEPGSQRKIPVFTEDANFGQISYQHAHVHIPTDIYEGSTIVL 180

Db 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIHQAAVHIPTDIYEGSTIVL 180
Qy 181 NELNWTSSALDEVEFKKREEDSLWQVFGSGATGLARYYPASPWVDNSRTPNKIDLYDVR 240
Db 181 NELNWTSSALDEVEFKKREEDSLWQVFGSGATGLARYYPASPWVDNSRTPNKIDLYDVR 240
Qy 241 RPWYIQGAASPKDMLILVDVSGVSGTLKLRITSVSEMLETSLDDDFVNVASFNNAQD 300
Db 241 RPWYIQGAASPKDMLILVDVSGVSGTLKLRITSVSEMLETSLDDDFVNVASFNNAQD 300
Qy 301 VSCFQHLVQANVRNKKVUKDAVNNTAKGIDYKKGFSFAFEQLLNNVSRANCNKIIML 360
Db 301 VSCFQHLVQANVRNKKVUKDAVNNTAKGIDYKKGFSFAFEQLLNNVSRANCNKIIML 360
Qy 361 FTDGGEERAQEIFNKYNDKKVRFRFVSGQHNVERGPIQWACENKGYEIPISGAIR 420
Db 361 FTDGGEERAQEIFNKYNDKKVRFRFVSGQHNVERGPIQWACENKGYEIPISGAIR 420
Qy 421 INTQBYLDVLRPMVLADGKAKQVQWNTVNYLDALGLVITGTLPVFNITQGFENKTNL 480
Db 421 INTQBYLDVLRPMVLADGKAKQVQWNTVNYLDALGLVITGTLPVFNITQGFENKTNL 480
Qy 481 NOLILGVMGVDVSLDIKRLTPRFTLCPNGYYFAIDPNGYVLLHPNLPKNPKSQEPVTL 540
Db 481 NOLILGVMGVDVSLDIKRLTPRFTLCPNGYYFAIDPNGYVLLHPNLPKNPKSQEPVTL 540
Qy 541 DFLDALENDIKVEIRNKMIDGESKTFRLVKSQDRIYDKGNRTYTWTVPVNGTDYSL 600
Db 541 DFLDALENDIKVEIRNKMIDGESKTFRLVKSQDRIYDKGNRTYTWTVPVNGTDYSL 600
Qy 601 ALVLPYTFYIKAKLETTIQAARKKMKDSEFLKPDNFEESGYTFIAPRDYCNLDKI 660
Db 601 ALVLPYTFYIKAKLETTIQAARKKMKDSEFLKPDNFEESGYTFIAPRDYCNLDKI 660
Qy 661 SDNTEFLNFEIDRTPNPNNSADLNRLVLDAGFTNELVQYWSKQKNKGVKAR 720
Db 661 SDNTEFLNFEIDRTPNPNNSADLNRLVLDAGFTNELVQYWSKQKNKGVKAR 720
Qy 721 FVVTGGITRVYPRKAGENQWENPETEYEDSKRSLDNDNVFTAPYFNKSGPGAYESGI 780
Db 721 FVVTGGITRVYPRKAGENQWENPETEYEDSKRSLDNDNVFTAPYFNKSGPGAYESGI 780
Qy 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFKTSIRDCAGPVCCKRNSDVMDCVI 840
Db 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFKTSIRDCAGPVCCKRNSDVMDCVI 840
Qy 841 LDGQFLMANHDDYTNQIGRFFGIDPSLMRHLVNSVYAFNKSVDYQSVCEPGAAPKQ 900
Db 841 LDGQFLMANHDDYTNQIGRFFGIDPSLMRHLVNSVYAFNKSVDYQSVCEPGAAPKQ 900
Qy 901 GAGHSAYVPSVADILQIGWATAAASILQOFLSLFPRLLEAVENDDDFASLSKQ 960
Db 901 GAGHSAYVPSVADILQIGWATAAASILQOFLSLFPRLLEAVENDDDFASLSKQ 960
Qy 961 SCITQTOYFFNDKSPSGVLDGNCNCRIFHGEKLMNTNIFIMVESKGCPCDTRL 1018
Db 961 SCITQTOYFFNDKSPSGVLDGNCNCRIFHGEKLMNTNIFIMVESKGCPCDTRL 1018

RESULT 4

US-08-311-363-25
; Sequence 25, Application US/08311363
; Patent No. 5876958
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: Human Calcium Channel Compositions and
; METHODS
; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311.363
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-51506
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1091 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-311-363-25

Query Match 100.0%; Score 5346; DB 2; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAAGCLLALTITLQSLIGPSSSEPPFSVATIKSWDKMQEDLVTLAKTAGVNLVDI 60
Db 1 MAAGCLLALTITLQSLIGPSSSEPPFSVATIKSWDKMQEDLVTLAKTAGVNLVDI 60
Qy 61 YEKQDLYTVEPNARQLVEIARADIEKLLSNRSKALVSLALEAEKVQAAHQRREDFASN 120
Db 61 YEKQDLYTVEPNARQLVEIARADIEKLLSNRSKALVSLALEAEKVQAAHQRREDFASN 120
Qy 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIHQAAVHIPTDIYEGSTIVL 180
Db 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIHQAAVHIPTDIYEGSTIVL 180
Qy 181 NELNWTSSALDEVEFKKREEDSLWQVFGSGATGLARYYPASPWVDNSRTPNKIDLYDVR 240
Db 181 NELNWTSSALDEVEFKKREEDSLWQVFGSGATGLARYYPASPWVDNSRTPNKIDLYDVR 240
Qy 241 RPWYIQGAASPKDMLILVDVSGVSGTLKLRITSVSEMLETSLDDDFVNVASFNNAQD 300
Db 241 RPWYIQGAASPKDMLILVDVSGVSGTLKLRITSVSEMLETSLDDDFVNVASFNNAQD 300
Qy 301 VSCFQHLVQANVRNKKVUKDAVNNTAKGIDYKKGFSFAFEQLLNNVSRANCNKIIML 360
Db 301 VSCFQHLVQANVRNKKVUKDAVNNTAKGIDYKKGFSFAFEQLLNNVSRANCNKIIML 360
Qy 361 FTDGGEERAQEIFNKYNDKKVRFRFVSGQHNVERGPIQWACENKGYEIPISGAIR 420
Db 361 FTDGGEERAQEIFNKYNDKKVRFRFVSGQHNVERGPIQWACENKGYEIPISGAIR 420
Qy 421 INTQBYLDVLRPMVLADGKAKQVQWNTVNYLDALGLVITGTLPVFNITQGFENKTNL 480
Db 421 INTQBYLDVLRPMVLADGKAKQVQWNTVNYLDALGLVITGTLPVFNITQGFENKTNL 480
Qy 481 NOLILGVMGVDVSLDIKRLTPRFTLCPNGYYFAIDPNGYVLLHPNLPKNPKSQEPVTL 540
Db 481 NOLILGVMGVDVSLDIKRLTPRFTLCPNGYYFAIDPNGYVLLHPNLPKNPKSQEPVTL 540

541 DFLDAELNDIKVEIRKMKIDGESGKFTLTKSODERYIDKGNRTYTWTPVNGTDYSL 600
Db 541 DFLDAELNDIKVEIRKMKIDGESGKFTLTKSODERYIDKGNRTYTWTPVNGTDYSL 600
QY 601 ALVLPYTFYIIKAKLEETITQARSKKGMKDSITLKPONFEESGYTFIAPRDYCNLDKI 660
Db 601 ALVLPYTFYIIKAKLEETITQARSKKGMKDSITLKPONFEESGYTFIAPRDYCNLDKI 660
QY 661 SDNTEFLNFEIDRKTPNPNPCNADLINRVLLDAGFTNELVQYNSKQKNIKVAK 720
Db 661 SDNTEFLNFEIDRKTPNPNPCNADLINRVLLDAGFTNELVQYNSKQKNIKVAK 720
QY 721 FVYTDGGITRVYKKEAGENQENPETYEDSFYKRSIDNDNYVFTAFYFNKSGPAYESGI 780
Db 721 FVYTDGGITRVYKKEAGENQENPETYEDSFYKRSIDNDNYVFTAFYFNKSGPAYESGI 780
QY 781 MYSKAVEIYIQGLKLPVAVGKIDVNSWIENTFTKTSIRDPACAGPYCDCKRNSDVMDCVI 840
Db 781 MYSKAVEIYIQGLKLPVAVGKIDVNSWIENTFTKTSIRDPACAGPYCDCKRNSDVMDCVI 840
QY 841 LDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI SYAFNKSVDYQSVCEPGAAPKQ 900
Db 841 LDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI SYAFNKSVDYQSVCEPGAAPKQ 900
QY 901 GAGHSAYVPSVADILQIGWATAAASWILQOFLLSITPRLEAVEMEDDDFTASLSKQ 960
Db 901 GAGHSAYVPSVADILQIGWATAAASWILQOFLLSITPRLEAVEMEDDDFTASLSKQ 960
QY 961 SCITEQTOYFFNDNDSKFSGLVDCGNCRSIFHGEKLMNTNLFIMVESKGTCTCDTRL 1018
Db 961 SCITEQTOYFFNDNDSKFSGLVDCGNCRSIFHGEKLMNTNLFIMVESKGTCTCDTRL 1018

RESULT 5

US-08-713-118-4
; Sequence 4, Application US/08713118
; Patent No. 6040436
; GENERAL INFORMATION:
; APPLICANT: Franco, Rodrigo
; APPLICANT: Sun Chen, Ai Ru
; APPLICANT: Suey, David J.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL
; TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713.118
; FILING DATE: 16-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mata, Elizabeth W.
; REGISTRATION NUMBER: 38,236
; REFERENCE/DOCKET NUMBER: ACC96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1091 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-713-118-4
Query Match 99.9%; Score 5342; DB 3; Length 1091;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1017; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MAAGCLLALTLLTQSLILGTPSEEPFPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
Db 1 MAAGCLLALTLLTQSLILGTPSEEPFPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
QY 61 YEKYQDLYTVEPNARQOLVEIARDEKLLSNRSKALVSLAEAEKVQAAHQREDFASN 120
Db 61 YEKYQDLYTVEPNARQOLVEIARDEKLLSNRSKALVSLAEAEKVQAAHQREDFASN 120
QY 121 EYVYNAKDDLDPEKNDSEPGSQRIKPVFTEDANFRQISYQHAHVHPTDIYEGSTIVL 180
Db 121 EYVYNAKDDLDPEKNDSEPGSQRIKPVFTEDANFRQISYQHAHVHPTDIYEGSTIVL 180
QY 181 NELNWTSALEDEVFKKNEEDPSLLMQVFGSATGLARYYPASPVWDNSRTPNKIDLYDVR 240
Db 181 NELNWTSALEDEVFKKNEEDPSLLMQVFGSATGLARYYPASPVWDNSRTPNKIDLYDVR 240
QY 241 RPYIIOGAASPKDMLILVDVSGSVGLTLKLI RTSVSEMLETSLDDDFVNVASFNSNAQD 300
Db 241 RPYIIOGAASPKDMLILVDVSGSVGLTLKLI RTSVSEMLETSLDDDFVNVASFNSNAQD 300
QY 301 VSCFQHLVQANVNKKVLDKAVNNITAKGTDYKGFSAFQOLLNYSRANCNKIIML 360
Db 301 VSCFQHLVQANVNKKVLDKAVNNITAKGTDYKGFSAFQOLLNYSRANCNKIIML 360
QY 361 FTDGGEERAQEIFNKYKDKKVRFRFSVQGHNYERGIOMMACENKGYIYEIPSGAIR 420
Db 361 FTDGGEERAQEIFNKYKDKKVRFRFSVQGHNYERGIOMMACENKGYIYEIPSGAIR 420
QY 421 INTQEYLDVLGRPMVLGAKAKOVQNTNVLDALEGLVITGTLPVFNITGQENKTNLK 480
Db 421 INTQEYLDVLGRPMVLGAKAKOVQNTNVLDALEGLVITGTLPVFNITGQENKTNLK 480
QY 481 NQILGLVMGVDSLEDIKRLTPRFTLCPNGYYPADIPNGYVLLHPLNLPKNPKSQBPVTL 540
Db 481 NQILGLVMGVDSLEDIKRLTPRFTLCPNGYYPADIPNGYVLLHPLNLPKNPKSQBPVTL 540
QY 541 DFLDAELNDIKVEIRKMKIDGESGKFTLTKSODERYIDKGNRTYTWTPVNGTDYSL 600
Db 541 DFLDAELNDIKVEIRKMKIDGESGKFTLTKSODERYIDKGNRTYTWTPVNGTDYSL 600
QY 601 ALVLPYTFYIIKAKLEETITQARSKKGMKDSITLKPONFEESGYTFIAPRDYCNLDKI 660
Db 601 ALVLPYTFYIIKAKLEETITQARSKKGMKDSITLKPONFEESGYTFIAPRDYCNLDKI 660
QY 661 SDNTEFLNFEIDRKTPNPNPCNADLINRVLLDAGFTNELVQYNSKQKNIKVAK 720
Db 661 SDNTEFLNFEIDRKTPNPNPCNADLINRVLLDAGFTNELVQYNSKQKNIKVAK 720
QY 721 FVYTDGGITRVYKKEAGENQENPETYEDSFYKRSIDNDNYVFTAFYFNKSGPAYESGI 780
Db 721 FVYTDGGITRVYKKEAGENQENPETYEDSFYKRSIDNDNYVFTAFYFNKSGPAYESGI 780
QY 781 MYSKAVEIYIQGLKLPVAVGKIDVNSWIENTFTKTSIRDPACAGPYCDCKRNSDVMDCVI 840
Db 781 MYSKAVEIYIQGLKLPVAVGKIDVNSWIENTFTKTSIRDPACAGPYCDCKRNSDVMDCVI 840
QY 841 LDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI SYAFNKSVDYQSVCEPGAAPKQ 900
Db 841 LDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI SYAFNKSVDYQSVCEPGAAPKQ 900
QY 901 GAGHSAYVPSVADILQIGWATAAASWILQOFLLSITPRLEAVEMEDDDFTASLSKQ 960
Db 901 GAGHSAYVPSVADILQIGWATAAASWILQOFLLSITPRLEAVEMEDDDFTASLSKQ 960
QY 961 SCITEQTOYFFNDNDSKFSGLVDCGNCRSIFHGEKLMNTNLFIMVESKGTCTCDTRL 1018

Db 961 SCITEQYFFDNDKSPFSGVLDGCGNSRIFHGEKLMNTNLIIFIMVESKGTCPDTRL 1018
|||||

RESULT 6

US-09-452-007-4
; Sequence 4, Application US/09452007
; Patent No. 6140485
; GENERAL INFORMATION:
; APPLICANT: Franco, Rodrigo
; APPLICANT: Sun Chen, Ai Ru
; APPLICANT: Suet, David J.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL
; TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/452.007
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/713.118
; FILING DATE: 16-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mata, Elizabeth W.
; REGISTRATION NUMBER: 38,236
; REFERENCE/DOCKET NUMBER: ACC96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1091 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-452-007-4

Query Match 99.9%; Score 5342; DB 4; Length 1091;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1017; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MAAGCLLALTTLFSLIGSPSSPEPPSATIKSWDKMQEDLVTLAKTAGVNLVDI 60
|||
DB 1 MAAGCLLALTTLFSLIGSPSSPEPPSATIKSWDKMQEDLVTLAKTAGVNLVDI 60
|||
QY 61 YEKYQDLTYVEPNNAQLVEIAARDEIKLLNSRKALYSALAEKVOAAHQWREDFASN 120
|||
DB 61 YEKYQDLTYVEPNNAQLVEIAARDEIKLLNSRKALYSALAEKVOAAHQWREDFASN 120
|||
QY 121 EVVYVNAKDDLDPEKNDSEPSQRIKPVFIEDANFGRIQSYOHAHVHIPTDIYEGSTIVL 180
|||
DB 121 EVVYVNAKDDLDPEKNDSEPSQRIKPVFIEDANFGRIQSYOHAHVHIPTDIYEGSTIVL 180
|||
QY 181 NELNWTLSALDEVFKKNDREDSLLMQVFGSATGLARYYPASPWDNSTRTPNKIDLYDYRR 240
|||
DB 181 NELNWTLSALDEVFKKNDREDSLLMQVFGSATGLARYYPASPWDNSTRTPNKIDLYDYRR 240
|||
QY 241 RPWYIQGAASPKDMLILVDVSGVSGSLTKLIRTSVSEMLETLDSDDDFVNVASFNSNAQD 300
|||
DB 241 RPWYIQGAASPKDMLILVDVSGVSGSLTKLIRTSVSEMLETLDSDDDFVNVASFNSNAQD 300
|||

QY 301 VSCFQHLVQANVRNKKVYLKDAVNNITAKGIDYKKGFSFAFQQLLNVNVRANCKIIML 360
|||
DB 301 VSCFQHLVQANVRNKKVYLKDAVNNITAKGIDYKKGFSFAFQQLLNVNVRANCKIIML 360
|||
QY 361 FTGGERAQEIEFNKYNKDKKRVFRFVSQGHNYERGIQWMACENKGYIYEIPSGAIR 420
|||
DB 361 FTGGERAQEIEFNKYNKDKKRVFRFVSQGHNYERGIQWMACENKGYIYEIPSGAIR 420
|||
QY 421 INTQEYLDVLGRPMVLAGDKAKQVQWNTNVLDALEGLVITGTLVPFNITGQFENKLNK 480
|||
DB 421 INTQEYLDVLGRPMVLAGDKAKQVQWNTNVLDALEGLVITGTLVPFNITGQFENKLNK 480
|||
QY 481 NOLLGVMGVDVSLDIKRLTPRETLCPNGYIYFAIDNGVYLLHPNLQPKNPKSQEPVTL 540
|||
DB 481 NOLLGVMGVDVSLDIKRLTPRETLCPNGYIYFAIDNGVYLLHPNLQPKNPKSQEPVTL 540
|||
QY 541 DFLDAELENDIKVEIRNMIDGESGKFTFTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600
|||
DB 541 DFLDAELENDIKVEIRNMIDGESGKFTFTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600
|||
QY 601 ALVLPYTSFYIIRAKLEETITQARSKGKMKDSTLKPDPNFEESGYTFIAPRDYCNDLKI 660
|||
DB 601 ALVLPYTSFYIIRAKLEETITQARSKGKMKDSTLKPDPNFEESGYTFIAPRDYCNDLKI 660
|||
QY 661 SDNTEFLNFEIDRKTNNPCNADLINRVLLDAGFTNELVQNTWSKOKNIKGVKAR 720
|||
DB 661 SDNTEFLNFEIDRKTNNPCNADLINRVLLDAGFTNELVQNTWSKOKNIKGVKAR 720
|||
QY 721 FVYTDGGITRVYPKEAGENMOENPETYEDSFYKRSKLDNDNTVFTAFYFNKSGPAYESGI 780
|||
DB 721 FVYTDGGITRVYPKEAGENMOENPETYEDSFYKRSKLDNDNTVFTAFYFNKSGPAYESGI 780
|||
QY 781 MVSKAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTSIRDPCAGPCVDCCKNSVMDCVI 840
|||
DB 781 MVSKAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTSIRDPCAGPCVDCCKNSVMDCVI 840
|||
QY 841 LDDGGFLLMANHDDYTNOIGRFFGEIDPSPLMRHLVNSVYAFNKSIDYQSVCEPGAAPKQ 900
|||
DB 841 LDDGGFLLMANHDDYTNOIGRFFGEIDPSPLMRHLVNSVYAFNKSIDYQSVCEPGAAPKQ 900
|||
QY 901 GAGHRSAYVPSVADILQIGMWATAAASILQOFLSLTFFPRLEAEMEDDDFTASLSKQ 960
|||
DB 901 GAGHRSAYVPSVADILQIGMWATAAASILQOFLSLTFFPRLEAEMEDDDFTASLSKQ 960
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QY 961 SCITEQYFFDNDKSPFSGVLDGCGNSRIFHGEKLMNTNLIIFIMVESKGTCPDTRL 1018
|||
DB 961 SCITEQYFFDNDKSPFSGVLDGCGNSRIFHGEKLMNTNLIIFIMVESKGTCPDTRL 1018
|||

RESULT 7
US-08-455-543A-54
; Sequence 54, Application US/0845543A
; Patent No. 5792846
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,543A
FILING DATE: May 31, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 1086 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-455-543A-54
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Query Match 99.3%; Score 5306.5; DB 1; Length 1086;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1013; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 1 MAAGCLLALTFLFOSLLIGPSEPPFSAVTKSWDKMQEDLVTLAKTASGVNOLVDI 60
DB 1 MAAGCLLALTFLFOSLLIGPSEPPFSAVTKSWDKMQEDLVTLAKTASGVNOLVDI 60
QY 61 YEKYQDYVTPENNAQLVEIARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120
DB 61 YEKYQDYVTPENNAQLVEIARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120
QY 121 EVVYNAKDDLPKNDSPGSGORIKPFIEDANFGROIYSQHAHVHIPTDIYEGSTIVL 180
DB 121 EVVYNAKDDLPKNDSPGSGORIKPFIEDANFGROIYSQHAHVHIPTDIYEGSTIVL 180
QY 181 NELNWTSALEDVFKKNREDPSLLMQVFGSATGLARYYPASPDVNSRTPNKIDLDYDVR 240
DB 181 NELNWTSALEDVFKKNREDPSLLMQVFGSATGLARYYPASPDVNSRTPNKIDLDYDVR 240
QY 241 RPWYIOGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300
DB 241 RPWYIOGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFQOLLNINVRANCNKIIML 360
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DB 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFQOLLNINVRANCNKIIML 360
QY 361 FTDGGEERAQEIFNKYNKDKKVVFRFSYQGHNYERGPQIOMACENKGYIYEIPSIGAIR 420
DB 361 FTDGGEERAQEIFNKYNKDKKVVFRFSYQGHNYERGPQIOMACENKGYIYEIPSIGAIR 420
QY 421 INTQEYLDVLGRPMVLADGKAKOVQWNTNYLDALGLVITGTLPVFNITQGFENKTLK 480
DB 421 INTQEYLDVLGRPMVLADGKAKOVQWNTNYLDALGLVITGTLPVFNITQGFENKTLK 480
QY 481 NQILGVMGVDSLEDIKRLTPRETLCPNGYFPAIDPNQVLLHPNLPKNPKSQBPVTL 540
DB 481 NQILGVMGVDSLEDIKRLTPRETLCPNGYFPAIDPNQVLLHPNLPKNPKSQBPVTL 540
QY 541 DFLDAELNDIKVEIRNKMIDGESGKFTRTLKVSQDERYIDKGNRTYTWTVPNGTDYSL 600
DB 541 DFLDAELNDIKVEIRNKMIDGESGKFTRTLKVSQDERYIDKGNRTYTWTVPNGTDYSL 600
QY 601 ALVLPYISFYIYKAKLEETITQARSKKGMKDSSETLKPONFEESGYTFTAPRDYCNDLKI 660
DB 601 ALVLPYISFYIYKAKLEETITQARSKKGMKDSSETLKPONFEESGYTFTAPRDYCNDLKI 660
QY 661 SDNTEFLNENEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQNVWSKQNIKGVKAR 720
DB 661 SDNTEFLNENEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQNVWSKQNIKGVKAR 720
QY 721 FVVTGGITRVYPKEAGENQENPETEYEDSFYKRSLDNDNYFTAPYFNKSGPGAYESGI 780
DB 721 FVVTGGITRVYPKEAGENQENPETEYEDSFYKRSLDNDNYFTAPYFNKSGPGAYESGI 780
QY 781 MYSKAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTSIRDPCAGPVCDCRNSDVMDCVI 840
DB 781 MYSKAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTSIRDPCAGPVCDCRNSDVMDCVI 840
QY 841 LDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNSIYAFNKSVDYQSVCPGGAAPKQ 900
DB 841 LDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNSIYAFNKSVDYQSVCPGGAAPKQ 900
QY 901 GAGHSAYVPSVADILQIGWATAAASILQQLFLLSITFPRLEAVEMEDDDFTASLSKQ 960
DB 901 GAGHSAYVPSVADILQIGWATAAASILQQLFLLSITFPRLEAVEMEDDDFTASLSKQ 960
QY 961 SCITEQTYFFDNDKSFSGVLDCGNCGRIFHGEKLMNTNLIIFIMVESKGTCTCDTRL 1018
DB 961 SCITEQTYFFDNDKSFSGVLDCGNCGRIFHGEKLMNTNLIIFIMVESKGTCTCDTRL 1018
QY 996 SCITEQTYFFDNDKSFSGVLDCGNCGRIFHGEKLMNTNLIIFIMVESKGTCTCDTRL 1013
DB 996 SCITEQTYFFDNDKSFSGVLDCGNCGRIFHGEKLMNTNLIIFIMVESKGTCTCDTRL 1013

RESULT 8
US-08-223-305C-54
; Sequence 54, Application US/08223305C
; Patent No. 5851824
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
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SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA: US/08/223.305C
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868.354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745.206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620.250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482.384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603.751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176.899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 52516 (P519739)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 1086 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-223-305C-54

Query Match 99.3%; Score 5306.5; DB 2; Length 1086;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1013; Conservative 0; Mismatches 0; Gaps 1;
QY 1 MAAGCLLALTTLFQSLTIGPSSPEPPPSAVTIKSWVDKMQEDLVTLAKTAGSVNQLVDI 60
DB 1 MAAGCLLALTTLFQSLTIGPSSPEPPPSAVTIKSWVDKMQEDLVTLAKTAGSVNQLVDI 60
QY 61 YEKYQDLYTVEPNNAQVLEIAARDIEKLLSNRSLVSLALEAEKVQAAHQWREDFASN 120
DB 61 YEKYQDLYTVEPNNAQVLEIAARDIEKLLSNRSLVSLALEAEKVQAAHQWREDFASN 120
QY 121 EVVYNAKDDLPKNDSPGSGRQKPFIEDANFGROIYSQYHAAVHIPTDIYEGSTIVL 180
DB 121 EVVYNAKDDLPKNDSPGSGRQKPFIEDANFGROIYSQYHAAVHIPTDIYEGSTIVL 180
QY 181 NELNWTSADEYFKKNNREDPDLWQVFGSATGLARYYPASFPWVNSRTPNPKIDLYDVR 240
DB 181 NELNWTSADEYFKKNNREDPDLWQVFGSATGLARYYPASFPWVNSRTPNPKIDLYDVR 240
QY 241 RPWYIQGAASPKDMLILVDVSGVSLTLKLTIRTSYSEMLETLSDDDFNVASFNSNAQD 300
DB 241 RPWYIQGAASPKDMLILVDVSGVSLTLKLTIRTSYSEMLETLSDDDFNVASFNSNAQD 300
QY 301 VSCFHLVQANVRNKKVLKDVANNITAKITDYKKGFSFAFQQLLNYNVSRANCKNIIML 360
DB 301 VSCFHLVQANVRNKKVLKDVANNITAKITDYKKGFSFAFQQLLNYNVSRANCKNIIML 360
QY 361 FTDGGERAEQEIFNKYKDKVVRFFSVGQHNRYERGPQIOWMACENKGYIYEIPSGAIR 420

DB 361 FTDGGERAEQEIFNKYKDKVVRFFSVGQHNRYERGPQIOWMACENKGYIYEIPSGAIR 420
QY 421 INTOEYLDVLRPMVLAGDKAKOVQWNTNVYLDALGLVITGTLPVENITGQFENKTNLK 480
DB 421 INTOEYLDVLRPMVLAGDKAKOVQWNTNVYLDALGLVITGTLPVENITGQFENKTNLK 480
QY 481 NQLILGVMGVDVSLIEDIKRLTPREFTLCPNGYFFAIDPNGYVLLHPNLPKPKSQEPVTL 540
DB 481 NQLILGVMGVDVSLIEDIKRLTPREFTLCPNGYFFAIDPNGYVLLHPNLPKPKSQEPVTL 540
QY 541 DFLDAELENDIKVEIRNMKIDGESKTEFTFLVKSQDRIYDKGNRYITWTVPVNGTDSL 600
DB 541 DFLDAELENDIKVEIRNMKIDGESKTEFTFLVKSQDRIYDKGNRYITWTVPVNGTDSL 600
QY 595 DFLDAELENDIKVEIRNMKIDGESKTEFTFLVKSQDRIYDKGNRYITWTVPVNGTDSL 595
QY 601 ALVLPYTFYFYIKAKLEETITQARSKKGMKDSKTLKPDNFEESGYTTFIAPRDYCNLDKI 660
DB 596 ALVLPYTFYFYIKAKLEETITQARSKKGMKDSKTLKPDNFEESGYTTFIAPRDYCNLDKI 655
QY 661 SDNTEFLNFEFTDRKTPNPNPCNADLINRVLLDAGFTNELYQVYWSKQKNIKGVKAR 720
DB 656 SDNTEFLNFEFTDRKTPNPNPCNADLINRVLLDAGFTNELYQVYWSKQKNIKGVKAR 715
QY 721 FVTDGGITRVYPKEAGENWOENPETYEDSYKRSKLDNDNTVFTAPYFNKSGPGAYESGI 780
DB 716 FVTDGGITRVYPKEAGENWOENPETYEDSYKRSKLDNDNTVFTAPYFNKSGPGAYESGI 775
QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSNIENFTKTSIRDPCAGPVCCKRNSDVMDCVI 840
DB 776 MYSKAVEIYIOGKLLKPAVVGKIDVNSNIENFTKTSIRDPCAGPVCCKRNSDVMDCVI 835
QY 841 LDDGGFLMANHDDYTNOIGRFFGEIDPDLMRHLNIVSYAFNKSVDYQSVCEPGAAPKQ 900
DB 836 LDDGGFLMANHDDYTNOIGRFFGEIDPDLMRHLNIVSYAFNKSVDYQSVCEPGAAPKQ 895
QY 901 GAGHRSAYVPSVADILQIGWATAAANSILOQFLLSLFPLLEAVEMEDDDFTASLSKQ 960
DB 896 GAGHRSAYVPSVADILQIGWATAAANSILOQFLLSLFPLLEAVEMEDDDFTASLSKQ 955
QY 961 SCITEOTOYFFDNDKSPSGVLDGNCNCRIFHGEKLMNTNLIIFIMVESKGTGCPDTRL 1018
DB 956 SCITEOTOYFFDNDKSPSGVLDGNCNCRIFHGEKLMNTNLIIFIMVESKGTGCPDTRL 1013

RESULT 9
US-08-455-543A-56
; Sequence 56, Application US/08455543A
; Patent No. 5792846
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455.543A
; FILING DATE: May 31, 1995
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/223,305
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 1084 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: Internal
US-08-455-543A-56

Query Match 98.9%; Score 5289.5; DB 1; Length 1084;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1010; Conservative 0; Mismatches 1; Indels 7; Gaps 1;
QY 1 MAAGCLLALTTLFQSLILGPSEEPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
DDB 1 MAAGCLLALTTLFQSLILGPSEEPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
QY 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDFASN 120
DDB 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDFASN 120
QY 121 EYVYNAKDDLOPEKNDSEFGSQRIPKVEDANFORQISYQAAHVIPTDIYEGSTIVL 180
DDB 121 EYVYNAKDDLOPEKNDSEFGSQRIPKVEDANFORQISYQAAHVIPTDIYEGSTIVL 180
QY 181 NELNMTSALDEVEKKNREDDPSLLWQVFGSATGLARYYPASPWVDNSRTPNKIDLDYDVR 240
DDB 181 NELNMTSALDEVEKKNREDDPSLLWQVFGSATGLARYYPASPWVDNSRTPNKIDLDYDVR 240
QY 241 RPWYIQGAASPKDMLILVDVSGSVGLTKLINTSVSEMLETSLDDDFVNVASFNSNAQ 300
DDB 241 RPWYIQGAASPKDMLILVDVSGSVGLTKLINTSVSEMLETSLDDDFVNVASFNSNAQ 300
QY 301 VSCFQHLVQANRNKVKLVDAVNNITAKITDYKKGFSFAFEOQLLYNVSRANCKIIML 360
DDB 301 VSCFQHLVQANRNKVKLVDAVNNITAKITDYKKGFSFAFEOQLLYNVSRANCKIIML 360
QY 361 FTDGGERAQEITFNKYNKDKVYVFRFSYGOHNYERGPQIOWACENKGYIYEIPSTIGAIR 420
DDB 361 FTDGGERAQEITFNKYNKDKVYVFRFSYGOHNYERGPQIOWACENKGYIYEIPSTIGAIR 420

QY 421 INTQEYLDVLGRPMVLADGKAKQVQWNTNVYLDALGLVITGTLPVFNITGQFENKTNLK 480
DDB 421 INTQEYLDVLGRPMVLADGKAKQVQWNTNVYLDALGLVITGTLPVFNITGQFENKTNLK 480
QY 481 NQLILGVMGVDVSLDIKRLTPRETLCPNGYIFADPNGYVLLHPNLPKPKSQEPVTL 540
DDB 481 NQLILGVMGVDVSLDIKRLTPRETLCPNGYIFADPNGYVLLHPNLPKPKSQEPVTL 540
QY 541 DFLDAELENDIKVEIRNKMIDGESGKFTFTLVKSQDERYIDKGNRTYTTVPVNGTDYSL 600
DDB 541 DFLDAELENDIKVEIRNKMIDGESGKFTFTLVKSQDERYIDKGNRTYTTVPVNGTDYSL 600
QY 601 ALVLPYTSFYIIRAKLEETITQARKSKGKMDSETLPDMPFESGYTFIAPRDYCNLDKI 660
DDB 601 ALVLPYTSFYIIRAKLEETITQARKSKGKMDSETLPDMPFESGYTFIAPRDYCNLDKI 660
QY 661 SDNTEFLNFEFIDRKTNNPSCNADLNRLVLLDAGFTNELVQNYWSKOKNIKGVKAR 720
DDB 661 SDNTEFLNFEFIDRKTNNPSCNADLNRLVLLDAGFTNELVQNYWSKOKNIKGVKAR 720
QY 721 FVYTDGGITRVYKPEAGENQENPETYEDSFYKSLDNDNYVFTAPYFNKSGPGAYESGI 780
DDB 721 FVYTDGGITRVYKPEAGENQENPETYEDSFYKSLDNDNYVFTAPYFNKSGPGAYESGI 780
QY 781 MYSKAVEIYIOGKLLKPAVVGIIKIDVNSWIENFTKTSIRDPGAGVCDCKRNSDVMDCVI 840
DDB 781 MYSKAVEIYIOGKLLKPAVVGIIKIDVNSWIENFTKTSIRDPGAGVCDCKRNSDVMDCVI 840
QY 841 LDGGFLLMANHDDYTNQIGRFFGEIDPGLMRHLVNI SVYAFNKSIDYQSVCEPGAAPKQ 900
DDB 841 LDGGFLLMANHDDYTNQIGRFFGEIDPGLMRHLVNI SVYAFNKSIDYQSVCEPGAAPKQ 900
QY 901 GAGHSAYVPSVADILQIGWATAAASIIQQFLSLTFFPRLLEAVEMEDDDFTASLSKQ 960
DDB 901 GAGHSAYVPSVADILQIGWATAAASIIQQFLSLTFFPRLLEAVEMEDDDFTASLSKQ 960
QY 961 SCITEQTYFFDNDKSKFSFSGVLDCGNC SRIFHGEKLMNTNLIIFIMVESKGTCPDTRL 1018
DDB 961 SCITEQTYFFDNDKSKFSFSGVLDCGNC SRIFHGEKLMNTNLIIFIMVESKGTCPDTRL 1018
RESULT 10
US-08-223-305C-56
Sequence 56, Application US/08223305C
Patent No. 5851824
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/223,305C
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 52516 (P519739)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 1084 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-223-305C-56

Query Match 98.9%; Score 5289.5; DB 2; Length 1084;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1010; Conservative 0; Mismatches 1; Indels 7; Gaps 1;
Qy 1 MAAGCLLALTTLFQSLGSSPEPPSAVTIKSWDKMQEDLVTLAKTAGVGNQLVDI 60
Db 1 MAAGCLLALTTLFQSLGSSPEPPSAVTIKSWDKMQEDLVTLAKTAGVGNQLVDI 60
Qy 61 YEKYQDLYTVEPNARQLVEAARDIEKLLNSRKALYSLSALEAEKVQAAHQWREDFASN 120
Db 61 YEKYQDLYTVEPNARQLVEAARDIEKLLNSRKALYSLSALEAEKVQAAHQWREDFASN 120
Qy 121 EVVYVNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROIYSQHAHVHPTDIYEGSTIVL 180
Db 121 EVVYVNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROIYSQHAHVHPTDIYEGSTIVL 180
Qy 181 NELNWTSSALDEVFKKREEDPSLLMQVFGSATGLARYYPASPDWNSRTPNKIDLYDVR 240
Db 181 NELNWTSSALDEVFKKREEDPSLLMQVFGSATGLARYYPASPDWNSRTPNKIDLYDVR 240
Qy 241 RPWYTOGAASPKDMLILYDVSGVSGLTGLKIRTSVSEMLETSLDDDFVNVASFNSAQD 300
Db 241 RPWYTOGAASPKDMLILYDVSGVSGLTGLKIRTSVSEMLETSLDDDFVNVASFNSAQD 300
Qy 301 VSCFOHLVQANVRNKKLVKDAVNNTAKGIDYKKGFSFAPEQLLNYNVSRANCNKIIML 360
Db 301 VSCFOHLVQANVRNKKLVKDAVNNTAKGIDYKKGFSFAPEQLLNYNVSRANCNKIIML 360
Qy 361 FTDGGEERAQEIFNKYNKDKKVRFRFVSQGHNYERGIQWMACENKGYVEIPSIGAIR 420
Db 361 FTDGGEERAQEIFNKYNKDKKVRFRFVSQGHNYERGIQWMACENKGYVEIPSIGAIR 420
Qy 421 INTQEYLDVLRPMVLADKAKQVQWNTNYLDALGLGLVITGLPVFNITGOFENKTNLK 480
Db 421 INTQEYLDVLRPMVLADKAKQVQWNTNYLDALGLGLVITGLPVFNITGOFENKTNLK 480
Qy 481 NQLILGVMGVDVSLSDIKRLTPFTLCPNGYVFAIDPNGYVLLHPNLPKPKSQEPVTL 540

Db 481 NQLILGVMGVDVSLSDIKRLTPFTLCPNGYVFAIDPNGYVLLHPNLPKPKSQEPVTL 540
Qy 541 DFLDAELENDIKVEIRNKMIDGESGKTFRTLVKSQDERYIDKGNRTYTWTPVNGTDSL 600
Db 541 DFLDAELENDIKVEIRNKMIDGESGKTFRTLVKSQDERYIDKGNRTYTWTPVNGTDSL 600
Qy 601 ALVLPYTSFYIIRAKLEETITQARSKKGMKDSITLAKPDNFEESGYTFIAPRDYCNLDKI 660
Db 601 ALVLPYTSFYIIRAKLEETITQARSKKGMKDSITLAKPDNFEESGYTFIAPRDYCNLDKI 660
Qy 661 SDNNTTEFLNFEIDRKTNNPCNADLINRVLLDAGFTNELYONYWSKOKNIKGVKAR 720
Db 661 SDNNTTEFLNFEIDRKTNNPCNADLINRVLLDAGFTNELYONYWSKOKNIKGVKAR 720
Qy 721 FVYTDGGITRVYPKEAGENWQENETEDSYKBSLNDNDNYFTAPYENKSGPGAYESGI 780
Db 721 FVYTDGGITRVYPKEAGENWQENETEDSYKBSLNDNDNYFTAPYENKSGPGAYESGI 780
Qy 781 MYSKAVEIYIQGKLLKPAVVGIKIDVANSWIENFTKTSIRDPCAGPVCDCRNSDVMDCVI 840
Db 781 MYSKAVEIYIQGKLLKPAVVGIKIDVANSWIENFTKTSIRDPCAGPVCDCRNSDVMDCVI 840
Qy 841 LDGGLFLMANHDDYTNOIGRFFGEIDPDLMRHLVNSVYAFNKSVDYQSVCEPGAAPKQ 900
Db 841 LDGGLFLMANHDDYTNOIGRFFGEIDPDLMRHLVNSVYAFNKSVDYQSVCEPGAAPKQ 900
Qy 901 GAGHRSAYVPSVADILQIGWATAAANSILOOFLLSLTPRLLAEVEMEDDDFTASLSKQ 960
Db 901 GAGHRSAYVPSVADILQIGWATAAANSILOOFLLSLTPRLLAEVEMEDDDFTASLSKQ 960
Qy 961 SCITEQTYQFFDNDKSPSGVLDGCGNCSRIEFGHEKLMNTNLIIFIMVESKGTCPDTRL 1018
Db 961 SCITEQTYQFFDNDKSPSGVLDGCGNCSRIEFGHEKLMNTNLIIFIMVESKGTCPDTRL 1018
Qy 994 SCITEQTYQFFDNDKSPSGVLDGCGNCSRIEFGHEKLMNTNLIIFIMVESKGTCPDTRL 1011
Db 994 SCITEQTYQFFDNDKSPSGVLDGCGNCSRIEFGHEKLMNTNLIIFIMVESKGTCPDTRL 1011

RESULT 11
US-08-455-543A-53
Sequence 53, Application US/08455543A
Patent No. 5792846
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,543A
FILING DATE: May 31, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206

;; FILING DATE: 15-AUG-1991
;; PRIORITY APPLICATION DATA: US 07/620,250
;; FILING DATE: 30-NOV-1990
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US 07/482,384
;; FILING DATE: 20-FEB-1990
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US 07/603,751
;; FILING DATE: 04-APR-1989
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/US89/01408
;; FILING DATE: 04-APR-1989
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US 07/176,899
;; FILING DATE: 04-APR-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Seidman, Stephanie L.
;; REGISTRATION NUMBER: 33,779
;; REFERENCE/DOCKET NUMBER: 6362-52517
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619)238-0999
;; TELEFAX: (619)238-0062
;; INFORMATION FOR SEQ ID NO: 53:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1103 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; FRAGMENT TYPE: internal
US-08-455-543A-53

Query Match 98.6%; Score 5270; DB 1; Length 1103;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 1010; Conservative 0; Mismatches 1; Indels 26; Gaps 2;

QY	1	MAAGCLLALTTLFOSLLIGSPSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI	60
DB	1	MAAGCLLALTTLFOSLLIGSPSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI	60
QY	61	YEKYODLYTVEPNARQLVETAAARDIEKLLNSRKALVSLALEAEKVQAAHQWREDFASN	120
DB	61	YEKYODLYTVEPNARQLVETAAARDIEKLLNSRKALVSLALEAEKVQAAHQWREDFASN	120
QY	121	EVVYNKADDDLPKNDSEPGSQRIKPVFIEDANFGROISYQHAHVHTDIYEGSTIVL	180
DB	121	EVVYNKADDDLPKNDSEPGSQRIKPVFIEDANFGROISYQHAHVHTDIYEGSTIVL	180
QY	181	NELNWTSLADVEFKKNEEDPSLLWQVFGSATGLARYTPASFWVDNSRTPNKKIDLYDVR	240
DB	181	NELNWTSLADVEFKKNEEDPSLLWQVFGSATGLARYTPASFWVDNSRTPNKKIDLYDVR	240
QY	241	RPWYIQGAASPKDMLLVDSVSGVSLTKLIRTSVSEMLETSLDDDFVNVASNSNAQD	300
DB	241	RPWYIQGAASPKDMLLVDSVSGVSLTKLIRTSVSEMLETSLDDDFVNVASNSNAQD	300
QY	301	VSCFQHLVQANVRNKVLDKAVNNITAKGIDYKKGFSFAFEQLLNVSRANCKIIML	360
DB	301	VSCFQHLVQANVRNKVLDKAVNNITAKGIDYKKGFSFAFEQLLNVSRANCKIIML	360
QY	361	FTDGEERAQEIFNKYKDKKVRFRSVGQHNTYERGPIONMACENKGYEIPISGAIR	420
DB	361	FTDGEERAQEIFNKYKDKKVRFRSVGQHNTYERGPIONMACENKGYEIPISGAIR	420
QY	421	INTQYLDVLGRPVLAGDKAKQVQWNTVLDLLEGLVITGTLPVNTIQPFENKTLK	480
DB	421	INTQYLDVLGRPVLAGDKAKQVQWNTVLDLLEGLVITGTLPVNTIQPFENKTLK	480
QY	481	NQLILGVGVDSVLEDKRLTPRTLCNPGYFAIDPNGVYLLHPNLPK-----	530
DB	481	NQLILGVGVDSVLEDKRLTPRTLCNPGYFAIDPNGVYLLHPNLPKPIGVGIPTIN	540

QY	531	-----NPKSQEPVTLDFDLAELENDIKVEIRNKMIDGESGEKTFRTLVKSQDERYI	581
DB	541	LRKRPNIQPKSQEPVTLDFDLAELENDIKVEIRNKMIDGESGEKTFRTLVKSQDERYI	600
QY	582	DGNRTYTWTPVNGTDYSLALVLPYTSFYIKAKLEETITQARSKGKMKDSETLKPDNF	641
DB	601	DGNRTYTWTPVNGTDYSLALVLPYTSFYIKAKLEETITQARY-----SETLKPDNF	653
QY	642	EESGYTFIAPRDYCNLDKISDNTEFLNNEFIDRTKTPNNPSCNADLINRVLDAGFTN	701
DB	654	EESGYTFIAPRDYCNLDKISDNTEFLNNEFIDRTKTPNNPSCNADLINRVLDAGFTN	713
QY	702	ELVQNYWSKQKNIKGVKARFVTDGGITRVYPKEAGENMOENPETEYEDSYKSLDNDNY	761
DB	714	ELVQNYWSKQKNIKGVKARFVTDGGITRVYPKEAGENMOENPETEYEDSYKSLDNDNY	773
QY	762	VFTAPYFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKTSIRDP	821
DB	774	VFTAPYFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKTSIRDP	833
QY	822	CAGPVCDCCKRNSDVMDCVILDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNISVYA	881
DB	834	CAGPVCDCCKRNSDVMDCVILDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNISVYA	893
QY	882	FNKSYDYQSVCEPGAAPKOGAGHRSAYVPSVADILQIGMWATAAASILQOFLLSLTFPR	941
DB	894	FNKSYDYQSVCEPGAAPKOGAGHRSAYVPSVADILQIGMWATAAASILQOFLLSLTFPR	953
QY	942	LLEAVEMEDDDFTASLSKQSCITEQTQYFFDNDKSFSGVLDGCGNCSRIIPHGEKLMNTNL	1001
DB	954	LLEAVEMEDDDFTASLSKQSCITEQTQYFFDNDKSFSGVLDGCGNCSRIIPHGEKLMNTNL	1013
QY	1002	IFIMVESKGTCPDTRL 1018	
DB	1014	IFIMVESKGTCPDTRL 1030	

RESULT 12
US-08-223-305C-53
; Sequence 53, Application US/08223305C
; Patent No. 5851824
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/223,305C
; FILING DATE: April 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 52516 (P519739)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1103 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-223-305C-53

Query Match 98.6%; Score 5270; DB 2; Length 1103;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 1010; Conservative 0; Mismatches 1; Indels 26; Gaps 2;

QY 1 MAAGCLLALTTLFOSLLIGPSSEPPFSAVTIKSWDKMOEDLVTLAKTAGVNLVDI 60
DB 1 MAAGCLLALTTLFOSLLIGPSSEPPFSAVTIKSWDKMOEDLVTLAKTAGVNLVDI 60
QY 61 YEKYQDLTYVEPNNAQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHWRDFA 120
DB 61 YEKYQDLTYVEPNNAQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHWRDFA 120
QY 121 EYVYNAKDDLPENKNDSPGSGRIKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180
DB 121 EYVYNAKDDLPENKNDSPGSGRIKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180
QY 181 NELNWTSAALDEYFKKNREDDPSLLAQVFGSATGLARYYPASPDVNSRTPNKIDLYDVR 240
DB 181 NELNWTSAALDEYFKKNREDDPSLLAQVFGSATGLARYYPASPDVNSRTPNKIDLYDVR 240
QY 241 RPWYIQAASPKDMLTILVDVSGVSGLTILKLRISVSEMLETSLDDDFVNVASFNSNAQD 300
DB 241 RPWYIQAASPKDMLTILVDVSGVSGLTILKLRISVSEMLETSLDDDFVNVASFNSNAQD 300
QY 301 VSCFOHLVQANVRNKKVLKDVANNITAKGITYKGFSEFAPQLLNYNVSRANCKNIIML 360
DB 301 VSCFOHLVQANVRNKKVLKDVANNITAKGITYKGFSEFAPQLLNYNVSRANCKNIIML 360
QY 361 FTDGGEERAQELFNKYNKDKKVRVRFVSGQHYERGPQWACENKGYEYIPIGSAIR 420
DB 361 FTDGGEERAQELFNKYNKDKKVRVRFVSGQHYERGPQWACENKGYEYIPIGSAIR 420
QY 421 INTQEYLDVLRGPMVLGDKAKQVQWNTVYLDALGLVITGLPVFNITGQFENKTNLK 480
DB 421 INTQEYLDVLRGPMVLGDKAKQVQWNTVYLDALGLVITGLPVFNITGQFENKTNLK 480
QY 481 NQILGVMGVDVSLIEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHPNLQPK----- 530
DB 481 NQILGVMGVDVSLIEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHPNLQPKPIGVGPTIN 540

QY 531 -----NPKSQEPVTLDFLDAELENDIKVEIRNKMIDGESGEKTFRTLKVSQDERYI 581
DB 541 LRKRPNIQPKSQEPVTLDFLDAELENDIKVEIRNKMIDGESGEKTFRTLKVSQDERYI 600
QY 582 DGNRTYTTPVNGTDYSLALVLTPTYSFYIKAKLEETITQARSKGKMKDSETLKPDNF 641
DB 601 DGNRTYTTPVNGTDYSLALVLTPTYSFYIKAKLEETITQARSKGKMKDSETLKPDNF 653
QY 642 EESGYTFIAPRDYCNLDKISDNNTFLLNFEFIDRKTTPNPNPCNADLINRVLLDAGFTN 701
DB 654 EESGYTFIAPRDYCNLDKISDNNTFLLNFEFIDRKTTPNPNPCNADLINRVLLDAGFTN 713
QY 702 ELVQYWSKQKNIKGVKARFVYVTDGTRVYVYKAGENQWENPETYEDSFYKRSLDNDNY 761
DB 714 ELVQYWSKQKNIKGVKARFVYVTDGTRVYVYKAGENQWENPETYEDSFYKRSLDNDNY 773
QY 762 VFTAPYFNKSGPAYESGIMVSKAVEIYIQGLLKPVAVGKIDVNSWNIENFTTSIRDP 821
DB 774 VFTAPYFNKSGPAYESGIMVSKAVEIYIQGLLKPVAVGKIDVNSWNIENFTTSIRDP 833
QY 822 CAGPVCDCRNSDVMDCVILDDGGFLLMANHDDVTNIGRFFGEIDPSLMRHLNYSIYA 881
DB 834 CAGPVCDCRNSDVMDCVILDDGGFLLMANHDDVTNIGRFFGEIDPSLMRHLNYSIYA 893
QY 882 FNKSYDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAAWSILOQFLLSLTTPR 941
DB 894 FNKSYDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAAWSILOQFLLSLTTPR 953
QY 942 LLEAVEMEDDDFTASLSKQSCITEQTQYFFDNDKSFSGVLDGNCGRIFHGEKLMNTNL 1001
DB 954 LLEAVEMEDDDFTASLSKQSCITEQTQYFFDNDKSFSGVLDGNCGRIFHGEKLMNTNL 1013
QY 1002 IFIMVESKGTCPCDTRL 1018
DB 1014 IFIMVESKGTCPCDTRL 1030
RESULT 13
US-08-455-543A-55
; Sequence 55: Application US/08455543A
; Patent No. 5792846
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08455543A
; FILING DATE: May 31, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/223,305
; FILING DATE: April 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seigman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 1079 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
FRAGMENT TYPE: Internal
US-08-455-543A-55

Query Match 98.2%; Score 5250; DB 1; Length 1079;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1005; Conservative 0; Mismatches 1; Indels 12; Gaps 2;

Qy	1	MAAGCLLATLTFLQSLIGSSSEPPFSAVTIKSWDKMQEDLVTLAKTAGVGNQLVDI	60
Db	1	MAAGCLLATLTFLQSLIGSSSEPPFSAVTIKSWDKMQEDLVTLAKTAGVGNQLVDI	60
Qy	61	YEKQDLYTVEPNARQLVETAAARDIEKLLNSRKALVSLALEAEKVQAAHQWREDFASN	120
Db	61	YEKQDLYTVEPNARQLVETAAARDIEKLLNSRKALVSLALEAEKVQAAHQWREDFASN	120
Qy	121	EWYVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIYSQHAHVHPTDIYEGSTIVL	180
Db	121	EWYVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIYSQHAHVHPTDIYEGSTIVL	180
Qy	181	NELNWTSALEDFVKKNRDEPSLLQWFGSATGLARYPASPVDNSTRPNKIDLYVRR	240
Db	181	NELNWTSALEDFVKKNRDEPSLLQWFGSATGLARYPASPVDNSTRPNKIDLYVRR	240
Qy	241	RPWTIOGAASPKMDILVDVSSVSGTLKLRISVSEMLETSLDDDFVNVASNSNAQD	300
Db	241	RPWTIOGAASPKMDILVDVSSVSGTLKLRISVSEMLETSLDDDFVNVASNSNAQD	300
Qy	301	VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQQLINYNVSRANCKIIML	360
Db	301	VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQQLINYNVSRANCKIIML	360
Qy	361	FTDGEERAQEIFKNYKDKKVRFRFSVGOHNTYERGPIONMACKNGYYEIPSIGAIR	420
Db	361	FTDGEERAQEIFKNYKDKKVRFRFSVGOHNTYERGPIONMACKNGYYEIPSIGAIR	420
Qy	421	INTQYLDVLGRPWLADGKAKQVQWNVYLDLELGLVITGLTPVFNITQGFENKTLK	480
Db	421	INTQYLDVLGRPWLADGKAKQVQWNVYLDLELGLVITGLTPVFNITQGFENKTLK	480
Qy	481	NQLILGVNGVDVSLDKRLTPRFTLCPNGYYFAIDPNGYVLLHPNLQPKNSQEPVTL	540
Db			

Db	481	NQLILGVNGVDVSLDKRLTPRFTLCPNGYYFAIDPNGYVLLHPNLQPKNSQEPVTL	535
Qy	541	DFLDAELENDIKVEIRNKNMIDGESGEKTRTLVKSDERYIDKGNRTYTWTPVNGTDYSL	600
Db	536	DFLDAELENDIKVEIRNKNMIDGESGEKTRTLVKSDERYIDKGNRTYTWTPVNGTDYSL	595
Qy	601	ALVLTYSFYIYKAKLEETITQARSKKGMKDSKSEILKPDNPFESGYTFIAPRDYCNLDKI	660
Db	596	ALVLTYSFYIYKAKLEETITQARSKKGMKDSKSEILKPDNPFESGYTFIAPRDYCNLDKI	648
Qy	661	SDNTEFLNFEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVQNYWSKQNIKGVKAR	720
Db	649	SDNTEFLNFEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVQNYWSKQNIKGVKAR	708
Qy	721	FVVDGGITRVYPKEAGENWQENPETYEDSFYKRLDNDNVYFTAPYFNKSGPGAYESGI	780
Db	709	FVVDGGITRVYPKEAGENWQENPETYEDSFYKRLDNDNVYFTAPYFNKSGPGAYESGI	768
Qy	781	MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIEFTKTSIRDPGAGPVCDCRNSDYMDCVI	840
Db	769	MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIEFTKTSIRDPGAGPVCDCRNSDYMDCVI	828
Qy	841	LDDGGFLLMANHDDYTNOIGREFGEIDPSLMRHLVNI SVYAFNKSYDQSVCEPGAAPKQ	900
Db	829	LDDGGFLLMANHDDYTNOIGREFGEIDPSLMRHLVNI SVYAFNKSYDQSVCEPGAAPKQ	888
Qy	901	GAGHSAYVPSVADILQIGMWATAAAWSILOQFLSLTFPRLEAVEDEDDFTASLSKQ	960
Db	889	GAGHSAYVPSVADILQIGMWATAAAWSILOQFLSLTFPRLEAVEDEDDFTASLSKQ	948
Qy	961	SCITEQTOYFFDNDKSPSGVLDGCGNCSRIHFHGEKLMNTNLIFIMVESKGTCPDTRL	1018
Db	949	SCITEQTOYFFDNDKSPSGVLDGCGNCSRIHFHGEKLMNTNLIFIMVESKGTCPDTRL	1006

RESULT 14
US-08-223-305C-55
Sequence 55, Application US/082233305C
Patent No. 5851824
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/223,305C
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 52516 (P519739)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0099
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1079 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-223-305C-55

Query Match 98.2%; Score 5250; DB 2; Length 1079;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1005; Conservative 0; Mismatches 1; Indels 12; Gaps 2;
QY 1 MAAGCLLALTTLFOSLLIGPSSEPPFSAVITKSWDKQEDLVTLAKTAGSVNQLVDI 60
Db 1 MAAGCLLALTTLFOSLLIGPSSEPPFSAVITKSWDKQEDLVTLAKTAGSVNQLVDI 60
QY 61 YEKYQDLTYVEPNNAQRLVEIARIEKLLSNRSKALYSLEAEKVAQAQWREDFASN 120
Db 61 YEKYQDLTYVEPNNAQRLVEIARIEKLLSNRSKALYSLEAEKVAQAQWREDFASN 120
QY 121 EYVYNAKDDLDPEKNDSEPGSQRKPFVIEDANFGROISYQHAHVHTDIYEGSTIVL 180
Db 121 EYVYNAKDDLDPEKNDSEPGSQRKPFVIEDANFGROISYQHAHVHTDIYEGSTIVL 180
QY 181 NELNWTSSALDEVFKKNREEDPSLLWQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240
Db 181 NELNWTSSALDEVFKKNREEDPSLLWQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240
QY 241 RPWYTOGAASPKDMLILVDVSGSVGLTKLIRTSYSEMLETSLDDDFVNVASFNSAQD 300
Db 241 RPWYTOGAASPKDMLILVDVSGSVGLTKLIRTSYSEMLETSLDDDFVNVASFNSAQD 300
QY 301 VSCFOHLVQANVRNKKVLKADAVNNITAGKITDYKGFSPAFEPOLLNLYNVRANCNKIIML 360
Db 301 VSCFOHLVQANVRNKKVLKADAVNNITAGKITDYKGFSPAFEPOLLNLYNVRANCNKIIML 360
QY 361 FTDGGEERAQEIFKNYKDKKVRFRFSYQGHNYERGPQIOWMACENKGYEYIPSGAIR 420
Db 361 FTDGGEERAQEIFKNYKDKKVRFRFSYQGHNYERGPQIOWMACENKGYEYIPSGAIR 420
QY 421 INTQEYLDVLRPMVLGADKAKQVQWNTYLDALGLVITGTLVPFNITGQFENKTNLK 480
Db 421 INTQEYLDVLRPMVLGADKAKQVQWNTYLDALGLVITGTLVPFNITGQFENKTNLK 480
QY 481 NQILGVMGVDVSLIEDIKRLTFRFTLCPNGYFAIDPNGYVLLHNPLOPKNPKSOEPTVL 540
Db 481 NQILGVMGVDVSLIEDIKRLTFRFTLCPNGYFAIDPNGYVLLHNPLOPKNPKSOEPTVL 540
QY 541 DFLDAELENDIKVEIRNKMIDGESGKFTRLVKSQDERYIDKGNRTYTWTPVNGTDSL 600
Db 536 DFLDAELENDIKVEIRNKMIDGESGKFTRLVKSQDERYIDKGNRTYTWTPVNGTDSL 595

RESULT 15
US-08-435-675B-5
; Sequence 5, Application US/08435675B
; Patent No. 5710250
; GENERAL INFORMATION:
; APPLICANT: Ellis, Steven Bradley
; APPLICANT: Williams, Mark E.
; APPLICANT: Harpold, Michael Miller
; APPLICANT: Schwartz, Arnold
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,675B
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,083
; FILING DATE: 28-SEP-1994
; APPLICATION NUMBER: US 07/914,231
; FILING DATE: 13-JUL-1992
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 08-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-53193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:

INFORMATION FOR SBO ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1106 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-435-675B-5

Query Match 96.1%; Score 5137.5; DB 1; Length 1106;
Best Local Similarity 94.8%; Pred. No. 0;
Matches 986; Conservative 13; Mismatches 12; Indels 29; Gaps 4;

QY	1	MAAGCLLALTLTQFS--LLIGSSSEPPFSAVITKSWDKMDEDLVTLAKTAGVGNOLV	58
Db	1	MAAGRPLAWTLTLQAWLILIGSSSEPPFSAVITKSWDKMDEDLVTLAKTAGVGNOLV	60
QY	59	DIYEKYODLVTPNNARQLVEAARDIEKLLNSRKALYSALAEKVAQAHHQWREDF	118
Db	61	DIYEKYODLVTPNNARQLVEAARDIEKLLNSRKALYRLALEAEKVAQAHHQWREDF	120
QY	119	SNEVYINAKDDLDPEKNDSEPGSQRIKPVFIEDANFGQISYQHAHAVHIPTDIYEGSTI	178
Db	121	SNEVYINAKDDLDPEKNDSEPGSQRIKPVFIEDANFRQVSYQHAHAVHIPTDIYEGSTI	180
QY	179	VLNELNWTSSALDEVFKNREEDPSLWQVFGSATGLARYYPASFWVDNSRTPNKKIDLYD	238
Db	181	VLNELNWTSSALDDVFKNREEDPSLWQVFGSATGLARYYPASFWVDNSRTPNKKIDLYD	240
QY	239	RRRPWTIQGAASPKDMLILVDVSGVSGTLKLRISVSEMLETLSDDDDFNVASFNSA	298
Db	241	RRRPWTIQGAASPKDMLILVDVSGVSGTLKLRISVSEMLETLSDDDDFNVASFNSA	300
QY	299	QDYSCFOHLVQANVRNKKVLLKDAVNNTAKGIDYKKGFSFAFEQLNLYNVSFRANCKII	358
Db	301	QDYSCFOHLVQANVRNKKVLLKDAVNNTAKGIDYKKGFSFAFEQLNLYNVSFRANCKII	360
QY	359	MLFTDGEERAQEIFNKNKDKKRVFRFSVGHQHYERGIQWACENKGYEYIPEISGA	418
Db	361	MLFTDGEERAQEIFAKYNNKDKKRVFTSVGQHYDRGPIQWACENKGYEYIPEISGA	420
QY	419	IRINTOEYLDVLRPMVLADGKAKQVQWNTNYLDALGLVITGTLVPFNITGQFENKTN	478
Db	421	IRINTOEYLDVLRPMVLADGKAKQVQWNTNYLDALGLVITGTLVPFNITGQFENKTN	480
QY	479	LKNQLILGVMGVDVSLIEDIKRLTPRTLCPNGYFFAIDPNGYVLLHPNLQPK-----	530
Db	481	LKNQLILGVMGVDVSLIEDIKRLTPRTLCPNGYFFAIDPNGYVLLHPNLQPKIGVGIPT	540
QY	531	-----NPKSQEPVTLDFDAELENDIKVEIRNKNMIDGESGEKTPRTLKVSQDER	579
Db	541	INLKRKRRPNVQNPKSPQEPVTLDFDAELENDIKVEIRNKNMIDGESGEKTPRTLKVSQDER	600
QY	580	YIDKGNRTYTWTPVNGTDY-SLALVLPYTSFYIKAKLETITQARSKKGMKDSQTLKP	638
Db	601	YIDKGNRTYTWTPVNGTDYSSALVLPYTSFYIKAKIETITQARY-----SETLKP	653
QY	639	DNPEESGYTFIAPRDYCNDLKISDNNTEFLNENFIDRKTNNPNSCNADLINRVLLDAG	698
Db	654	DNPEESGYTFIAPRDYCSDLKPSDNNTEFLNENFIDRKTNNPNSCNTDLINRVLLDAG	713
QY	699	FTNELVQNTWSKQKNIKGKARFVVDGGITRVYPKEAGENWQENPETYBDSFYKRSLDN	758
Db	714	FTNELVQNTWSKQKNIKGKARFVVDGGITRVYPKEAGENWQENPETYBDSFYKRSLDN	773
QY	759	DNVYFTAPYFNKSGPAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSI	818
Db	774	DNVYFTAPYFNKSGPAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSI	833
QY	819	RDPACGVPDCKRNSDVMDCVILDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNIS	878

Db	834	RDPACGVPDCKRNSDVMDCVILDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNIS	893
QY	879	VYAFNKSYDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAAWSILOQFLLSLT	938
Db	894	VYAFNKSYDYQSVCEPGAAPKQAGHRSAYVPSIADILQIGWATAAAWSILOQFLLSLT	953
QY	939	FPRLLAEVEMEDDDFTASLSKQSCITEQTQYFFONDSSKFSFVLDCCGNCSTRIFHGEKLMN	998
Db	954	FPRLLAEADMEDDDFTASMSKQSCITEQTQYFFONDSSKFSFVLDCCGNCSTRIFHGEKLMN	1013
QY	999	TNLIFIMVESKGTCPCDTRL	1018
Db	1014	TNLIFIMVESKGTCPCDTRL	1033

Search completed: July 23, 2001, 07:38:46
Job time: 513 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 23, 2001, 07:37:40 ; Search time 84.28 Seconds

(without alignments)
920.096 Million cell updates/sec

Title: US-09-397-548-15

Perfect score: 5346

Sequence: 1 MAAGCLLALTTLFQSLIG.....TNLIFMVESKTCPCDRL 1018

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_68.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	5346	100.0	1091	2 JH0565	calcium channel al
2	5145	96.2	1091	2 A44147	calcium channel pr
3	5132.5	96.0	1106	1 CHR9A2	calcium channel al
4	1085	20.3	1091	2 T30256	calcium channel al
5	607	11.4	734	2 S44617	C50C3.11 protein -
6	569.5	10.7	1148	2 T18770	probable calcium c
7	198	3.7	1450	2 C86880	hypothetical prote
8	194.5	3.6	886	2 S54355	inter-alpha-trypsi
9	185	3.5	885	2 S30350	inter-alpha-trypsi
10	164.5	3.1	889	2 JC5576	inter-alpha-trypsi
11	161	3.0	2706	2 T28155	variant-specific s
12	159	3.0	1984	2 A44396	p-type cation tran
13	157.5	2.9	575	2 D64998	hypothetical prote
14	155	2.9	1516	2 E71619	RAD2 endonuclease
15	155	2.9	2364	2 L40884	cytotoxin L - Clos
16	154.5	2.9	946	1 LVHU2	inter-alpha-trypsi
17	154.5	2.9	1315	2 T28679	fibrinogen-binding
18	153	2.9	932	2 JC5953	inter-alpha-inhibi
19	152	2.8	1291	2 S46431	botulinum neurotox
20	152	2.8	1291	2 A49777	botulinum neurotox
21	151.5	2.8	420	2 S76691	hypothetical prote
22	150.5	2.8	921	2 JC4625	inter-alpha-trypsi
23	150	2.8	654	2 A69656	methyl-accepting c
24	149	2.8	459	2 F64688	proteinase [EC 3.4
25	149	2.8	930	2 JX0368	inter-alpha-trypsi
26	148.5	2.8	2401	2 T28676	rhodopy protein -
27	148	2.8	964	2 S25855	DNA-directed DNA p
28	146.5	2.7	1285	2 B72430	hypothetical prote
29	146	2.7	4688	2 F82885	hypothetical prote

ALIGNMENTS

RESULT 1

JH0565

calcium channel alpha-2b chain precursor - human

C:Species: Homo sapiens (man)

C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug-1999

C:Accession: JH0565

R:Williams, M.E.; Feldman, D.H.; McCue, A.F.; Brenner, R.; Velicelebi, G.; Ellis, S.B. Neuron 8, 71-84, 1992

A:Title: Structure and functional expression of alpha1, alpha2, and beta subunits of A:Reference number: JH0564; MUID:92110010

A:Accession: JH0565

A:Molecule type: mRNA

A:Residues: 1-1091 <WIL>

A:Cross-references: GB:M76559; NID:g179761; PIDN:AAA51903.1; PID:g179762

A:Experimental source: basal ganglia

A:Note: Several conflicts are found between GenBank submission, authors' translation C:Comment: This protein is a subunit of the voltage dependent calcium channel.

C:Superfamily: calcium channel alpha-2 chain

C:Keywords: glycoprotein; phosphoprotein

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-1067/Product: calcium channel alpha-2b chain status predicted <CAL>

F:32,268,326,339,535,1087/Binding site: phosphate (Thr) (covalent) (by protein kinase F:91,142,250,625,817/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #

F:92,136,184,324,348,468,475,585,594,663,682,769,812,876,883,973,986/Binding site: ca F:501/Binding site: phosphate (Thr) (covalent) #status predicted

F:833/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status pre

Query Match 100.0%; Score 5346; DB 2; Length 1091;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAAGCLLALTTLFQSLIGPSSEPPFSAVTIKSWDKMQEDLVTLAKTAGVNLVDI 60

Db 1 MAAGCLLALTTLFQSLIGPSSEPPFSAVTIKSWDKMQEDLVTLAKTAGVNLVDI 60

Qy 61 YEKYODLYTVPNNARQIVETAAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120

Db 61 YEKYODLYTVPNNARQIVETAAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120

Qy 121 EYVYNNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRLISYQHAHVHTPTDIYEGSTVL 180

Db 121 EYVYNNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRLISYQHAHVHTPTDIYEGSTVL 180

Qy 181 NELNWTSALEDVFKKNREDDPSLLMQVFGSATGLARYYPASFPWVDSNRTPNKNIDLYDVR 240

Db 181 NELNWTSALEDVFKKNREDDPSLLMQVFGSATGLARYYPASFPWVDSNRTPNKNIDLYDVR 240

Qy 241 RPWYIQGAASPKDMLILVDVSGSVSGLTKLIRTSVSEMLEFTLSDDDFVNVASFNSNAQD 300

Db 241 RPWYIQGAASPKDMLILVDVSGSVSGLTKLIRTSVSEMLEFTLSDDDFVNVASFNSNAQD 300

QY 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGIDTYKKGFSAFEPQLLNINVSFRANCNKIIML 360
DB 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGIDTYKKGFSAFEPQLLNINVSFRANCNKIIML 360
QY 361 FTDGGEERAQEIFNKYNKDKKVRVFRFSGVGHNYERGPFIQWACENKGYIYEIPSIGAIR 420
DB 361 FTDGGEERAQEIFNKYNKDKKVRVFRFSGVGHNYERGPFIQWACENKGYIYEIPSIGAIR 420
QY 421 INTQEYLDVGRPMVLGADKAKOVQWNTNYLDALBGLVITGTLVPFNITGQFENKTNLK 480
DB 421 INTQEYLDVGRPMVLGADKAKOVQWNTNYLDALBGLVITGTLVPFNITGQFENKTNLK 480
QY 481 NOLILGVMGVDVSLIEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHNPLOKPKKSOEPTVL 540
DB 481 NOLILGVMGVDVSLIEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHNPLOKPKKSOEPTVL 540
QY 541 DFLDAELENDDIKVEIRNKMIDGESGKFTLTKVKSQDERTLVPVNGTDYSL 600
DB 541 DFLDAELENDDIKVEIRNKMIDGESGKFTLTKVKSQDERTLVPVNGTDYSL 600
QY 601 ALVLPITYSFYIIKAKLEETITQARSKKGMKDSSETLKPDPNFEEGYTFIAPRDYCNDLKI 660
DB 601 ALVLPITYSFYIIKAKLEETITQARSKKGMKDSSETLKPDPNFEEGYTFIAPRDYCNDLKI 660
QY 661 SDNTEFLNFEFIDRKTTPNPNPCNADLINRVLLDAGFTNVLVQNSKQKNIKGVKAR 720
DB 661 SDNTEFLNFEFIDRKTTPNPNPCNADLINRVLLDAGFTNVLVQNSKQKNIKGVKAR 720
QY 721 FVVTGGITRVYPKEAGENWQENPETEYDSFYKRSLDNDNVTFTAPYFNKSGPGAYESGI 780
DB 721 FVVTGGITRVYPKEAGENWQENPETEYDSFYKRSLDNDNVTFTAPYFNKSGPGAYESGI 780
QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSHNIENFTKTSIRDPKAGVPCDCKRNSDVMDCVI 840
DB 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSHNIENFTKTSIRDPKAGVPCDCKRNSDVMDCVI 840
QY 841 LDGGEFLMANHDDVTNQIGRFFGEIDPMSLRHLNINISYAFNKSVDYQSVCEPGAAPKQ 900
DB 841 LDGGEFLMANHDDVTNQIGRFFGEIDPMSLRHLNINISYAFNKSVDYQSVCEPGAAPKQ 900
QY 901 GAGHSAYVPSVADILQIGWATAAAMSILQOFLSLTPRLLLEAEMEDDDFTASLSKQ 960
DB 901 GAGHSAYVPSVADILQIGWATAAAMSILQOFLSLTPRLLLEAEMEDDDFTASLSKQ 960
QY 961 SCITEQTOFFNDKSKFSGLVDCGNCISIFHGEKLMNTNLIIFIMVESKGTCPDCTRL 1018
DB 961 SCITEQTOFFNDKSKFSGLVDCGNCISIFHGEKLMNTNLIIFIMVESKGTCPDCTRL 1018

RESULT 2
A44147
calcium channel protein alpha-2 chain precursor - rat
N:Alternate names: dihydropyridine-sensitive L-type
N:Contains: calcium channel alpha-2 chain
C:Species: Rattus norvegicus (Norway rat)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 20-Aug-1999
C:Accession: A44147
R:Kim, H.L.; Kim, H.; Lee, P.; King, R.G.; Chin, H.
Proc. Natl. Acad. Sci. U.S.A. 89, 3251-3255, 1992
A:Title: Rat brain expresses an alternatively spliced form of the dihydropyridine-sensitive
A:Reference number: A44147; MUID:92228762
A:Accession: A44147
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1091 <KIM>
A:Cross-references: GB:M86621; NID:g203954; PIDN:AAA41088.1; PID:g203955
C:Superfamily: calcium channel alpha-2 chain
C:Keywords: calcium; glycoprotein; ion channel; transmembrane protein

Query Match 96.2%; Score 5145; DB 2; Length 1091;
Best Local Similarity 95.8%; Pred. No. 2.6e-302;
Matches 976; Conservative 22; Mismatches 19; Indels 2; Gaps 2;

RESULT 3
CHRB2
calcium channel protein alpha-2 chain precursor - rabbit

QY 1 MAAGCLLALTLTLOSLLIGPSSPEPPSAVTIKSWDKMOEDLVTLAKTAGVNLVDI 60
DB 1 MAAGCLLALTLTLOSLLIGPSSPEPPSAVTIKSWDKMOEDLVTLAKTAGVNLVDI 60
QY 61 YEKYQDLTYVEPNNAQLVEAARDIEKLLSNRSKALYSALAEAEKQAAHQWREDFASN 120
DB 61 YEKYQDLTYVEPNNAQLVEAARDIEKLLSNRSKALYSALAEAEKQAAHQWREDFASN 120
QY 121 EVVYNKADDDLOPEKNDSEPSQRIKPVFIEDANFGROIYSQHAHVHIPTDIYESTIVL 180
DB 121 EVVYNKADDDLOPERNESESGSQRIKPVFIEDANFGROIYSQHAHVHIPTDIYESTIVL 180
QY 181 NELNWTSAALDEVEKKNREDDSLMQVFGSATGLARYYPASVWDNSRTPNKIDLYDVR 240
DB 181 NELNWTSAALDEVEKKNREDDSLMQVFGSATGLARYYPASVWDNSRTPNKIDLYDVR 240
QY 241 RPWYIQAASPKDMLILVDVSGVSGLTCLKLIRTSVSEMLETLDSDDFVNVASFNSAQD 300
DB 241 RPWYIQAASPKDMLILVDVSGVSGLTCLKLIRTSVSEMLETLDSDDFVNVASFNSAQD 300
QY 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGIDTYKKGFSAFEPQLLNINVSFRANCNKIIML 360
DB 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGIDTYKKGFSAFEPQLLNINVSFRANCNKIIML 360
QY 361 FTDGGEERAQEIFNKYNKDKKVRVFRFSGVGHNYERGPFIQWACENKGYIYEIPSIGAIR 420
DB 361 FTDGGEERAQEIFNKYNKDKKVRVFRFSGVGHNYERGPFIQWACENKGYIYEIPSIGAIR 420
QY 421 INTQEYLDVGRPMVLGADKAKOVQWNTNYLDALBGLVITGTLVPFNITGQFENKTNLK 480
DB 421 INTQEYLDVGRPMVLGADKAKOVQWNTNYLDALBGLVITGTLVPFNITGQFENKTNLK 480
QY 481 NOLILGVMGVDVSLIEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHNPLOKPKKSOEPTVL 540
DB 481 NOLILGVMGVDVSLIEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHNPLOKPKKSOEPTVL 540
QY 541 DFLDAELENDDIKVEIRNKMIDGESGKFTLTKVKSQDERTLVPVNGTDYSL 599
DB 541 DFLDAELENDDIKVEIRNKMIDGESGKFTLTKVKSQDERTLVPVNGTDYSL 599
QY 600 LALVLPITYSFYIIKAKLEETITQARSKKGMKDSSETLKPDPNFEEGYTFIAPRDYCNDLK 659
DB 600 LALVLPITYSFYIIKAKLEETITQARSKKGMKDSSETLKPDPNFEEGYTFIAPRDYCNDLK 659
QY 660 ISDNTEFLNFEFIDRKTTPNPNPCNADLINRVLLDAGFTNVLVQNSKQKNIKGVK 719
DB 660 ISDNTEFLNFEFIDRKTTPNPNPCNADLINRVLLDAGFTNVLVQNSKQKNIKGVK 719
QY 720 REVVTGGITRVYPKEAGENWQENPETEYDSFYKRSLDNDNVTFTAPYFNKSGPGAYESG 779
DB 720 REVVTGGITRVYPKEAGENWQENPETEYDSFYKRSLDNDNVTFTAPYFNKSGPGAYESG 779
QY 780 INVSKAVEIYIOGKLLKPAVVGKIDVNSHNIENFTKTSIRDPKAGVPCDCKRNSDVMDCV 839
DB 780 INVSKAVEIYIOGKLLKPAVVGKIDVNSHNIENFTKTSIRDPKAGVPCDCKRNSDVMDCV 839
QY 840 ILDDGGFLMANHDDVTNQIGRFFGEIDPMSLRHLNINISYAFNKSVDYQSVCEPGAAPK 899
DB 840 ILDDGGFLMANHDDVTNQIGRFFGEIDPMSLRHLNINISYAFNKSVDYQSVCEPGAAPK 899
QY 900 QGAGHSAYVPSVADILQIGWATAAAMSILQOFLSLTPRLLLEAEMEDDDFTASLSK 959
DB 900 QGAGHSAYVPSVADILQIGWATAAAMSILQOFLSLTPRLLLEAEMEDDDFTASLSK 959
QY 960 QSCITEQTOFFNDKSKFSGLVDCGNCISIFHGEKLMNTNLIIFIMVESKGTCPDCTRL 1018
DB 960 QSCITEQTOFFNDKSKFSGLVDCGNCISIFHGEKLMNTNLIIFIMVESKGTCPDCTRL 1018

N: Alternate names: dihydropyridine-binding protein, 140K
C: Species: Oryctolagus cuniculus (domestic rabbit)
C: Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 22-Jun-1999
C: Accession: S10579; A39518; A33409
R: Ellis, S.B.; Williams, M.E.; Ways, N.R.; Brenner, R.; Sharp, A.H.; Leung, A.T.; Campbell
Science 241, 1661-1664, 1988
A: Title: Sequence and expression of mRNAs encoding the alpha(1) and alpha(2) subunits of
A: Reference number: S10579; MUID: 88336904
A: Accession: S10579
A: Molecule type: mRNA
A: Residues: 1-1106 <ELL>
A: Cross-references: EMBL:M21948; NID: g164762; PIDN: AAA81562.1; PID: g164763
A: Note: 57-Asn, 106-Lys, and deletion of 620-Ser were also found
R: Jay, S.D.; Sharp, A.H.; Kahl, S.D.; Vedvick, T.S.; Harpold, M.M.; Campbell, K.P.
J. Biol. Chem. 266, 3287-3293, 1991
A: Title: Structural characterization of the dihydropyridine-sensitive calcium channel al
A: Reference number: A39518; MUID: 91131638
A: Accession: A39518
A: Molecule type: protein
A: Residues: 961-973 <JAY>
A: Note: this sequence represents the amino end of a glycosylated peptide that appears at
e at the amino end and identical molecular weights (17K) following deglycosylation
R: Hamilton, S.L.; Hawkes, M.J.; Brush, K.; Cook, R.
Biochemistry 28, 7820-7828, 1989
A: Title: Subunit composition of the purified dihydropyridine binding protein from skelet
A: Reference number: A33409; MUID: 90122765
A: Accession: A33409
A: Status: preliminary
A: Molecule type: protein
A: Residues: 27-44, 'S', 46-47 <HAM>
C: Superfamily: calcium channel alpha-2 chain
C: Keywords: calcium; disulfide bond; glycoprotein; ion channel; membrane protein; phosph
F: 1-26/Domain: signal sequence #status predicted <SIG>
F: 27-1106/Product: calcium channel alpha-2 chain #status predicted <MAT>
F: 94, 138, 186, 336, 350, 470, 477, 606, 615, 678, 697, 784, 827, 891, 898, 988, 1001, 1081/Binding site:

Query Match 96.0%; Score 5132.5; DB 1; Length 1106;
Best Local Similarity 94.7%; Pred. No. 1.5e-301;
Matches 985; Conservative 14; Mismatches 12; Indels 29; Gaps 4;

Qy 1 MAAGCLLALTILFQS--LLIGPSSEEPFSAVTIKSWDKMQEDLVILAKTASGVNQLV 58
Db 1 MAAGPLAATLTQAWLILIGPSSEEPFSAVTIKSWDKMQEDLVILAKTASGVHQLV 60
Qy 59 DIYEKQDLYTVEPNARQLVEIARDEKLLSNRSKALVSLALEAEKVQAQAHQWREDF 118
Db 61 DIYEKQDLYTVEPNARQLVEIARDEKLLSNRSKALVRLALEAEKVQAQAHQWREDF 120
Qy 119 SNEVYNAKDDLDPEKNDSEPGSQRIKPVFTIEDANFRQISYQHAHVHPTDIYEGSTI 178
Db 121 SNEVYNAKDDLDPEKNDSEPGSQRIKPVFTIEDANFRQISYQHAHVHPTDIYEGSTI 180
Qy 179 VLNELNWTSALEDEKKNREEDPSLLQVFGSATGLARYYPASWPVNSRPNKIDLDYDV 238
Db 181 VLNELNWTSALEDDVFKKNREEDPSLLQVFGSATGLARYYPASWPVNSRPNKIDLDYDV 240
Qy 239 RRRPWYIOGAASPKDMLILVDVSGVSLGLTKLITFSVSEMLETSDDDFVNVSFNSNA 298
Db 241 RRRPWYIOGAASPKDMLILVDVSGVSLGLTKLITFSVSEMLETSDDDFVNVSFNSNA 300
Qy 299 QDVSCFQHLVQANRNKVLKDVANNITAKGITDYKKGFSFAFEQLLNYSRANCRNII 358
Db 301 QDVSCFQHLVQANRNKVLKDVANNITAKGITDYKKGFSFAFEQLLNYSRANCRNII 360
Qy 359 MLFTDGGERAQEIKNYKDKKVRFRFSGQHNRYERGPTQWMAKCNKGYIYEIPSGA 418
Db 361 MLFTDGGERAQEIKNYKDKKVRFRFSGQHNRYERGPTQWMAKCNKGYIYEIPSGA 420
Qy 419 TRINTQEYLDVLRPWLADGAKQVQNTNYLDALGLVITGTPLPNTITGQFENKTN 478
Db 421 TRINTQEYLDVLRPWLADGAKQVQNTNYLDALGLVITGTPLPNTITGQFENKTN 480

Qy 479 LKNQLILGVMGVDSLEDIKRLTPRTFLCPNGYYFAIDPNGVYLLHPNLQPK----- 530
Db 481 LKNQLILGVMGVDSLEDIKRLTPRTFLCPNGYYFAIDPNGVYLLHPNLQPKPIGVGPT 540
Qy 531 -----NPKSQEPVTLDFDAELENIDKVEIRKMKIDGESGEKTFRLVKSQDER 579
Db 541 INLRKRRPNVQKSPQEPVTLDFDAELENIDKVEIRKMKIDGESGEKTFRLVKSQDER 600
Qy 580 YIDKGNRTYTPVNGTDY-SLALVLPYFYFYIKAKLEETITQARSKKGMKMDSETLKP 638
Db 601 YIDKGNRTYTPVNGTDYSSALVLPYFYFYIKAKLEETITQARY-----SETLKP 653
Qy 639 DNFEESGTYTAPRYCNDLKISDNTEFLNFNFIDIRKTPNPNNSCNADLNRLVLLDAG 698
Db 654 DNFEESGTYTAPRYCNDLKISDNTEFLNFNFIDIRKTPNPNNSCNADLNRLVLLDAG 713
Qy 699 FTNELVQNWSKQKNIKGVKARFVYTDGITRVYKPEAGENQENPETYEDSFYKRSLDN 758
Db 714 FTNELVQNWSKQKNIKGVKARFVYTDGITRVYKPEAGENQENPETYEDSFYKRSLDN 773
Qy 759 DNYVETAPYFNKSGPAYESGIMVSKAVEIYIQGKLLPAPVYGIKIDVNSWIENFTKTSI 818
Db 774 DNYVETAPYFNKSGPAYESGIMVSKAVEIYIQGKLLPAPVYGIKIDVNSWIENFTKTSI 833
Qy 819 RDPGAGPVCDCKRNSDMVDCVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNIS 878
Db 834 RDPGAGPVCDCKRNSDMVDCVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNIS 893
Qy 879 VYAFNKSYDYQSVCEPAGAPKOGAGHRSAYVPSADIILQIGHWATAAAWSILQQFLLSLT 938
Db 894 VYAFNKSYDYQSVCEPAGAPKOGAGHRSAYVPSADIILQIGHWATAAAWSILQQFLLSLT 953
Qy 939 FPRLEAVEMEDDDFTASLSKQSCITEQTYFFDNDKSFSGVLDGCGNCSRFHGEKLMN 998
Db 954 FPRLEAADMEDDDFTASLSKQSCITEQTYFFDNDKSFSGVLDGCGNCSRFHGEKLMN 1013
Qy 999 TNLIFIMVESKGTCPDTRL 1018
Db 1014 TNLIFIMVESKGTCPDTRL 1033

RESULT 4
T30256
calcium channel alpha-2-delta-C chain - mouse
C: Species: Mus musculus (house mouse)
C: Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 20-Jun-2000
C: Accession: T30256
R: Klugbauer, N.; Lacinova, L.; Marais, E.; Hobom, M.; Hofmann, F.
J. Neurosci. 19, 648-691, 1999
A: Title: Molecular diversity of the calcium channel alpha2delta subunit.
A: Reference number: 420794
A: Accession: T30256
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: mRNA
A: Residues: 1-1091 <KLJ>
A: Cross-references: EMBL:AJ010949; PIDN:CAA09423.1
A: Experimental source: brain
C: Superfamily: calcium channel alpha-2 chain

Query Match 20.3%; Score 1085; DB 2; Length 1091;
Best Local Similarity 28.7%; Pred. No. 2.3e-57;
Matches 309; Conservative 222; Mismatches 416; Indels 128; Gaps 40;

Qy 3 ACCLLALITLTLFQSLIGPSSEEPFSAVTIKSWDKMQEDLVILAKTASGVNQLV 62
Db 14 ASALLA-TALLYAALGVVRSQQIPLSV-VKLWASAFSGGEIKRSTAAKYSSQLQKKTK 71
Qy 63 KYODLYTVEPNARQLVEIARDEKLLSNRSKALVSLALEAEKVQAQAHQWREDFASNEV 122
Db 72 EYKDVATEIEDGLQVKKLAKIMEEMFHKSEAVRRLVEAAEEAHLKHEFDADL---QY 128
Qy 123 VYINAK--DDLDPKNDSEPGSQRIKPVIEDANFR-QISYQHAHVHPTDIYEGSTIV 179

Db 129 EYFNAVILNERDGNFLELGEFT---LAPNDHFNPLPVNISLSDVQVPTNNYKNDPAI 185
QY 180 LNELNWTSADEVFVKRNEEDPSLLQVFGSATGLARYYPASPVVDNDRTPNKLIDYVR 239
Db 186 VNGVWSESLNKFVNDPDRDPSLIQWFGSAGKFRQYPGIKWEPDE---NGVIAFDCR 242
QY 240 RRPWTIOGAASPKDMLILVDVSGSVGLTLKIRTSVSEMLETSLDDDFVNVASFNNAQ 299
Db 243 NRKWTIOATSPKDVILVDVSGSMKGLRLTIKATQTSILDTLGDGDDFFNIITYNEELH 302
QY 300 DYS-CFO-HLVQANVRNKKVLKADANNITAKGIDTYKKGFSFAFQOLLNYNVSRAN--CN 355
Db 303 YYPECLNGTLVQDRNTKHFREHDKLFAKGIOMLDLALNEAFNILDNFNITGGSTCS 362
QY 356 KIIMLTGDEGEAROEIENKYN-KDKYRVRFSVQGHYERGPQIOWMACENKGYEYRIP 414
Db 363 QAIMLITDGAVDYTIIPAKYNNPDKVRIFTYLIGREAPADNKLKMACANKGFFTOIS 422
QY 415 SIGAIRINTQEVLDVGRPMVLADKAKQVQWNTVYLD-----ALELGLVI--TGT 463
Db 423 TLADVOENMYELHLSRPKVI--DQEHVVMTEAYIDSTLPQAOKLADDOGLVMTTVA 480
QY 464 LPVENITGOFENKTNKQILQILGVMDVSLIEDIKRLTPRETLCPNGYFAIDPNGYVLL 523
Db 481 MPVFS-----KQNETRSKG--ILGVVGTDPVVKELTKTIPYKLGIGHGAFALTNGYILT 535
QY 524 HFNLOP---KNPKSOEP---VTLDLDAELNEDIKYIRKIMIDGESGKFTFTLVKSODE 578
Db 536 HPELRPLYEGKRRKPNYSYVDLSEVEDREDVV-LRNAMVNRKTGK--FSMEVK---- 588
QY 579 RYIDKGNRT-----YTTPVNGTDSLALVLPT-YSFYIIKALEETITQARSKKGMK 631
Db 589 KTVDKGRVLMVNTDYYIDIRKTFPSGLVALSRHGKYFF-----RGNVT 634
QY 632 DSETLKPDPNEESGTYFIAPRYCN-DLKISONTEFLNNEFIDRTPNPNPCNADLI 690
Db 635 IEGL--HLEHPDVSADENSYCWTDLHPEHRHLSQLEAIKLYLKGREP-LLOCDKELI 691
QY 691 NRVLIDAGTNELVQNYWS-----KQKNIKGVKARFVVDGIGTRVYP----- 733
Db 692 QEVLPDA-VVSAPIEAYWTSLALNKSNSDKGEVAFGLTRGLSRINLFVGAEOQTND 750
QY 734 -KEAGENQENPETEDSYKSLDN--DNYVETAPY-----FNKSGPGAYESGIWVKAV 786
Db 751 FLKAGDKENIFNADHPLWYRAAEOIAGSFYISPFSTGTYNKS-----NVYTAESI 804
QY 787 EYIQGKLLKPAVVGKIDVNSWIEFTKTSIRDCAGPVCCKRNSDVMDCVILDDGDF 846
Db 805 QLLDERKSPVAAVGIOMKLEFFQRFKFTASQCASLDCKCSISCDDETVNCLIDNNGF 864
QY 847 LLMANHDDYTNOIGRPFGBIDPSLRHLNYSVYAFNKSVDYQSVCEPGAAPKQAGHRS 906
Db 865 ILVS--EDYT-QTGDPFGEVGAVMKLLTMGSFKRITLYDQAMCR---ANKSSDSAH 918
QY 907 AYVPSVADILQGWATAAASWILQOFLSLFPRLLEAVEMEDDDFTASLSK-----QS 961
Db 919 GLUDPYKAEF-----SAAKWIMTELVLVLEF---NLCSSWHSMDTAKAOKLQTLPEP 968
QY 962 CITEQTYEFDNDKSFSGVLDGNGCSRIFHGKELMNTNLIFIMVESKTCPCDT 1016
Db 969 CTEYPAFVSERTIKETTGNICEDCSKSFVIOQTPSSNLFVWVYDS--SCICES 1021

RESULT 5

S44617
C50C3.11 protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C:Accession: S44617
R:Favella, A.D.
submitted to the EMBL Data Library, May 1993
A:Description: Sequence of the C. elegans cosmid C50C3.

A:Reference number: S44618
A:Accession: S44617
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-734 <FAV>
A:Cross-references: EMBL:L14433; NID:g289649; PID:g289650
C:Genetics:
A:Introns: 24/2; 87/3; 175/1; 259/1; 290/3; 346/3; 460/3; 538/3

Query Match 11.4%; Score 607; DB 2; Length 734;
Best Local Similarity 26.6%; Pred. No. 8.7e-29;
Matches 180; Conservative 127; Mismatches 258; Indels 112; Gaps 20;

QY 47 LAKTASGVNQLVDIYEKYODLYTVEPNARQLVEAARDIEKLLNRS-----KALVSLAL 102
Db 36 MKETFSKISHETILKQNEKLEVEEQFOPRAELKSKHRIEDYLKVRSPAYKAKIS--L 93
QY 103 EAEKVOAAHONREDFASNEVYVYNAKDDLDPEK-NDSEPGSORIKP-----VFIEDANF 155
Db 94 EARSVRNDSTVNDPOSQSFIREMSAKQGDGTIYESNHLGRLLKVNKYSNLTQANAF 153
QY 156 -GRQISYQHAHVHIPTDIEGSTIVLNELNWTSADEVFVKRNEEDPSLLQVFGSATGL 214
Db 154 YLPTSSVSSAVHIPTPLYDRNEDLLRKIDW-SDIDAVYRTNREETKDLAFQFCSEAGY 212
QY 215 ARYPASPMV-DNSRTPNKKIDLYVRRRPWYTOGAASPKDMLILVDVSGSVGLTLKLR 273
Db 213 MRYYPAAASFWDNQ--DEHLDLDFCRNTEWYINSATNSKNVILMLDMSGMLGQRYEVAK 270
QY 274 TSVSEMLETSLDQDDFVNVASFNNSA--QDVSCFOHLVQANVRNKKVLKADANNITAKGI 330
Db 271 QTEIALETSLSHNDNFNIMTFSKNTFLDGCNGTGLLQATWNRKALKRRKMDTQSESK 330
QY 331 TDYKGFSAFQQLNLYN-----VSRANCKIIMLTGDEGEAROEIENKYNKDKKRVYF 385
Db 331 AYEKALPLAFSVLLDINNNGGDNRRGACENVIMLTIDGAPNAYKKIFDYNADKKRVF 390
QY 386 RFSVQOHYNERGPIOWMACENKGYEYIETPSIGAIRINTQEYL-----DVLGRPMVLADKA 441
Db 391 TELVGEAIDFNEVREMACNRRGYVMVHANMADVDKEIHIIYRMRVRYVGRYKESQGLS 450
QY 442 KQVQWNTVYLDALGLL--VITGTLPVFNITGOFENKTN----- 478
Db 451 ---WTVGVRELYLPPEIFAEPVPIITNQSFVAVNMKASRRKIRLOKSEARSMEVTVV 507
QY 479 ---LKNQILGVMDVDSLEDIKRLTPRETLCPNGYIYFAIDPNGYVLLHPLNPKNP--- 532
Db 508 SYPVIVNETFMGVAAVNIPLEVAQKSHPANIGSKSYFFMLDQNGFVMTHPOLRPIDPFT 567
QY 533 ---KQSEPVTLDPLD-----AELENDIKVEIRNKMID 561
Db 568 KYHKQNNMMDLELEVQONVRSSQSAQVSDLVCEGANYAECVDDLRKAVRKMID 627
QY 562 GFSGKTFRTLVKSODERY---IDK---GNRTYTTPVNGTDSLALVLPYYSFYIKA 614
Db 628 CNQSD-----VQQLDVLVATELLDRVYQTNYYIAECINHANFVLGLAVAKGDDIRVK 681
QY 615 KLEETITQARSKKGMK 631
Db 682 K-----QKKYDFGRVK 692

RESULT 6

T18770
Probable calcium channel protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C:Accession: T18770; 125249
R:Sulston, J.
submitted to the EMBL Data Library, June 1995
A:Reference number: Z19019
A:Accession: T18770

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1148 <N1>

A:Cross-references: EMBL:Z49907; PIDN:CAA90091.1; GSPDB:GN00020; CESP:T24F1.6

A:Experimental source: clone B0491

R:Chui, C.

submitted to the EMBL Data Library, June 1995

A:Reference number: Z2004

A:Accession: T25249

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1148 <N1>

A:Cross-references: EMBL:Z49912; PIDN:CAA90141.1; GSPDB:GN00020; CESP:T24F1.6

A:Experimental source: clone T24F1

C:Genetics:

A:Gene: CESP:T24F1.6

A:Map position: 2

A:Introns: 91/2; 131/3; 170/3; 283/1; 322/2; 410/3; 487/1; 563/1; 602/3; 654/3; 683/3; 7

Query Match 10.7%; Score 569.5; DB 2; Length 1148;

Best Local Similarity 21.5%; Pred. No. 3.2e-26;

Matches 234; Conservative 216; Mismatches 406; Indels 233; Gaps 42;

QY 37 VDKMOEDLVTLA-----KTASGVNQLVDYIEKYQDLYTVENPNNAROLVEIAARDI 86

Db 99 VDTIEAPASIAQSANTLRDFQTQSRLVQEEFKLPDIKSKKEDAAEKLVRATEHL 158

QY 87 EKLNSNRKALVSLALEAEKVAQAAHQRDEFNASNEVYNNAKDDLDPKNDSEPOSQR-- 144

Db 159 DRLTNNRVDAKLKASSAESA--DEYDDQAYAVPQADKRCE 201

QY 145 --IKPVFEDANFGRIQYQH---AAVHIPDIYEGSTIVNELNWTSA--LDEYFKNR 197

Db 202 AYMKKNESDMHFVSNM--VEHNSKSGIHTVESYQCDPRVMDRFDWTGKHKLEKMTSDNK 260

QY 198 EEDPSLLMQVGSATGLARYPASPWVDSNRTPNKIDLYVRRRPWYIOGAASPKDMLIL 257

Db 261 EKAPMGHQYIGTSGTGRMPRRHW--KVEPTPIIDLPDRFRPWFVNAESVVPKDIIVFL 319

QY 258 VDVSQSVSLGLKILRTSVSEMLETSDDDFVNVSFNSAOD--VSCFOH--LVQANVRNK 315

Db 320 LDYSGSVGPTMHLIKITMILSLPSNDYFGFYNNHFNPIISCRANTPMPATTNNK 379

QY 316 KVLKAVANNITAKGITDYKKGFSFAEOL---LNTNVS-----RANCKIIMLFDGEE 367

Db 380 KVFFELGNLEEKDOAHATPLKFLSLDLVLRGNLDSQSLFADYRSEGHKLLIIFTDGVD 439

QY 368 RAQEIFN---KYNKDKVVRFRFSGQHYERGPQWACENKGYIYEIPSGAIRINTQ 424

Db 440 WPHQILDEEFOTRNSGLIRIFGSMGYGTSLLPQQYACKSHGYSYSEIDSMYKQSR 499

QY 425 EYLDVLRPMVLADKAK-----QVQWTVYLDLLEGLVITCTLPVNTGOFENKT 477

Db 500 TIQNVLSQ---VRGDELGTNAEKREPSWTQLYMTQGTGPIVTLUSPLT-----SQ 551

QY 478 NLKNQILIGVAGVDVSLIEDIKRLTFRFLPCPNGYIFAIDPNGYVLLHPNLQ--PKNPK--- 533

Db 552 IWRDQKLAGVAIDISIEFKHLP--TSSEQMVGIVDNGMLIYHQLQIPKTEVHCV 609

QY 534 -----SQEPV-----TLDFLDAELENDIKVETRN 557

Db 610 RRSACYDAQVKQKAGSLRVHYGFSDEVRVLRVGLIDSPTLDMYDLEGGDTAIRDLR 669

QY 558 KMDGESGEFTLVKQODERYIDKGRNTYTWTPVNGFDYSALV--LPTYSFYIKAK 615

Db 670 -----RITTKCYEARAKDNKSEKSHIKSPFFLVIVNNIQLKTVIIDS 717

QY 616 LREETITQ-----ARSKKGMKMDSETLKPDPNFESGYFTIAPRDYC--NDLKISDNN 665

Db 718 QELGLTDNKLVTFFPRDVCQWKLDEAAHDFRV--WSDISEKEICAQDDMLRAPFT 775

QY 666 EPLLNFNEFIDRKTNNPNSCNADLRNVLDDAGFTNELVQNVWSKOKNIKVKARFVVD 725

Db 776 KGLGSWTOSWPKSDIEHTTC-----LLAQYPENASVPHVNS-----FVTR 817

QY 726 GGITRVYKEAGENQWENPETEYEDSFYKSLDNDNYFTAFYFNKSGPGAYESGIMVSKA 785

Db 818 SKLTAFYPTCSSHDMKAVNKKFDEI--KLTDNDFV---QFSMR-----SESLIYRT 866

QY 786 VEYIQGLKLPVAVGIIKIDVN---SWIENTFKTISIRPCAGPVCDCRNSD-----VMD 837

Db 867 IADYNNRL---AVVGTQWKENFFDQYDFDFT-----RQNPDKWIKRQE 908

QY 838 CVILDDGGFLLMANHDDTYNIGREFGEIDPSLMRLHVNISVYAENKSYDVQSVCE--PGA 896

Db 909 CSIITRNHGVIASSAHRAPAHAKF---DPQLFESLVKVNLDVNSTWTEVQSECKAKRV 964

QY 897 APKQAGHRSA-----YVPSVADIQIGWATAAASILQOFL-----SLTFP 940

Db 965 APWSAAPGSSSILRYFVTSIFKLAKTSFWR-----NLLESALTIVDAQPSMTGNTCTFO 1019

QY 941 RL--LEAVEMEDDDPTASLSKOSCTEQTYFFDNDKSFSGVLDCGNCSTRIFHGEKLMN 998

Db 1020 KIKPPECRCFMFFHYRMTLN---ITKQLQ-----LTGMSTCSRYSYAKLY---PVPH 1063

QY 999 TNLFIWVE 1007

Db 1064 TTLSLIAD 1072

RESULT

C86880

hypothetical protein yvcC [imported] - Lactococcus lactis subsp. lactis (strain IL140

C:Species: Lactococcus lactis subsp. lactis

C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001

C:Accession: C86880

R:Botolin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissensbach, J.; Eh

Genome Res. in press, 2001

A:Title: The complete genome sequence of the lactic acid bacterium.

A:Reference number: A86625

A:Accession: C86880

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1450 <SPO>

A:Cross-references: GB:AB005176; NID:gl2725093; PIDN:AAK06141.1; GSPDB:GN00146

A:Experimental source: strain IL1403

C:Genetics:

A:Gene: yvcC

Query Match 3.7%; Score 198; DB 2; Length 1450;

Best Local Similarity 21.0%; Pred. No. 0.0012;

Matches 242; Conservative 149; Mismatches 439; Indels 322; Gaps 56;

QY 37 VDKMOEDLVTLAKTAGVGNOLVDYIEKYQDLYTVENPNNARQLVEIAARDIEK-----L 89

Db 69 INKTENDLKLKFKFEGNQPIEBE--NESWTLKEKNT-----IISDFERENEGKIYL 120

QY 90 LSNRSKALVSLALEAEKVAQAAHWR---EDFA-----SNEVVYNA 127

Db 121 RANNSISLNLLEIQDAKLIENDQEVISEDILAKKESTIFSLYIPENNKADSKEDKNKT 180

QY 128 KDDLDPKNDSPFGSORIKP---VFIEDANFGRIQISYQHAHVH----- 167

Db 181 EEVLWNSSQEETVSQLKDSQLAFSPFNFGIKASFNDLAQNYENISPEYQDETGISP 240

QY 168 ----IPTDIYESTIVNELNWTLSALDVEYFKKNREDPSLLMQVFSATGLARYYPASPW 223

Db 241 NISWITP-----CNTIVVNHQGNF-----SSQWDGVNSNN--GEATNLSYIEYAG 287

QY 224 VDN-----SRTPNKIDLY--DVRRRPMYIOGAASPKDMLILYDVSGVSLTLK 270

Db 288 VNNPVDALRYKAKETETGLYDVVNLVRGN---VQNPIKPVDIVLIDMSGSMQAKET 344

QY 271 LIRTSVSEMLETLSD--DFNVN--ASFNSNAQDVSCFQHLVQANVRNKKVYKLD----A 321

Db 345 AVRGVDFSTLQNTAWADYVNVGIVCSFGNVVTCASGVIIVPI--DKVSESHVKS 402
Qy 322 VNNITA---KGITDYKGFSAFAPOLLNYSRANKIIMFLDTGGEEAQAEIFNKYNK 378
Db 403 INQALAPOFGSGTFTQLGRKGTEML---EQDSSDNQMKMLMTDQ---VPTESYKVN 455
Qy 379 DKYR--VFRSVGHNYERG---PIQ---WACENKGYEYI-----PSGATIRNTOE 425
Db 456 ASKVDNVYIGOSFABSRDEPGNTSKIOSPYVKDINGGNSIEIRDTWAATIGEAIEISKQ 515
Qy 426 YLDVLRGPMVLADQ-----KAKQVQWTVNYLDALGLVITGTLVPFNITGOF 474
Db 516 ISEIHTLQIQLGNDGYSLSQBEVKSRTSLIATGLYQDANSN-----DITDYLK 565
Qy 475 NKTN-----LKNQILGVGVDSVLEDIKRLTPRTFLCPNGYFAIDPNGYVLLHPN 526
Db 566 NOANVLSRFNTITNGLLDPLGAOFKDKTK-----FEITSVG-----604
Qy 527 LOPKNPKSQEPVTLDFDAELENDIKVEIRNMIDGESKTFRTLKVSQDERYIDKGNR 586
Db 605 -----EDSINLPTGINKEGLEISLNI--GKNOEVOIHQVRLNTETDDFKTNY 653
Qy 587 TY-----TWTPVNGT--DYSIALVLPYSFYIYKAKLE-----ETITQARSKK 627
Db 654 WYQMGETTLTP--NGSNPDKNVFGVPSAKSGGINLTLEKQWLANSENI PENVELLIGRR 712
Qy 628 GKMDSE-----TLKPDNFBESGTYFIAPDYCNLDKISDNNTFELLNFNFBIDRKTNN 682
Db 713 SAQISSDWTKVTTLKEDDEWSQLENPKYILGEBEYIEIKDEIVLN--SEYDWTITIGE 771
Qy 683 PSCNADLNRLVD---AGFTNELVQWYMSKQKIKGVKARFVYTDGTRVYPKEAGE 738
Db 772 DKTITANIEKFLQLIKTSNHDNEPLSEVEFVLKNSQGEEDKAVTN-----EKGE 822
Qy 739 -NWOENPETEYDFYKRLSDNDVYFTAPYFNKSGPGAYSGIMVSK-----AVEIYIQ 791
Db 823 ILFDKTRNLNVEEYQHEIKSPGHSLEGPWKTKT--EFENGQPIIKVDGEQIALDEHYN 879
Qy 792 GKLLPAPVVGKIDVNSWIEFTKTSIRDPAGVCDCKRNSVDMCVILD-----DG-- 844
Db 880 KFMIS--LNTINDIN--VEEF-----RNSVTIDKRAVDSEELDGAV 917
Qy 845 -GFLMANHDDVTNOIGRFFGEIDPFLMRHLVNISVYAFNKSVDYQSVCEPGAAPKQAG 903
Db 918 FNLYQIESVDELTLQKPL--EITNLLPGL-----YALQESVSPNGYTRDDEV 964
Qy 904 H--RSAYVPSVADILQIGWATAAAWSILOQFL-----IDPFLDENESGKNGLVNEENGDLHLTLIFY 1015
Db 965 HFRVYKFGNSIVAIGSEG-----IDPFLDENESGKNGLVNEENGDLHLTLIFY 1015
Qy 940 ----PRLEAVEMEDDDFTASLSKQSC--ITQOTQYFFNDS-----KFSGVLDGNCRSRI 990
Db 1016 NOAVPPLQLEVDKIDDDFTSLAGVSFELTRLGRKSTDSVKRINSFDRILKTFN--NE 1073
Qy 991 FHGEKL--MNTNL 1001
Db 1074 FTGETIALKNSL 1085
RESULT 8
S54355
inter-alpha-trypsin inhibitor heavy chain 3 precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 04-Feb-2000
C:Accession: S54355
R:Chan, P.; Risler, J.L.; Raguenez, G.; Sallier, J.P.
Biochem. J. 305: 505-512, 1995
A:Title: The three heavy-chain precursors for the inter-alpha-inhibitor family in mouse.
A:Reference number: S54353; MUID:95194326
A:Accession: S54355
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA

A:Residues: 1-886 <CHA>
A:Cross-references: EMBL:X70393; NID:g695635; PIDN:CAA49843.1; PID:g695636
C:Superfamily: inter-alpha-trypsin inhibitor complex component II

Query Match 3.6%; Score 194.5; DB 2; Length 886;
Best Local Similarity 19.9%; Pred. No. 0.00091;
Matches 185; Conservative 138; Mismatches 347; Indels 261; Gaps 44;

Qy 27 FPSAVITKSVDDKMOEDLVTLAKTAGSVQNVLDYIEKYQDLYTYEPNNARQLVEIARAADI 86
Db 98 YPGNVKEVAQKQYKAVSOCKTAG---LVKASGRKLEKFTVSNNVAAGSKVTFELTY 153
Qy 87 EKLLSNSKALVSLALEAEKVAQAHQWREDFASNEVVYNAKDDLDPEKNDSEPSQRIK 146
Db 154 EELL--KRNGKYEMLYKQPKQLVRHFEID-----AHIFEP-----Q 189
Qy 147 PVFTEDANFRQISVQHAHVHIPTDIYEGSTIVLNMELNWTISALDEVFKKNEEDPSLLMQ 206
Db 190 GISMLDAE-----ASFITNDL--LGSALTQSF-----214
Qy 207 VFGSATGLARYYPASPWDNSRT--PNKID-----LYDVRRRP-----WYI-- 245
Db 215 -----SGKKGVSPKPSLDQOOSCTCTDSLNGDFTIVDYNRESGPNVQIVNGFYVHF 269
Qy 246 --OG--AASPKDMLILDVSGSVGLTKLIRTSVSEMLETISDDEDFNVASFNSNAODV 301
Db 270 FAPGLPVVKNIVFVIDVSGSMGRKIQTREALKILDDVKEDDYLNFILFST---DV 326
Qy 302 SCFO--HLVQANVRNKKVLKDAVNNITAKGITDYKGFSAFEPQLNLYNVSRAN-----C 354
Db 327 TTWKDHLVQATPANLKEAKTFVKNIHQDSMTNINDGLKGIEML--NKAREDHVTPERS 383
Qy 355 NKIIMLFTDG---GEERAQEIFNKYNK--DKKVVRFVSFGQHNHYERGPQWMAECENKG 408
Db 384 TSIIMLTDGANTGESRPEKIQENVRNAIGGKPLYNLGFG--NNLNTNLETALENHG 442
Qy 409 YYETPSIGAIRINTQEVLDVLRGPMVLADGKAKQVQWTVNYLDALGL--VITGTLPV 466
Db 443 LARRIYEDSDANLQLOGVEEVANPLL-----TNVEVEYEPENAILDLTNSYPH 491
Qy 467 FNITGQFENLKNQLILGVGVDSVLEDIKRLTPRTFLCPNGYFAIDPNGYVLLHPN 526
Db 492 F-----YDG-----SEIVVAGRLVDRNMDN-----FKADVKGHGALN-- 523
Qy 527 LOPKNPKSQEPVTLDFDAELENDIKVEIRNMIDGESK--TFRTLKVSQDERYIDKG 584
Db 524 ---DLTPEEVDMEEMDAALK-----EGYIFGDIERLWAYLTIEQLLEKRNKAG 572
Qy 595 NRTYTPVNGTDYSLA--LVLPYTSFYIYKAKLEETITQARSKKMKDSE-----LK 637
Db 573 DEKENIT--AEALDLSLKYHFTPLTSWVTPKPEDNEDQTSIADNAGEAFAETITMSFLT 631
Qy 638 PDNFEESGTYFIAPDYCNLDKISDNNTFELLNFNFBIDRKTNNPNSCNADLINRVLLDA 697
Db 632 TQOSSQSPYIV-----DGDPHFIQI-----PGKNDSCIFNIDEKP 668
Qy 698 GFTNELVQWYMSKQKNIKGVKARFVYTDGTRVYPKAGENWQENPETEYDFSKRSLD 757
Db 669 GTVLRLIQD-----PVT--GIT-VTGQIIG-----KRS-- 694
Qy 758 NDNVYFTAPYFNKSGPGAYSGIMVSKAVEIYIOCKLLKPAVVGIKIDVNSWIEFTKTS 817
Db 695 NASSRTGTYFGKLGITNWMDFRVEVTEKILG-----TGAEIJSFSLDVTVTQ 747
Qy 818 IRDPCAGPVCCKRNSVDMCVILDG--GFLMAN-----HDDYTNQIGRFFGEIDP 868
Db 748 ----TGLSVINRKNKVV--VSFGDGSIFVILLHQVKKHPVHQDFLG-----FYVVD 795
Qy 869 SLMRHLVNISVYAFNKSVDYQSV--CEPGAAP 898
Db 796 HRMSAQTHGLLQGFQFPDFKVFGRPGSDP 826

RESULT 10
JC5576
inter-alpha-trypsin inhibitor heavy chain 3 - golden hamster
C/Species: Mesocricetus auratus (golden hamster)
C/Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 17-Mar-1999
C/Accession: JC5376; PC486
F:Nakatani, T.; Suzuki, Y.; Yamamoto, T.; Sinohara, H.
J. Biochem. 122, 71-82, 1997
A/Title: Molecular cloning and sequencing of cDNAs encoding three heavy-chain precursors in inhibitor heavy chain family.
A/Reference number: JC5574; MUID:97420688
A/Accession: JC5376
A/Molecule type: mRNA

A;Residues: 1-889 <NAK>
A;Cross-references: DDBJ:D89287
A;Experimental source: liver
A;Accession: PC4486
A:Molecule type: protein
A;Residues: 34-53;449-475;509-526 <NA2>
C;Comment: In the plasma three inter-alpha-trypsin inhibitor heavy chains 1, 2 and 3 were found that the complexes play important role for pancreatic cancer.
C;Superfamily: inter-alpha-trypsin inhibitor complex component II
F;236-239,664-865/Disulfide bonds: #status predicted

Query Match 3.1%; Score 164.5; DB 2; Length 889;
Best Local Similarity 23.2%; Pred. No. 0.059;
Matches 66; Conservative 56; Mismatches 112; Indels 51; Gaps 11;

QY 202 SLLWQVGSATGLARYYPASPFDNSPT-PNKID-----LYDYRRR-PWTIOGA-- 248
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 211 SALTKSFSGKGHVSFKPS---LDQQRSCTPCTDSLNGDFTIVDVNRPSPGNVQVVG 267
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 249 -----ASPKDMLILVDVSGSVGLTLKLIRTSVSEMLETSLDDDFNVASFNS 296
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 268 YFVHFPAQGLPVVPKNIVFIDISGSMAGRKIQOTRVALLKILDDMKQDYLNFLEST 327
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 297 NAQVSCFOHLVQANVRKKVLKDANNITAKGITDKKGFSAFEQLN----YVNSRA 352
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 328 GV--TTWKDSLVQATPANLEEARTFVRSISDQGWTINDDLGRIMLTDAREQHTVPER 385
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 353 NCNKIIMLFTDG----GEERAQEIFNKYNKDKKVRFPSVG-QHNRYERGIQMACEKN 407
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 386 STSIIML-TDGDANTGESRPEKTQENVRKAIEGRFPFLYNLGFGNNLNYNFLETMALENH 444
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 408 GYYEIPESIGAIRINTQYLDVLCGRPMVLADGKAKAQVQWNTNYLD 452
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 445 GVARIYEDSANLOQGFYEAVANPLL-----TNVEVE 478
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 11
T28155
variant-specific surface protein 1 - malaria parasite (Plasmodium falciparum) (fragments)
N;Alternate names: erythrocyte membrane binding protein 1 (EMPI)
C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C;Accession: T28155
R;Rowe, J.A.; Moulds, J.M.; Newbold, C.I.; Miller, L.H.
Nature 388, 232-295, 1997
A;Title: Plasmodium falciparum rosetting is mediated by PfEMP1 and requires complement in vitro
A;Reference number: Z20477; MUID:97373957
A;Accession: T28155
A;Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A;Residues: 1-2706 <ROW>
A;Cross-references: EMBL:Y13402; PIDN:CAA73831.1
A;Experimental source: strain IT 4/25/75
C;Genetics:
A;Introns: 2493/3
A;Note: R29R+var1

Query Match 3.0%; Score 161; DB 2; Length 2706;
Best Local Similarity 18.2%; Pred. No. 0.55;
Matches 183; Conservative 137; Mismatches 345; Indels 338; Gaps 46;

QY 36 WYDKMQEDLVTLAKTAGCVGNOLVDIYKYQDLVTVEPNNA-----RQL 78
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 308 WFDEWAEEFCRIKI-----KLENVKKECRD-----EPNNKYCSGDGHDKRTYLRKDNFI 358
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 79 VEIARDETEKLLSNRSKALVSLAEAEKVQAHAHQWREDFASNVEYYYNAKDDLOPEKND 138
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 359 IDLNCPRNACSNITK-----WIEIRKQFDKQKRK--YWNEL---KIKNISNNEK 408
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 139 E-----PGSORIKVPFIEDANFGRIQSIGHAAVHIPTDIYEGSTIVLNLNWTLSALDE 191
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

R; Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
Pierce, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
Science 282, 1126-1132, 1998
A; Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A; Reference number: A71600; MUID:99021743
A; Accession: E71619
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-1516 <GAR>
A; Cross-references: GB:AE001383; GB:AE001362; NID:G3845135; PIDN:AACT71842.1; PID:G3845135
A; Experimental source: clone 3D7
C; Genetics:
A; Gene: PFE0265C

Query Match 2.9%; Score 155; DB 2; Length 1516;
Best Local Similarity 18.9%; Pred. NO. 0.51;
Matches 178; Conservative 133; Mismatches 291; Indels 340; Gaps 52;

Qy	119	SNEVYVYNAKDDLD--PEKNDSEPGSQRKPVFIEDANFGROISYQHOAAHVHTPTDIYEGS	176
Db	517	NDVVIIEHNNNNNIYDNKYVNECSSEKINDGNSKNIN-----ILEPNNL-DTS	567
Qy	177	TIYVNLNWTSSALDE--VEFKKAREDPSSLW-----QVGSATGLARYYPASPWYDNST	229
Db	568	NIFL-----EGDEYKYVYNKEEIRIPLFKEINKEIF-----EKL	603
Qy	230	PNKID--LYDVRRRPWY---IQGAASPKDMLILVDVSGVSLT-LKLIFT-----	274
Db	604	PLAKYOIQLDIKEE-WYTDNRIRAIKSKDDM---DYFSQVLEYVYRMKTDFFEIKL	658
Qy	275	--SVSEMLETLSDDPVN---VASPNSNAQDVSCFQHLVQAVNRNKKVKLDAVN--NIT	326
Db	659	KIRMAENIOSVEGELLINDLSKNTDNIKYNVLOK-KSKKKKKPLNDILANTYNT	717
Qy	327	A-----KGITDYKKGFSFAFEQLL-NYNVSRANCHNIIMLFDGGEERAQEIF	373
Db	718	TESKYQDLYVKGSESKEDIKQIDFVTOCYRRNDLIIRTHDK-----SOLF	764
Qy	374	N--KYNKDKRVRFPSVQGH-----NYERGIOWMACENKGYEYIPSGAIRINTQE	425
Db	765	KNIKIDNNKKYEIYNLELQEEINEKKYNNKNNND---SNKTFP-----LATENEF	812
Qy	426	YLDVLRGPVWLAGDK---AKQVQWT-----NYVLDALEGLVITGTLPVFNIT	470
Db	813	KKOLLDDSDQIFGDSLLADIKEYNTADMLDNNNENKSLYEDGENF---ITRNEP---IT	866
Qy	471	QOFENKTNL-----KNOLLGVMGVDVSLSDIKRLTPRFTLCPN---G	510
Db	867	NEYEEKNNIIYISDEQYNEEDIIFKDKIKEKENNDTSSDFENCVSQOEKIVYNEKIEE	926
Qy	511	YFPAID---PNGVYLHPNLQPNKPSQEPVT-----LDFLD--AELEN-----DI	551
Db	927	YNNKNDKSKSSSSSIIEIKYKKEKDELVPNLVCLLDEFEHNDLENNYIVSSDDM	986
Qy	552	KVEIRKMDIGESGEKFTFTLVKSODERYIDKGNRTYTWTPVNGTDYSLALVLTSEFY	611
Db	987	KTNVSKNNITG-----VK--ENKVDKTNVEY-----	101
Qy	612	IKAKLEETTOARSKKG-----KKMDETLKPDNFESGVTF-----IAPRDCYN	656
Db	1011	-----DKGDDGVIBISFEDSHKLEESKFDNDNNIYDNDDELEKNLSKDYIS	1055
Qy	657	DLKISDNTTEFLNF-----NEFIDRKTNPNS-----CNADL	689
Db	1058	D--VDKNHVNNIYIERGEDERENEVENKIOSTESHKSNFICITENKSLRKOYMSKEDI	1111
Qy	690	IN-RVLIDAGFTNELQVNTYSKQKNIKGVKARFVTDGGITRVYKPEAGENQENPETYE	748
Db	1116	SNVRILKSDDINNLKSQNYE-----ILLD-----KKQVMDNFQMIEQNN	1155
Qy	749	DSFYKRSLDNDNTVFTAPFNKSGPGAYSGGIWVSKAVEIYI-----OCKLLK	796

Db 1157 DKLKEDKLDE-----GAYFEYLEDNKLIIDSYIKETNKENEEELIKEYYKKLK 1201

Qy 797 PAVYGKIKIDVNSWIE---NFTKTS-IRDP-C-AGPVCDCRKSNDVMDCVILDDGGFLLMAN 851
 :
Db 1202 KNNTEINDNDDKLLLNFFGIPYIQSPCEAAQAQCSYLANKNVCDALIIDSDSVLVFSG 1361

Qy 852 HDDYTNOIGRRFFE-----IDPSL---MRHLVNISV 879
 :
Db 1362 ---KTVIKNFFNKKKTVEVYEKKAIBEKLGLYQEELINISL 1299

RESULT 15
I40884
cytotoxin L - Clostridium sordellii
C:Species: Clostridium sordellii
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 15-Oct-1999
C:Accession: I40884
Gene 161, 57-61, 1995
A:Title: Cloning and characterization of the cytotoxin L-encoding gene of Clostridium
A:Reference number: I40884; MUID:95369733
A:Accession: I40884
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-2364 <RES>
A:Cross-references: EMBL:X82638; NID:g1000694; PIDN:CAA57959.1; PID:g1000695
C:Superfamily: cpl repeat homology
C:Keywords: cytotoxin

Query Match 2.9%; Score 155; DB 2; Length 2364;
Best Local Similarity 18.7%; Pred. NO. 1;
Matches 217; Conservative 132; Mismatches 342; Indels 46

Qy	12	TLFQSLIGSSPEPPSAVTIKSWDKMQEDLVTLAKTASGVNOLDVIYEKYQDLTYVE	71
Db	1137	TLDDKKIIMPODO-----LVLSEID-FNNNSITLKG-----EINRAE	1173
Qy	72	PNNARQLVETAAARDIEKLLSNRS-----KALVS-----LALAEKVQAAHQRWEDFASNEV	123
Db	1174	GGSGHTLTUD---DIDHFFSSPSITYRKFWLSIYDLVNIKKIKI-----DPSKDLMW	1221
Qy	124	YYNAKD-----DLDPEKNDEPQSQRKP-----VFIEDANFGR-	157
Db	1222	LPNAPNRVFGYEMGWPGRSLD-----NDGTKLLDIRRHYEQFVVRVFAFIADATIKL	1278
Qy	158	QISVQHAHVHPIDIYEGSTIVLNLNWTFSALDVEYFKNREEDPSLLMQVGSATGLARY	217
Db	1279	KPRYEDTVNRINDGNTRSFIV-----PVIITEQIRKN-----LSYSFYGS--GGSYS	1324
Qy	218	YPASPWVDNSRTPNKIDLVYRRRPWYIQGAASPKDMLILVDVSGSVGLKLIIRTSVS	277
Db	1325	LSLSYPNN-----IDLNVENDTW-----VIDVDNVKNITIESEDTQKG	1365
Qy	278	EMLETTLDDDFNVVASFNSNAODVSCFHLVQANVRNKKVLKDAVNNITAK---GITYDK	334
Db	1366	ELTENI-----LSKLINTEDNKII--LNNHTINFYGDINESN	1399
Qy	335	KGFSFAPEQLLNYN-----YSRA-----NCKNIIMLFTD-----GGEERAQ	370
Db	1400	RFISLFSILEDINIIEIDLVSYSKYILLSCNCKLIENSSDIQOKIDHIGENGHEQKY	1459
Qy	371	EIPN-----KYN-----KDKKVRVFRFSGVQHNYERGPQIWMACENKNGYVEIPSIGAIR	420
Db	1460	IPYSIDNETKNGFYDYSKKEGLFTAEPFSNESIIRN--IYMPDSNNLFIYSSKDLKDIR	1517
Qy	421	INTQEYLDVLRPWLJAGKAKQ-----VQWTVNVLDALEGLVITGTLPL	465
Db	1518	IINK-----GDVKLLITGNFYKDMKVSLSFTIEDTNTIKLNGVYLDE-----NGVAQ	1564
Qy	466	VFNITQGFENKTNKOLLILGVMGVDVSLIEDIKRLTPRETLCPNGYFPAIDPNGVYLLHP	525
Db	1565	ILKFMNNAKSALNTSNLMFNESINIK-----NIFYNNLPDNIETILDT	1609

[illegible]

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QY 526 NLOPKNPKSQEPVTLDFLDAELENDIKVEIRNMKIDGESGEXTFTFLVKSQDERYIDKGN 585
Db 1610 NF-----IISGNSIGQFE-LICDCKN-----1631
QY 586 RYTWTPVNGDYSLALVPTYSFYIKAKLBETITQARSKKGMKDSLTLPDNEESG 645
Db 1632 -----IQP-----YFINKIKET-----SYTLVYGNQON--1655
QY 646 YTFIAPDYCNLDKISDNTEFLNENE---FIDR---KTPNPNPCNADLIN-----691
Db 1656 -LIVESYHLDD---SGNLSVINFESQKLYGIDRYVNVKVIAPNLYTDEINITPVYKP 1711
QY 692 -----RVLLDAGFTNE-----LVQNYW-----SKOKNIKGVKARFVVT 724
Db 1712 NYICPEVILDANYINEKINVININDLSIRYVWMDNGSDLILIANSEEDNQPVKIRFV--1769
QY 725 DGGITRVYPERAGE-----NQENPE-----TYEDSFYKR-----SLDNDNY 761
Db 1770 -----NVFKSDTAADKLSFNFSKQDVSVSKIIISTFSLAAYSDFDYEFGLVSLDND--1822
QY 762 VFTAPYFNKSGPGAYESGIMVSKAVIYIQGKL--LKPAVVVGKIDVNSWIENFTKTSIR 819
Db 1823 -----YFYINSGNMYVSGL-----IYINDSLYFKP-----PKNNLITGFTTI---1860
QY 820 DPCAGPVCDCKRNSVDMCVILDDGFLLMANHDDYTNOIGRFFGEIDPFLMRHLVNSIV 879
Db 1861 -----DGN-----KYVFDPTKGAASIGBI-----TIDGKD 1886
QY 880 YAFNKSYDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAAWSILQOFLSLTF 939
Db 1887 YFEN-----KQG-----ILQGVINTSDG---LKYFAPAGTL 1915
QY 940 PRLEAVEME-----DDDFASLSKQCITEOTOYFFFDNDSKFSFGLDCG 985
Db 1916 DENLEGESVNFICKLIDGKIYYFEDNYRAAV-EWKLDDETYYFNPKTGEALKGLHQIG 1974
QY 986 NCSRIFHGEKLMNTNLIFI 1004
Db 1975 DNKYFFDDNGIMOTGFTTI 1993

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Search completed: July 23, 2001, 07:37:58
Job time: 495 sec


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FT TRANSMEM 1067 1086 POTENTIAL.
FT CARBOHYD 92 92 N-LINKED (GLNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLNAC. . .) (POTENTIAL).
FT CARBOHYD 184 184 N-LINKED (GLNAC. . .) (POTENTIAL).
FT CARBOHYD 324 324 N-LINKED (GLNAC. . .) (POTENTIAL).
FT CARBOHYD 348 348 N-LINKED (GLNAC. . .) (POTENTIAL).
FT CARBOHYD 475 475 N-LINKED (GLNAC. . .) (POTENTIAL).
FT CARBOHYD 585 585 N-LINKED (GLNAC. . .) (POTENTIAL).
FT CARBOHYD 594 594 N-LINKED (GLNAC. . .) (POTENTIAL).
FT CARBOHYD 663 663 N-LINKED (GLNAC. . .) (POTENTIAL).
FT CARBOHYD 769 769 N-LINKED (GLNAC. . .) (POTENTIAL).
FT CARBOHYD 812 812 N-LINKED (GLNAC. . .) (POTENTIAL).
FT CARBOHYD 876 876 N-LINKED (GLNAC. . .) (POTENTIAL).
FT CARBOHYD 883 883 N-LINKED (GLNAC. . .) (POTENTIAL).
FT CARBOHYD 973 973 N-LINKED (GLNAC. . .) (POTENTIAL).
FT CARBOHYD 986 986 N-LINKED (GLNAC. . .) (POTENTIAL).
FT MOD_RES 501 501 PHOSPHORYLATION (BY CAPK)
FT MOD_RES 833 833 PHOSPHORYLATION (BY CAPK)
FT MOD_RES 833 833 PHOSPHORYLATION (BY SIMILARITY)
FT SEQUENCE 1091 AA; 123183 MW; 254E13EE29A47837 CRC64;

Query Match 100.0%; Score 5346; DB 1; Length 1091;
Best Local Similarity 100.0%; Pred. No. 2e-299;
Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAACLLALITLQSLIGSPSEPPSAVTIKSWDKMQEDLVTLAKTAGVGNQLVDI 60
DB 1 MAACLLALITLQSLIGSPSEPPSAVTIKSWDKMQEDLVTLAKTAGVGNQLVDI 60
QY 61 YEKQDLYTVEPNAROLVELAARDIEKLSNRKALVSLALEAEKVOAQAHOWREDPASN 120
DB 61 YEKQDLYTVEPNAROLVELAARDIEKLSNRKALVSLALEAEKVOAQAHOWREDPASN 120
QY 121 EVVYNKADLLDPEKNDSEPGSQRIKPVFIEDANFRQISVQHAHVHIPTDIYEGSTIVL 180
DB 121 EVVYNKADLLDPEKNDSEPGSQRIKPVFIEDANFRQISVQHAHVHIPTDIYEGSTIVL 180
QY 181 NELNWTALDVFVKKNEEDPSLLQVFGSATGLARYYPASPWWDSNRTNPKIDLYDVR 240
DB 181 NELNWTALDVFVKKNEEDPSLLQVFGSATGLARYYPASPWWDSNRTNPKIDLYDVR 240
QY 241 RPWTIOGAASPKMLILVDVSGVSGLTFLKIRTSVSEMLETSLDDDFVNVASFNSAQD 300
DB 241 RPWTIOGAASPKMLILVDVSGVSGLTFLKIRTSVSEMLETSLDDDFVNVASFNSAQD 300
QY 301 VSCFQHLVQAVNRNKKVLDKAVNNITAKGTDYKKGFSFAFEQLLNVRANCNKIIML 360
DB 301 VSCFQHLVQAVNRNKKVLDKAVNNITAKGTDYKKGFSFAFEQLLNVRANCNKIIML 360
QY 361 FTDGGEERAQEIFNKYNKKKVRVRESVGOHNYERGPQIWMACENKGYIYEIPSIGAIR 420
DB 361 FTDGGEERAQEIFNKYNKKKVRVRESVGOHNYERGPQIWMACENKGYIYEIPSIGAIR 420
QY 421 INTOEYLDVLRPNVLADKAKQVQWNTVNLDALEGLVITGLPVENITGQFENKTNLK 480
DB 421 INTOEYLDVLRPNVLADKAKQVQWNTVNLDALEGLVITGLPVENITGQFENKTNLK 480
QY 481 NQLILGVAGDVSLIEDIKRTPRTCLPCNGYFAIDPVGVLHPNLPQKNPKSQEPVTL 540
DB 481 NQLILGVAGDVSLIEDIKRTPRTCLPCNGYFAIDPVGVLHPNLPQKNPKSQEPVTL 540
QY 541 DFLDAELNDIKVEIRNKMIDGESGKFTFTLVKSQDERYIDKGNRTYTTPVNGTDYSL 600
DB 541 DFLDAELNDIKVEIRNKMIDGESGKFTFTLVKSQDERYIDKGNRTYTTPVNGTDYSL 600
QY 601 ALVLPYTSFYIIKAKLETTQOARSKGKMKDSETLPDNFPEESGYTFIAPROYCNDLKI 660
DB 601 ALVLPYTSFYIIKAKLETTQOARSKGKMKDSETLPDNFPEESGYTFIAPROYCNDLKI 660
QY 661 SDNTEFLNFEIDRKTNNPNSCNADLINRVLLDAGFTNELVQWYWSKQKNIKGVKAR 720

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DB 661 SDNTEFLNFEIDRKTNNPNSCNADLINRVLLDAGFTNELVQWYWSKQKNIKGVKAR 720
QY 721 FVYTDGGITRVYKPEAGENQENPETYEDSFYKSLDNDNYVFTAPYFNKSGPGAYESGI 780
DB 721 FVYTDGGITRVYKPEAGENQENPETYEDSFYKSLDNDNYVFTAPYFNKSGPGAYESGI 780
QY 781 MYSKAVEIYIOGKLLKPAVVGIIKIDVNSWIENTFTKTSIRDPACGAPVDCCKRNSVMDCVI 840
DB 781 MYSKAVEIYIOGKLLKPAVVGIIKIDVNSWIENTFTKTSIRDPACGAPVDCCKRNSVMDCVI 840
QY 841 LDGGFFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNLVSVAFNKSYDYQSVCEPGAAPKQ 900
DB 841 LDGGFFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNLVSVAFNKSYDYQSVCEPGAAPKQ 900
QY 901 GAGHRSAYPSVADILQIGWATAAANSILQQFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960
DB 901 GAGHRSAYPSVADILQIGWATAAANSILQQFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960
QY 961 SCITEQOYFFDNDKSFSGVLDGCGNSRIFPHGKLMNTNLIIFIMVESKGTCPDTRL 1018
DB 961 SCITEQOYFFDNDKSFSGVLDGCGNSRIFPHGKLMNTNLIIFIMVESKGTCPDTRL 1018

RESULT 2
CIC2_RAT
ID CIC2_RAT STANDARD; PRT; 1091 AA.
AC P54290;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-2/DELTA
DE SUBUNITS PRECURSOR.
DE CACNA2D1 OR CACNL2A OR CCHL2A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92228762; PubMed=1314383;
RA Kim H.L., Kim H., Lee P., King R.G., Chin H.;
RT "Rat brain expresses an alternatively spliced form of the
RT dihydropyridine-sensitive L-type calcium channel alpha 2 subunit.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:3251-3255(1992).
CC -1- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN
CC EXCITATION-CONTRACTION COUPLING.
CC -1- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:
CC ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS
CC HETERODIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM
CC A PRECURSOR FORM (BY SIMILARITY).
CC -1- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.
CC
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CC
CC EMBL; M86621; AAA1088.1;
CC InterPro: IPR002035;
CC Pfam; PF00092; wavy 1.
CC PROSITE; PS50234; VWFA_DOMAIN; 1.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Calcium channel; Glycoprotein; Phosphorylation; Signal;
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 944 L-TYPE CALCIUM CHANNEL ALPHA-2 SUBUNIT

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CHAIN	945	1091	(BY SIMILARITY) L-TYPE CALCIUM CHANNEL DELTA SUBUNIT (BY SIMILARITY).
FT TRANSMEM	445	468	POTENTIAL.
FT TRANSMEM	906	930	POTENTIAL.
FT TRANSMEM	1067	1086	POTENTIAL.
FT CARBOHYD	92	92	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	136	136	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	184	184	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	323	323	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	347	347	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	474	474	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	584	584	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	593	593	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	663	663	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	769	769	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	812	812	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	876	876	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	883	883	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	973	973	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	986	986	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES	500	500	PHOSPHORYLATION (BY CAPK)
FT MOD_RES	833	833	PHOSPHORYLATION (BY CAPK)
FT SEQUENCE	1091 AA;	123822 MW;	(BY SIMILARITY).
SQL			7054907D9D343B34 CRC64;

Query Match 96.2%; Score 5145; DB 1; Length 1091;
Best Local Similarity 95.8%; Pred. No. 7, le-288;
Matches 976; Conservative 22; Mismatches 19; Indels 2; Gaps 2;

QY	1	MAAGCLLALTFLQSLIGPSEPPFSAVTKSWDKMQEDVLTAKTASGVNQLVDI	60
DB	1	MAAGCLLALTFLQSLIGPSEPPFSAVTKSWDKMQEDVLTAKTASGVNQLVDI	60
QY	61	YKYOQLTVENPNARQLEIAARDIEKLLSNRSLVLALEAEKVAQAAHWRDFASN	120
DB	61	YKYOQLTVENPNARQLEIAARDIEKLLSNRSLVLALEAEKVAQAAHWRDFASN	120
QY	121	EVVYNNAKDDLPKNDSPGSGRIKPVFIEDANFGRQISYQAAVHIPTDIEGSTIVL	180
DB	121	EVVYNNAKDDLPKNDSPGSGRIKPVFIEDANFGRQISYQAAVHIPTDIEGSTIVL	180
QY	181	NELNMTSALDEYFKKREDDPSLLMQVFGSATGLARYYPASPVDNRSRPNKIDLYDVR	240
DB	181	NELNMTSALDEYFKKREDDPSLLMQVFGSATGLARYYPASPVDNRSRPNKIDLYDVR	239
QY	241	RPWYIGAAAPKMDLILVDVSGVSLGTLKLTSTVSEMLETSLDDDFVNVASFNSNAOD	300
DB	240	RPWYIGAAAPKMDLILVDVSGVSLGTLKLTSTVSEMLETSLDDDFVNVASFNSNAOD	299
QY	301	VSCFQHLVQANVRNKKVLKADAVNNITAKGTDYKKGFSFAFOLLNYSRANCNKIIML	360
DB	300	VSCFQHLVQANVRNKKVLKADAVNNITAKGTDYKKGFSFAFOLLNYSRANCNKIIML	359
QY	361	FTDGGEEARQAEIFKNYKDKKVRFRFSVQGHNYERGIQWMAACENKGYIYEIPSGAIR	420
DB	360	FTDGGEEARQAEIFKNYKDKKVRFRFSVQGHNYERGIQWMAACENKGYIYEIPSGAIR	419
QY	421	INTQEYLDVLGRPMVLADKAKQVQWNTNVDLALGLVITGTPLVNTITGQFENKTLK	480
DB	420	INTQEYLDVLGRPMVLADKAKQVQWNTNVDLALGLVITGTPLVNTITGQFENKTLK	479
QY	481	NQILGVMGVDVSLDIKRLTPFTLCPNGIYFAIDPQNGVLLHLPNLPKNPKSQBPVTL	540
DB	480	NQILGVMGVDVSLDIKRLTPFTLCPNGIYFAIDPQNGVLLHLPNLPKNPKSQBPVTL	539
QY	541	DFLDAELNDIKYIENKMKIDGESGKFTFLVKSQDERYIDKGNRTYTPVNGTDYDYS-	599
DB	540	DFLDAELNDIKYIENKMKIDGESGKFTFLVKSQDERYIDKGNRTYTPVNGTDYDYS	599
QY	600	LALVLPYTSFYIKAKLEETITQARSKKGMKDSITLKPDPNFESGYTFTIAPRDYCNDLK	659

DB	600	LALVLPYTSFYIKAKLEETITQARSKKGMKDSITLKPDPNFESGYTFTIAPRDYCNDLK	659
QY	660	ISDNTEFLNFEFIDRKTNNPSCNADLNRLVLLDAGFTNELVQNTWSOKNKGVKA	719
DB	660	PSDNTEFLNFEFIDRKTNNPSCNADLNRLVLLDAGFTNELVQNTWSOKNKGVKA	719
QY	720	RFVYTDGGITRVYPKEAGENQENPETYEDSFYKRSKLDNDNYVFTAPYFNKSGPGAYESG	779
DB	720	RFVYTDGGITRVYPKEAGENQENPETYEDSFYKRSKLDNDNYVFTAPYFNKSGPGAYESG	779
QY	780	IMVSKAVEIYIOGKLLKPAVVGIIKIDVNSWIENFTKTSIRDPGAGPVCDCRNSDVMDCV	839
DB	780	IMVSKAVEIYIOGKLLKPAVVGIIKIDVNSWIENFTKTSIRDPGAGPVCDCRNSDVMDCV	839
QY	840	ILDDGGFLLMANHHDDYTNOIGRFFGEIDPMSLRHLVNTSVYAFNKSVDYQSVCEPGAAPK	899
DB	840	ILDDGGFLLMANHHDDYTNOIGRFFGEIDPMSLRHLVNTSVYAFNKSVDYQSVCEPGAAPK	899
QY	900	QGAGHRSAYVPSVADILQIGMWATAAASILQOFLLSLTFPRLLEAVEMEDDDFTASLSK	959
DB	900	QGAGHRSAYVPSVADILQIGMWATAAASILQOFLLSLTFPRLLEAVEMEDDDFTASLSK	959
QY	960	QSCITEQTYFFPDNDKSFSGVLDGCGNSRIFPHGKLMNTNLIIFIMVESKGTCPDTRL	1018
DB	960	QSCITEQTYFFPDNDKSFSGVLDGCGNSRIFPHGKLMNTNLIIFIMVESKGTCPDTRL	1018

RESULT 3
CIC2_RABIT
ID CIC2_RABIT STANDARD; PRT; 1106 AA.
AC P13806;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-2/DELTA
DE SUBUNIT'S PRECURSOR.
GN CACNA2D1 OR CACNL2A OR CCHL2A.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88336904; PubMed=2458626;
RA Ellis S.B., Williams M.E., Ways N.R., Brenner R., Sharp A.H.,
Leung A.T., Campbell K.P., McKenna E., Koch W.J., Hui A.,
Schwartz A., Harpold M.M.;
RT "Sequence and expression of mRNAs encoding the alpha 1 and alpha 2
subunits of a DHP-sensitive calcium channel.";
RL Science 241:1661-1664(1988).
RN [2]
RP SEQUENCE OF 961-973.
RX MEDLINE=91131638; PubMed=1847144;
RA Jay S.D., Sharp A.H., Kahl S.D., Vedvick T.S., Harpold M.M.,
Campbell K.P.;
RT "Structural characterization of the dihydropyridine-sensitive calcium
channel alpha 2-subunit and the associated delta peptides.";
RL J. Biol. Chem. 266:3287-3293(1991).
RN [3]
RP SEQUENCE OF 961-975; 992-1000 AND 1033-1050.
RX MEDLINE=90368635; PubMed=2168391;
RA de Jongh K.S., Warner C., Catterall W.A.;
RT "Subunits of purified calcium channels. Alpha 2 and delta are encoded
by the same gene.";
RL J. Biol. Chem. 265:14738-14741(1990).
CC -1- FUNCTION: CONTRACTION COUPLING.
CC -1- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:
ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS
HETERODIMERS THAT ARE DISULFIDE-LINKED.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE

RA	Craxton M., Dear S., Du Z., Durbin R., Favell A., Fraser A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latraile P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R., Sims M., Smaldon N., Smith A., Smith M., Sonhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Watson R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,	DB	451	---WMTGVYRRLVLPRLPEFAEPVITINQSFVAMKMSRRKIRLQKSEARSMFVTV	507
RA		QY	479	-----LNQLILGVGVDSVLEKILKRLTPRTLCNPGYVEALDPNGYLLHPLNLPKPNP	532
RA		DB	508	SYPIVNETTGMVAANPIPLTEVAQKSHPANIGSKSYFFMLDQNGFVTHPQLRPIDPFT	567
QY		QY	533	--KSOEPVTLDFLD-----AELNDIKVEIRNMID	561
DB		DB	568	KYHKQNNMDLLELVGQNVRSQKQVSLVCSGANYAEVDLKRVRKMIID	627
QY		QY	562	GEGEKTRFLVKSQDERY-----IDK---GNRTTVPNGTDSLALVLTFFYFIKA	614
DB		DB	628	CNDS-----VOOLDVLYATELDRVYPTNTTYAECINHANFVLGLAVAKGDYRVK	681
QY		QY	615	KLEETIQARSKKMK 631	
DB		DB	682	K-----QKKYDFGRVK 692	
RESULT 5					
ITH3_MOUSE		ITH3_MOUSE		STANDARD;	PRT; 886 AA.
AC		AC	Q61704;		
DT		DT	15-JUL-1998 (Rel. 36, Created)		
DT		DT	15-JUL-1998 (Rel. 36, Last sequence update)		
DT		DT	01-OCT-2000 (Rel. 40, Last annotation update)		
DE		DE	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3).		
GN		GN	ITI H3.		
OS		OS	Mus musculus (Mouse).		
OC		OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC		OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX		OX	NBL_TaxID=10090;		
RN		RN	[1]		
RP		RP	SEQUENCE FROM N.A.		
RC		RC	STRAIN=C57BL/6N; TISSUE=Liver;		
RX		RX	MEDLINE=95194326; PubMed=7534067;		
RA		RA	Chan P., Risler J.-L., Raguenez G., Salier J.-P.;		
RT		RT	"The three heavy-chain precursors for the inter-alpha-inhibitor family in mouse: new members of the multicopper oxidase protein group with differential transcription in liver and brain."		
RL		RL	Biochem. J. 306:505-512(1995).		
CC		CC	-1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY SIMILARITY).		
CC		CC	-1- SUBUNIT: I-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN, BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2 AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.		
CC		CC	-1- TISSUE SPECIFICITY: EXPRESSED IN BOTH LIVER AND BRAIN.		
CC		CC	-1- PFM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY SIMILARITY).		
CC		CC	-1- SIMILARITY: BELONGS TO THE ITIH FAMILY.		
CC		CC	-1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.		
CC		CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
CC		CC	EMBL; X70393; CAA49843.1;		
DR		DR	MGI:96620; Itih3.		
DR		DR	InterPro; IPR002035;		
DR		DR	Pfam; PF00092; vwa; 1.		
DR		DR	PROSITE; PS50234; VWFA_DOMAIN; 1.		

KW Serine protease inhibitor; Repeat; Signal; Multigene family;
KW Glycoprotein.
FT SIGNAL 1 18 POTENTIAL.
FT PROPEP 19 30 BY SIMILARITY.
FT CHAIN 31 646 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN
FT H3.
FT PROPEP 647 886 BY SIMILARITY.
FT DOMAIN 279 439 VWFA.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 577 577 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT BINDING 646 646 CHONDROITIN 4-SULFATE, CROSS-LINK SITE
FT (BY SIMILARITY)
SQ SEQUENCE 886 AA; 96977 MW; 15955308C7F5030A CRC64;

Query Match 3.6%; Score 194.5; DB 1; Length 886;
Best Local Similarity 19.9%; Pred. No. 0.00089;
Matches 185; Conservative 138; Mismatches 347; Indels 261; Gaps 44;

Qy 27 FPSAVTKSWDKMOEDLVTLAKTAGSNQVQLDIYKYQDLYTVPEPNAROLVIAARDI 86
Db 98 YPGNVKEKVAQKQYKAVSOCKTAG----LVKASGRKLEKFTVSNVAAGSKVTFELTY 153
Qy 87 EKLLSNRSKALVSLALEAEKQAAHOREDFASNEVYVYNAKDDLDPEKNDSEPGSQRIK 146
Db 154 BELL-KRNKGKYLEMYLVQPKQVLRHFEID-----AHIFEP-----Q 189
Qy 147 PVFTEDNFRQISYQAAHVHPTDIYEGSTIVLNLNWTLSALDEVFKNREDEPSLIWQ 206
Db 190 GISMLDAE-----ASFIINDL-LGSALTKSF----- 214
Qy 207 VFGSATGLARYPASPWNDSRT-PNKID-----LYDVRRRP-----WYI-- 245
Db 215 -----SGKKGHVSKPDLDDQSCPTCTDLSLLNGDFTIYVDVNRSPGNQVINGYVFHF 269
Qy 246 --QG-AASPKDMLILVDVSGVSLTLLKLTSTVSEMLETSLDDDFVNVASFNQAQDV 301
Db 270 FAPQGLPVPRNIVFIDVSGSMGRKIQOTREALKLLDDVKEDDYLNFLFST--DV 326
Qy 302 SCFQ-HLVQAVNRNKKVLKDAVNNTAKITDYKKGFSFAFQOLLNVYSRAN-----C 354
Db 327 TTKWDHLVQATPANLKEAKTEPVKNIHQDSMTNINDGLLKGIEML---NKAREDHVTPERS 383
Qy 355 NKIIMLFTDG-----GEERAQIFNKYNK--DKKVVRFVSFGQHYERGPQWACENKG 408
Db 384 TSIITMLTDGANTGESRPEKIQENVRNAIGKFFLYNLGFG-NLNLNFTLELALENHG 442
Qy 409 YYPEISGAIRINTQEVLDVLRPMVLGDKAKQVQNTVYLDLALGLL--VTGTLPV 466
Db 443 LARIYEDSDANLQGGVEEVANPLL-----TNVEVEYPENAILDTRNSIPH 491
Qy 467 FNITQGFENKTNLKNLILGVGVDSVLSLEIDIKRLTPRETLCPNGYFAIDPNGVYLLHPN 526
Db 492 F-----YDG-----SEIVVAGLVDRNDN-----FKADYKGGHGAN-- 523
Qy 527 LQPNKPKSQEPVTLDFDALENDIKVIRNKMIDGESGEK--FTRLVKSODERYIDKG 584
Db 524 ----DLTTEEVDMEDDAALK-----ECCYIFGDIYERLWAYTLTQELLEKKRNAG 572
Qy 585 NRTYTWTPVNGTDYSLA--LVLPYTSFYIYKAKLEETITQARSKGKKMDSET-----LK 637
Db 573 DEKENIT-AEALDLSLKHYFTPLTSMVYTPKPEDNEDQTSIADNAGEAFATFTMSFLT 631
Qy 638 PDNFESGFTFAPRDYCNLDKISDNNTFEFLNFEFIDRKTTPNPNPCNADLINRVLLDA 697
Db 632 TQOSQSPYIVV-----DGDPHFIQI-----PGKNDSCFNIDEKP 668
Qy 698 GFTNELQVNYMSKQNIKGVKARFVTVTGGITRVYKPEAGENQWQENPETYDSFYKRSUD 757
Db 669 GTVRLIQD-----PVT--GIT-VTQGIIGD-----KRS-- 694
Qy 758 NDNYVFTAPFNKSGPAGYESIMYKAVEIYIQGLKLPVAVGIKIDVNSHIFNTKS 817

Db 695 NASRTGKTYFGKLGITNANWDFRVEVTEKIIILG-----TGAELSTFSLWDTVTVTQ 747
Qy 818 IRDPCAGFVCDCKRNSDVMDCVILDDG-GFLLMAN-----HDDYTNQIGRFFGEIDP 868
Db 748 ----TGLSVITNKKNMV--VSFGDGISFVILHQVWKKHPVHQDFLG-----FYVYDS 795
Qy 869 SLMRHLVNIISVYAFNKSYDYQSV-CEPGAAP 898
Db 796 HRMSAQTGHLIGQFPDFKVFQIRGSDP 826

RESULT 6
ITH3_HUMAN
ID ITH3_HUMAN STANDARD; PRT; 885 AA.
AC Q06033; Q99085;
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY
DE CHAIN H3) (SERUM-DERIVED HYALURONAN-ASSOCIATED PROTEIN) (SHAP).
GN ITIH3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93215656; PubMed=7681778;
RA Bourguignon J., Diarra-Mehrpour M., Thiberville L., Bost F.,
RA Sesboue R., Martin J.P.;
RT "human pre-alpha-trypsin inhibitor-precursor heavy chain. cDNA and
RT deduced amino-acid sequence.";
RL Eur. J. Biochem. 212:771-776(1993).
RN [2]
RP SEQUENCE OF 341-885 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89137072; PubMed=2465147;
RA Diarra-Mehrpour M., Bourguignon J., Sesboue R., Mattei M.-G.,
RA Passage E., Sallier J.P., Martin J.P.;
RT "Human plasma inter-alpha-trypsin inhibitor is encoded by four genes
RT on three chromosomes.";
RL Eur. J. Biochem. 179:147-154(1989).
RN [3]
RP SEQUENCE OF 30-49; 463-477 AND 497-515.
RX MEDLINE=89380192; PubMed=2476436;
RA Enghild J.J., Thøgersen I.B., Pizzo S.V., Salvesen G.;
RT "Analysis of inter-alpha-trypsin inhibitor and a novel trypsin
RT inhibitor, pre-alpha-trypsin inhibitor, from human plasma.";
RL J. Biol. Chem. 264:15975-15981(1989).
RN [4]
RP MEDLINE=91093267; PubMed=1898736;
RX Enghild J.J., Salvesen G., Hefta S.A., Thøgersen I.B.,
RA Rutherford S., Pizzo S.V.;
RT "Chondroitin 4-sulfate covalently cross-links the chains of the
RT human blood protein pre-alpha-inhibitor.";
RL J. Biol. Chem. 266:747-751(1991).
CC -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES.
CC -1- SUBUNIT: I-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,
CC BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-1) IS COMPOSED OF H1, H2
CC AND BIKUNIN. INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND
CC BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.
CC -1- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
CC 4-SULFATE BRIDGE TO THEIR C-TERMINAL ASPARTATE.
CC -1- SIMILARITY: BELONGS TO THE ITIH FAMILY.
CC -1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.

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CC or send an email to license@isb-sib.ch).

DR EMBL; X67055; CAA47439.1; -
DR EMBL; X14690; CAA32821.1; -
DR MIM; 146650; -
DR InterPro; IPR002035; -
DR Pfam; PF00092; vwa; 1.
DR PROSITE; PS50234; VWFA_DOMAIN; 1.
KW Serine protease inhibitor; Repeat; Signal; Multigene family;
KW Glycoprotein.
FT SIGNAL 1 ? POTENTIAL.
FT PROPEP 31 647
FT CHAIN 31 647
FT FT
FT FT
FT FT
FT PROPEP 648 885
FT DOMAIN 278 438
FT CARBOHYD 87 87
FT CARBOHYD 576 576
FT BINDING 647 647
FT BINDING 344 344
FT CONFLICT 357 357
FT CONFLICT 846 846
FT CONFLICT 885 AA; 99121 MW; BC63836F8F5E4A1B CRC64;
FT SEQUENCE 885 AA; 99121 MW; BC63836F8F5E4A1B CRC64;

Query Match 3.4%; Score 182; DB 1; Length 885;
Best Local Similarity 20.7%; Pred. No. 0.0046;
Matches 136; Conservative 102; Mismatches 239; Indels 180; Gaps 34;

QY 27 FSAVTKSWDKMQDLYTLAKTAGSVNQLVDIYEKYQDLYTPVNNAROLVIEAARDI 86
DB 97 YGKNVEKEVAKKQYKAVSQKTAG-----LVKASGRKL 131
QY 87 EKLNSRSLKAL---VSLAEAEKVAQAHQWREDFASNEVYVYNAKDDLPKNDSEPGSQ 143
DB 132 EKFTSVNVAAGSKYTFELTYELLKRHGK-----YEMLYKVQPK-----Q 173
QY 144 RIKPVIEDANFGRQISYQAAHVIPTDIYEGSTIVNLNWTSLDVEFKKREEDPSL 203
DB 174 LVKHFIE-----VDIFEQGI-----SMLD-----AEASF 200
QY 204 LKQVFGSA-----TGLARYPASPWVDSRT-PNKTD-----LYDVRRRP----- 242
DB 201 TNDLGSALTGKSFSGKKGHVSFKPSLDQQRSCPTCTDSLLNGDFTTYDVNRESPGNVQI 260
QY 243 ---WYI-----QC-AASPDKMLILVDVSGVSLTKLIRTSVSEMLETSLDDDFNVAS 293
DB 261 VNGYFVHFAPQGLPVVPRNVAFVDSISGMAGRKLEQKALLRIEDKMEEDYLNFL 320
QY 294 FNSAODVSCF-OHLVQAVNRNKKVLKDAVNNITAGITDYDKGFSFAEQLLNYSVR- 351
DB 321 FSG-----DVSTWKEHLVQATPENLQEARTEFKSMEDKGMTNINDGLRGISML---NKARE 374
QY 352 ----ANCHKIIMLFDG---GEERAQEIFNKYNK--DKKVFVFRFSVQGHNVGRPIQ 400
DB 375 EHRIPERSTIVMLDGDANVGSREPEIQENVRNAGKFFLYNLGFG-NLNINLFLE 433
QY 401 WNAENKGYEYIETPSGIRINTQEYLDVLRPMVLGADKAKQVQWNTVYLDALD----- 455
DB 434 NMALENHGFARRIYEDSDADLOQGYEEVAVNPL-LTGVEMEYPE--NAILDLTQNTYQH 490
QY 456 ----LGLVITGLTPVNTIGQFNKNLK-----NOLILGVMGVDVSLDIKRLTRPFTL 506
DB 491 FYDGSIEIVVAGRL-VDEDMNSF--KADVKGHGATNDL---TFTEEVDKMEK-----AL 539
QY 507 CPNGYFAIDPN-----GYVLHPNLQPK--NPKSQEPVTLDFDLAELENDIKVEIRN 557

Db 540 QERDYIFG---NYIERLWAYLTIEQLLEKRNKNAHGEEKENLTARALDLSLKHYHFTVPLTS 596
QY 558 KWDGSGEKTRTLVKSDERYI-DKGNRTYTWTPVN-GTDSYSLALVLTFTSYFYII 612
Db 597 MVTWKEP-----DNEDERAIDKPGDEATVPSPAMSYLTSYQPPQNPYYV 644

RESULT 7

ITIH3_RAT
ID ITIH3_RAT STANDARD; PRT; 887 AA.
AC Q63416;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY
DE CHAIN H3).
GN ITIH3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
RA Blom A., Fries E.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
CC SIMILARITY).
CC -!- SUBUNIT: 1-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,
CC BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2
CC AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND
CC BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.
CC -!- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
CC 4-SULFATE BRIDGE TO THEIR C-TERMINAL ASPARTATE (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE ITIH FAMILY.
CC -!- SIMILARITY: CONTAINS 1 VWFA DOMAIN.

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CC or send an email to license@isb-sib.ch).

DR EMBL; X83231; CAA58233.1; -
DR InterPro; IPR002035; -
DR Pfam; PF00092; vwa; 1.
DR PROSITE; PS50234; VWFA_DOMAIN; 1.
KW Serine protease inhibitor; Repeat; Signal; Multigene family;
KW Glycoprotein.
FT SIGNAL 1 21 POTENTIAL.
FT PROPEP 22 33 BY SIMILARITY.
FT CHAIN 34 647 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN
FT FT
FT PROPEP 648 887 BY SIMILARITY.
FT DOMAIN 282 442 VWFA.
FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 580 580 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT BINDING 647 647 CHONDROITIN 4-SULFATE, CROSS-LINK SITE
FT (BY SIMILARITY)
FT SEQUENCE 887 AA; 99097 MW; 3B9F0FF96D514096 CRC64;

Query Match 3.4%; Score 180.5; DB 1; Length 887;
Best Local Similarity 18.5%; Pred. No. 0.0057;
Matches 173; Conservative 139; Mismatches 350; Indels 275; Gaps 39;

QY 27 FPSAVTIKSWDKMOEDLVTLAKTAGSVNQLVDIYKYQDLYTVEPNAROLVEIARDI 86
Db 101 YPGSVKEVAQKQYKAVSQGTAG-----LVKASGRKLEKFTVSVNVAAGSKVIFELTY 156
QY 87 EKLKNSRKALVSLALEKQVAAHQWRED--FASNEVVVYNNAKDDLDPEKNDSEPGSQ 143
Db 157 BELL-KRNKGYEMVLKQPKLVHFEIDAHIFEPOGISMLDA-----199
QY 144 RIKPVFIEDANFGRIQSYQHAHVHIPTDIYEGSTIVLNELNWTGALDEVFKKNEEDPSL 203
Db 200 -----DASF-----ITNDL-LGSALTCSF-----217
QY 204 LWQVPGSATGLARYYPASPWNDSRT-PNKID-----LYDVRRP-----WY 244
Db 218 -----SGKKGHVSRFPKSLDQQRSCPTCTDSLLNGDFTIVDVNRESGNVQVINGYF 269
QY 245 I-----QG-AAAPKMDLILVDVSGSVSLTKLTKLRTSVSEMLETSDDDFVNVSFNSNA 298
Db 270 VHFPAQGLPVVPKNIATVIDVSGMSGRKIQOTREALKILDDMKEDYLNFLFSTGV 329
QY 299 QDVSCFQHLVQANVRNKKVLDAVNNITAKGIDYKKGFSFAFQLLNYSRAN-----353
Db 330 --TTWKHLVLRATPANLEEARAFVKNIRDSMTNINDGLLRGIEML-----NKAREDHLPVE 384
QY 354 -CNKIIMFTDG-----GEARQETPNKYNKDKKVRFRFSVG-QHNYERGPIQWACENK 407
Db 385 RSTSLVMTLDGDTGDSRPEKIQENYRNARIGKFPYLNGLFGNNLNFLESLALENH 444
QY 408 GYVYEPSIGAIRINTQBYLDVLRPMVLGDKAKQVQWTVYLDALBELG--VITGTLPL 465
Db 445 GFARIYEDSDASLOLQGFYEVANPLL-----TVELEYENALDUTRNSIP 493
QY 466 VFNITQFENKTNLKNQILGVMDVSDLEDKLRTFLPCNPYYPFAIDPNGYVLLHP 525
Db 494 HE-----YDG-----SEIVAGRLVDRNVN-----FKADVKGHALN- 526
QY 526 NLOPNKPSQEPVTLDFDAELNDIKVEIRNKMIDGSGEKT-----RTLVKSQDER 579
Db 527 -----DLTFTTEVDKMDAALK-----EGGYIFGDYIERLWAYLTIEOLLEKRNAR 574
QY 580 YTDKGNRYTTPVNGTDSLAL-LVLPTYFYIKAKLETITQARSKKMKMDSET-- 635
Db 575 GDEKENIT-----ABALSLKYHVTPLTSMVYKPDENEDQTAIDKPGEEAISASTA 629
QY 636 -LKPNDNFESGYFTIAPRDYCNLDKISDNTEFLNF--NEFIDRKTNPNSCNADLIN 691
Db 630 YLTSSQSSHSPIYV-----DGDPHFIQVPGKNDTICFNIDKPGTGLSLIQ 677
QY 692 RVLIDAGFTNELVQVNSKQKNKGVKARFVVDGITRVYPKEAGENWQENPETYEDSF 751
Db 678 DPVTGIATVGTQII-----GEGNNASSRTGKT-----704
QY 752 YKRLSDNDNVPTAPYFNKSGPGAYESGIMVSKAVEIYIQGLLKPVAVGIKIDVNSWIE 811
Db 705 -----YFKGLGTANAMDFRTEVTEKILGN-----GALSTFSMLD 742
QY 812 NFKTTSIRDPACPGVCDCKRNSDVNDVILDDG-GFLLMAN-----HDDYTNQIGRF 862
Db 743 TVTVTQ-----TGLSVTINRKNMV--VSFEDGISFVIVLHVQVKKHPVHQDFLG-----790
QY 863 FGEIDPSLMRLHVLNIVSVAFNKSQYQSV-CEPGAAP 898
Db 791 FYVVDSHRMSAQTHGLLQGFQFPDFKVDVPRGSDP 827

RESULT 8

ITH3_MESAU STANDARD; PRT: 886 AA.
AC P97280;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY
DE CHAIN H3) (HC3).
GN ITH3.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=97420688; PubMed=9276673;
RA Nakatani T., Suzuki Y., Yamamoto T., Sinohara H.;
RT "Molecular cloning and sequencing of cDNAs encoding three heavy-chain
RT precursors of the inter-alpha-trypsin inhibitor in Syrian hamster:
RT implications for the evolution of the inter-alpha-trypsin inhibitor
RT heavy chain family.";
RL J. Biochem. 122:71-82(1997).
CC -I- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
CC SIMILARITY).
CC -I- SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN.
CC BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2
CC AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND
CC BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.
CC -I- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
CC 4-SULFATE BRIDGE TO THEIR C-TERMINAL ASPARTATE (BY
CC SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE ITH FAMILY.
CC -I- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D89287; BAA13940.1; -
CC InterPro: IPR002035; -
CC DR Pfam: PF00092; vwa; 1.
CC DR PROSITE: PS50234; VWFA_DOMAIN; 1.
CC KW Serine protease inhibitor; Repeat; Signal; Multigene family;
CC Glycoprotein. 1 18 POTENTIAL.
FT SIGNAL 1 18 BY SIMILARITY.
FT PROPEP 19 30 INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN
FT CHAIN 31 646 H3.
FT FT PROPEP 647 886 BY SIMILARITY.
FT DOMAIN 279 439 VWFA.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 577 577 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT BINDING 646 646 CHONDROITIN 4-SULFATE, CROSS-LINK SITE
FT (BY SIMILARITY).
SQ SEQUENCE 886 AA; 99018 MW; AC0594C685257688 CRC64;

Query Match 3.1%; Score 164.5; DB 1; Length 886;
Best Local Similarity 23.2%; Pred. No. 0.047;
Matches 66; Conservative 56; Mismatches 112; Indels 51; Gaps 11;

QY 202 SLLQVFGSATGLARYYPASPWNDSRT-PNKID-----LYDVRRR-PWYIQA-- 248
Db 208 SALTAKSFSGKKGHVSKFSP-----LDQQRSCPTCTDSLLNGDFTIVDVNRESGNVQVNG 264
QY 249 -----ASPKDMLILVDVSGSVSGLTKLRTSVSEMLETSDDDFVNVSFNS 296
Db 265 YVHFPAQGLPVVPKNIATVIDVSGMSGRKIQOTREALKILDDMKEDYLNFLFST 324

QY 297 NAQVSCFQHLVQANVRNKKVLDKAVNNITAKGTDYKKGSFAFEQLLN-----YNSRA 352
Db 325 GV--TTWKDSLQVATPANLEARTFVRISDQGTNTINDGLLRMTDAREQHTVPER 382
QY 353 NCNKIIMLFTDG---GEERAQEIFNKYKDKKVRVERFSVG-CHNYERGPIONMACENK 407
Db 383 STSIILML-TDGDANTGESREPKLOENVRKAIEGRFPILYNGFNLLNLYNFLEIMALENH 441
QY 408 GYIYEIPISGAIRINTQBYLDVLRPMVLAGDKAKQVQWNTNVIYLD 452
Db 442 GVARRIYDSANLQLOQFGYEEVANPLL-----TNVEVE 475

RESULT 9
DPOL THEST
ID DPOL THEST STANDARD; PRT; 1829 AA.
AC 03845;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE DNA POLYMERASE (EC 2.7.7.7).
GN POL.
OS Thermococcus sp. (strain TY).
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Thermococcus.
OX NCBI_TaxID=86030;
RN [1]
RX MEDLINE=98094267; PubMed=9434178;
RA Niehaus F., Frey B., Antranikian G.;
RT "Cloning and characterisation of a thermostable alpha-DNA polymerase
from the hyperthermophilic archaeon Thermococcus sp. TY";
RL Gene 204:153-158(1997).
CC -1- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE -
N PYROPHOSPHATE + DNA(N).
CC -1- PPM: THIS PROTEIN UNDERGOES A PROTEIN SELF SPLICING THAT INVOLVES
A POST-TRANSLATIONAL EXCISION OF THE THREE INTERVENING REGION
(INTEINS) FOLLOWED BY PEPTIDE LIGATION.
CC -1- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; Y13030; CAA73475.1; -
DR InterPro; IPR002064; -
DR InterPro; IPR002203; -
DR Pfam; PF00136; DNA_pol_B; 4.
DR PRINTS; PR00379; INTEIN.
DR PROSITE; PS00116; DNA_POLYMERASE_B; FALSE_NEG.
DR PROSITE; PS00881; PROTEIN_SPLICING; 3.
KW Transferase; DNA-directed DNA polymerase; DNA replication;
KW DNA-binding; Hydrolase; Endonuclease; Autocatalytic cleavage;
KW Protein splicing.
FT CHAIN 1 409 DNA POLYMERASE, 1ST PART (POTENTIAL).
FT CHAIN 410 769 INTEIN I.
FT CHAIN 770 855 DNA POLYMERASE, 2ND PART (POTENTIAL).
FT CHAIN 856 1392 INTEIN II.
FT CHAIN 1393 1441 DNA POLYMERASE, 3RD PART (POTENTIAL).
FT CHAIN 1442 1598 INTEIN III.
FT CHAIN 1599 1829 DNA POLYMERASE, 4TH PART (POTENTIAL).
SQ SEQUENCE 1829 AA; 211875 MW; A113A8BC57EB9CB3 CRC64;

Query Match 3.0%; Score 161; DB 1; Length 1829;
Best Local Similarity 20.1%; Pred. No. 0.21;
Matches 172; Conservative 101; Mismatches 301; Indels 282; Gaps 39;

QY 16 SLLIGSPSEPPPS-----AVIKSWV-----DKMQEDLVTLA 48

Db 229 TLLGROKEHEPEKTHRMGDSFAVEIKGRIHFDFLPVVRRTINLPTYLEAVEYAVLGKT 288
QY 49 KTASGVNQLVDIYKYQDL-----YVEPNNAQVLETAARDIEKLLNSRKALVSLALE 103
Db 289 KSKLGAEIAAIAWETEESMKLAQYSMB--DARATYEL-----GKEFPFMEAE 334
QY 104 AEKQAAHQWREDFAS--NEVVIY-----NAKDDLDPEKNDSEPGSQRIKPVFI----- 150
Db 335 LAKLIGQSVQVDSRSTGNLVEWILLRVAYERNELAPKNPDEEEYRRRLRTYILGGYKE 394
QY 151 EDANFGROIYQHAHAVHIPTD---IYEGSTIV---LNLNWTLSALDEVFKKNREEDPSL 203
Db 395 PERGLWENIAYLDFRCH-PADTKVIVKKGIVNISDVKEGDIYLGIDG----- 441
QY 204 LMQVFGSATGLARYYPASPWDNSR---TPN-KIDLYVRRRPWTYIQGAASPKDMLILVD 259
Db 442 -WQ---RVKVKWKYHEGLKININGLKCTPNHKVPVVTENDRQTRI-----RDSLAKSF 491
QY 260 VSGSVGLTLKIRTSVSEMLETLSDDDFVNVASPSN----- 297
Db 492 LSGKVKG---KIITTKL-----FEKIAEFKNKPSEEEILKGLSELGIIAEGTL 537
QY 298 -AQVSCF-----OHLVQANV-RNKKVLKDAV-----NNITAKG----- 329
Db 538 LRKDIEYDSSRGKKRISHQYRVEITIGENEKELLERILYFDKLGIRPSVKKKGDTNA 597
QY 330 --ITDYKKGFSFAFEQLLNYNVSRANCKIIMLFYDGGEEAQAQEIFNKYKDKKVRVERF 387
Db 598 LKITTAKAVVLIQIEELK-NIESLYAPAVLRGF-----FERDATYNKIRS 642
QY 388 SV---GQHNVERGPIOWMACENKGY---YVEIPSIGAIRINTQYLDVLRPMVLAGDK 440
Db 643 TIVVTQGTNNKWKIDIVAKLLDSLSGIPYSRYEYKYEINGELTKHILEITGRD----- 695
QY 441 AKQVQWNTVYLDALGLVITGTLPVFNITQGF-----NKTNLKNQLILGVMGD 491
Db 696 -----GLILFTLVGFISSEKNEALEKAEVRENRLKNNSFYNLSTPE 739
QY 492 VSLIEDIKRLTPRTCPNGYFPAIDPNGVYLLHPNLQPNKPSQEPVILDFDLDAELNDI 551
Db 740 VSSEYKGEVYDLTLEGNPYFA---NG-ILTHNSLYPSIIVTHN-VSPDTLRE----- 789
QY 552 KVEIRKMDGSGEKTFTLVKSQDERYIDKGNRTYTTVPVNGTDYSLALVLPYSFY 611
Db 790 -----GCKNYDVAPIVG--YKECKDFPG----F 811
QY 612 IKAKLEETITQARSKKGMKDSKTLKPDNFESEY-----TFIAPRDCNDLKISD 662
Db 812 IPSILGELITMFEQIKKMK--ATIDPIEKKMLDYQRAVKLLANSILPNW---LPITE 866
QY 663 NNTFELLNPFNEDIRKTPNPNPCNADLINRVLLDAGFTNELVQWYWSKQNKIKGVKARFV 722
Db 867 NGEVAFVKIGEFIDRYMEQDKVFTVDNTEYVLEVDNIFAFSLNKESKSEIKKVKAL--- 924
QY 723 VTDGGITRVYPKEAGE 738
Db 925 -----IRHKYKEAYE 935

RESULT 10
ATXL PLAF
ID ATXL PLAF STANDARD; PRT; 1956 AA.
AC Q04956;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE PROBABLE CATION-TRANSPORTING ATPASE 1 (EC 3.6.1.-).
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.

Query Match 2.9%; Score 154.5; DB 1; Length 946;
Best Local Similarity 19.9%; Pred. No. 0.19;

FT	DISULFID	436	452	INTERCHAIN (PROBABLE).
FT	CONFLICT	84	84	P > T (IN REF. 2).
SEQ	SEQUENCE	1290 AA;	148734 MW;	71FBE379F97129E8 CRC64;
Query Match		2.8%;	Score 152;	DB 1; Length 1290;
Best Local Similarity		20.3%;	Pred. No. 0.42;	
Matches		205; Conservative	125; Mismatches	346; Indels 334; Gaps 54;
QY	106	KVQAQHWQRDEFPASVEVYVYNAKDDLDPEKNDSEFGSQRIK	----	PVIEDANFGR----- 157
DB	138	KTROGNNWVTGTSINPSVIITG	-----	PRENIIDPSTFTKLTNTTFAAOGFGALSIIIS 192
QY	158	-----QISYQAAHVIPTDIVEGS	-----	TIVLNLNWTSLDAVEFK---KNRE 198
DB	193	ISPRFMUTYGNAT	-----	NDVGEGRFSKFCMDPILIMHELN--HAMHNLGYGTAI PNQ 246
QY	199	EDPSLLMQVFGSATGLARYXP	-----	ASPVWDSRTPNKIDLYDVRRRPWYIOGAASPKD 253
DB	247	TISSVTSNIFFVSQYNVLEVAEIVAFGGPTID	---	LIPKSARKYPEERKALDYRSTAKRLN 304
QY	254	MLILVDVSG	-----	SVSGGLTKLIIR-----TSVSEMLETLSDDDFVNVASFNSNAQDVSCF 304
DB	305	SITTANPSSFNKYIGEYKQILIRKYRFVSESGEV	---	TVNKNKEVEL--YNELQTQIFTEF 360
QY	305	QHLVQANVRNKKV-LKDAVNNTAK	-----	GTTDYKKGFSPAFEOI-----LNVNYSR----- 351
DB	361	NYAKIYNQNRKTIYLSNVYTPVTANILDDNYDIQNGFNIPKSNLVLFMCQNLNRPAL	420	
QY	352	--ANCNKIIMLFT	-----	DGGEERAQEIENK-----YNKD-----KKRVYFR 386
DB	421	RKVPENMLYLFTEFKHKAIDG	---	RSLYNKTLDCRELLVKNKTDLPFIIGDISVKTDI 475
QY	387	FSVGQHYNERGPIOWMACENKGYVEIPSIGAIRI	---	NTQEY--LDVL----- 430
DB	476	FLRKDINEETEVI	-----	YPDNVSDQVILSKNTSEHGQDLDLYPSIDSESEILP 526
QY	431	GRPMVLADGKAKQVOWTN	---	VYLDALLEGVLITGTLPVNITGOFENKTN----- 478
DB	527	GENQVFDYDNRQNDYLSYYLESQKL	---	SDNVEDFTFSTRTEEAALNSAKYVTFYP 582
QY	479	--LKNQLILGVMG	-----	VDVSLIEDIKRLTPRETLCPNGYFAIDPNGYVLLHHPNLOPK 530
DB	583	TLANKVNAGVOGGLFWANDVWEFTTNILRKDTLDKISDVSAIIP	---	YIGPALNIS 638
QY	531	NPKSQEPPVTLDF	-----	LDAALENDI-----KVEIRKNKMIDGESGEKTFRTL 572
DB	639	NSVRGRNGTEAFATVGTVILLEAFPEFTIPALGAFVVIYSKQOERNEII	-----	KTIONC 692
QY	573	VKSQDERYIDKGNRTYTW	-----	TPVNGTDSLALVLTYSFYIRAKLSEITIQ 622
DB	693	LEQRTIKRKWD	---	SYEMWMTLSRIITQFNISYQWYDSL-NYQAGAIRAKID----- 742
QY	623	ARSKKGMKDSETLKP	---	DNFEESGYTFIAPRDYCNLDKISDNNTFEFLNFNEFI----- 675
DB	743	LEYKYSQSDKENIKSQVENLKN	-----	LDVKIS--EAMNINKFIREGCV 787
QY	676	-----	DRKTPNPSCNADLINRVILDA	----- 697
DB	788	TYLFKNMLPKVIDELNEFDRT	-----	KAKLIN--LIDSHNIIILVEGDKLIKAKVNSNF 839
QY	698	-----GTN	---	ELVQNYW-----SKQNKIKGVKARFVYTDGGITRVYKPEAGE 738
DB	840	QNTIPFNFTSYTNNSLLKDIINEXYFNNDINSKILSLQNKKNLTVDTSQ	-----	YNAEYSE 894
QY	739	--NWQENPETYEDSFYKRSLONDNVVFAPYENKSGPGAYESGIMVSKAVEYIIQGLLK	796	
DB	895	EGDVOLNP	-----	IF--PFDKLGSSGEDGKVIIVTQENINVIYNSMTE 935
QY	797	PAVVGIKIDVNSWIENFTKTSIRDPAGVCDCKRNSDVMOCVILDDGGFLMANHD	---	853
DB	936	SFSISFWTRINKWNSLPCYTIID	-----	SVKNSSWGSIIGIISNFLTFTLKQDNESQ 988

RESULT	15
ITH4_PIG	
ID	ITH4_PIG
AC	STANDARD; PRT; 921 AA.
CT	P79263;
DT	15-JUL-1998 (Rel. 36, Created)
DT	15-JUL-1998 (Rel. 36, Last sequence update)
DT	01-OCT-2000 (Rel. 40, Last annotation update)
DE	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H4 PRECURSOR (ITI HEAVY
DE	CHAIN H4) (INTER-ALPHA-TRYPsin INHIBITOR FAMILY HEAVY CHAIN-RELATED
DE	PROTEIN) (IHRP) (MAJOR ACUTE PHASE PROTEIN) (MAP).
GN	ITI4 OR IHRP.
OS	Sus scrofa (Pig).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX	NCBI_Taxid=9823;
[1]	
RN	SEQUENCE FROM N.A., AND SEQUENCE OF 28-36; 695-703 AND 710-722.
RP	TISSUE=Liver;
RC	MEDLINE=96271024; PubMed=8830057;
RA	Hashimoto K., Tobe T., Sumiya J.-I., Sano Y., Choi-Miura N.-H.,
RA	Ozawa A., Yasue H., Tomita M.;
RT	"Primary structure of the pig homologue of human IHRP: inter-alpha
RT	trypsin inhibitor family heavy chain-related protein.";
RL	J. Biochem. 119:577-584(1996).
[2]	
RN	PRELIMINARY SEQUENCE OF 267-556 FROM N.A.
RP	TISSUE=Liver;
RC	MEDLINE=90371455; PubMed=1697703;
RA	Buchanan T.G., Cabin D.E., Vickers S., Deutschman C.S., Delgado E.,
RA	Sussman M.M., Bulkley G.B.;
RT	"Molecular biology of circulatory shock. Part II. Expression of fo
RT	groups of hepatic genes is enhanced after resuscitation from
RT	cardiogenic shock."
RL	Surgery 108:559-566(1990).
[3]	
RN	SEQUENCE OF 28-54 AND 223-240.
RP	TISSUE=Serum;
RC	MEDLINE=96013138; PubMed=7556597;
FX	

RA Gonzalez-Ramon N., Alava M.A., Sarsa J.A., Pineiro M., Escartin A.,
 RA Garcia-Gil A., Lampreave F., Pineiro A.;
 RT "The major acute phase serum protein in pigs is homologous to human
 CC plasma kallikrein sensitive PK-120.";
 RT FEBS Lett. 371:227-230(1995).
 RL - - - FUNCTION: MAY BE INVOLVED IN ACUTE PHASE REACTIONS.
 CC - - - TISSUE SPECIFICITY: LIVER-SPECIFIC.
 CC - - - INDUCTION: LEVELS INCREASE SIGNIFICANTLY AFTER CARDIOGENIC
 CC SHOCK.
 CC - - - PMW: APPEARS TO BE BOTH N- AND O-GLYCOSYLATED (BY SIMILARITY).
 CC - - - PMW: CLEAVED BY PLASMA KALLIKREIN TO YIELD 55- AND 25-KDA
 CC FRAGMENTS.
 CC - - - SIMILARITY: BELONGS TO THE ITH FAMILY.
 CC - - - SIMILARITY: CONTAINS 1 VWFA DOMAIN.
 CC - - - CAUTION: REF.2 SEQUENCE IS INCORRECT DUE TO FRAMESHIFTS AND OTHER
 CC SEQUENCING ERRORS.
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 CC EMBL; U43164; AAD00024.1; -;
 CC EMBL; S82800; AAB46821.1; -;
 CC EMBL; M29507; -; NOT_ANNOTATED_CDS.
 CC InterPro; IPR002035; -;
 CC Pfam; PF00092; vwa; 1;
 CC PROSITE; PS05234; VWFA_DOMAIN; 1.

KW Serine protease inhibitor; Repeat; Signal; Multigene family;
KW Glycoprotein.

FT SIGNAL 1 27
FT CHAIN 28 921
FT DOMAIN 270 428
FT CARBOHYD 80 80
FT CARBOHYD 205 205
FT CARBOHYD 242 242
FT CARBOHYD 513 513
FT CARBOHYD 577 577
FT CONFLICT 49 50
FT CONFLICT 703 703
SQ SEQUENCE 921 AA; 102146 MW; E2BF95925DE8D07C CRC64;

Query Match 2.8%; Score 150.5; DB 1; Length 921;
Best Local Similarity 19.9%; Pred. No. 0.32; Mismatches 265; Gaps 36;
Matches 156; Conservative 100; Indels 265; Gaps 36;

QY 4 GCLLALTTL-----FQSLIGPSSEPPFPSPAYTIKSWVDK---MQED--- 43
DB 10 GLLLVPLLLAVLQSTAHKNDINIYSLTVDSKVSRRFAHTVVTSRVYVNGSAVQEAETQ 69
QY 44 -----LVTLAKTASGVNQLVDIYK--YODLYT-VEPNNAQOLVEIAARDIEKL--- 89
DB 70 MELPKKAFITNEFMIDGVTYGNIKERAAQEQYSAVARGESAGLVRAATGRKTEQFQVA 129
QY 90 LSNRSKALVSLAEAKVQAAHQWREDPASNEWVYNAKDDLDPEKNDSEPGSORIKPVF 149
DB 130 VSAVPAKVTFFELVEELARH-----LGVTELLKIQOQ-----QLVKHLQ 171
QY 150 IEDANFGRO-ISY-QHAAVHIPTDIYEGTIVLNE-----LNWTSALDEVFKKNREEDPSL 203
DB 172 MDIHIFEPQGISFLETSTFTNLAELATISONKTKAHIREKPTLSQO-QKSPEQEQEV 230
QY 204 L-----WQVFGSATG-----LARYPASPWVDSRTPNPKIDLYDVRPPWYIOG 247
DB 231 LOGNETVRYDVNRTVTGSGIQIENGIVFHYFAPEVW----- 266
QY 248 AASPDKMLLVDSVSGSLTKLIRTSYSEMLETSLDDDFVNVASFNSNAODVSCFOHL 307
DB 267 SAIPKNVIFVIDTSGSMRGKIQOTREALIKILGDLGSRQDNLVSFSGEAPR-----RA 322
QY 308 VOANVRNKKVLDAVNNTAKGITYDKGFSFAFEOQLNINYSRANCNKI-----IM 359
DB 323 VAASAENVEAKSYAAEIIHAQGTNINDAMLAVALQL-----ERANREELLPARSVTFII 377
QY 360 LFTDG-----GEERAQIFNKNKDKVRV-----PFRSVGQHNYERGPIQWMA 403
DB 378 LLTDGPTVGETNPSKI-----QKNVREAIQHSCLGFGFDVPYAFLEK-----MA 426
QY 404 CENKG-----YY-----YEIPSIGAIRINTQEYLDVL--GR 432
DB 427 LENGGLARIYEDSSALQLEDYQEVANPLRLVAFEYPS-NAVEEVTDQDNFRLEFKGS 485
QY 433 PMVLAG---DKAKQVQWNTVYLDALDELGLVITGTLVPFNITQGFENKTNLKNOLILG--- 486
DB 486 ELVAVGKLRDQSDV-----LSAKVRGQLHMENTVFMESRVAEOEAFLSPKY 534
QY 487 -----VMGDVYSLEDI--KRLTPRTLCPCNGYYPFPAIDPNGVYLLHPNL 527
DB 535 IPHSEMERLWAYLTIQQLLAQTVSASDAEKKALEARALSLSLNSYFVTPLTSMVITKEG 594
QY 528 QPNPKSQBPVTLDFDAELENDIKVEIRNKMIDGSEKTEFTFLVKSQDERVIDKGNRT 587
DB 595 QEQSQAERK-----YENGNRQGNTHSGHSSF-----QFHSVGDRT 630
QY 588 YTWTPVNGDYSALVLPYTFYIIKAKLEETITQARSKGKMKDSETLKPDPNFESGYT 647
DB 631 SRLTGGSSVD-----PVFS-----HRRGWKGQAQ-----GFEKMSY- 661
QY 648 FIAPR 652

Db 662 -LPPR 665

Search completed: July 23, 2001, 07:48:12
Job time: 573 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 23, 2001, 07:46:48 ; Search time 125.88 Seconds

(without alignments)
1069.960 Million cell updates/sec

Title: US-09-397-548-15

Perfect score: 5346

Sequence: 1 MAGCLLALTLFLFQSLIG.....TNLIFIVESKGTCPDCTRL 1018

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL16:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_unclassified:*
- 13: sp_vertebrate:*
- 14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5312.5	99.4	1110	4 Q9UIU0	Q9ui0 homo sapien
2	5288	98.9	1091	6 O77773	O77773 sus scrofa
3	5202	97.3	1091	11 Q9ERS3	Q9ers3 rattus norv
4	5134	96.0	1103	11 O08532	O08532 mus musculus
5	3570	66.8	745	4 Q9UDQ3	Q9udq3 homo sapien
6	2900	54.2	1150	4 Q9NY47	Q9ny47 homo sapien
7	2883.5	53.9	1156	11 Q9EOG2	Q9eqg2 mus musculus
8	2872.5	53.7	1143	4 Q9NY48	Q9ny48 homo sapien
9	2872.5	53.7	1145	4 Q9Y268	Q9y268 homo sapien
10	2851.5	53.3	1076	4 Q9UEW0	Q9uew0 homo sapien
11	2682	50.2	975	4 Q9NSA6	Q9nsa6 homo sapien
12	1085	20.3	1091	11 Q921L5	Q921l5 mus musculus
13	1015	19.0	997	4 Q9NY16	Q9ny16 homo sapien
14	923.5	17.4	2190	5 Q9NKG4	Q9nk64 drosophila
15	912.5	17.1	2172	5 Q9VJMO	Q9vjmo drosophila
16	889	16.6	1191	5 Q9VJN7	Q9vjn7 drosophila
17	884	16.5	1255	5 Q9NKG3	Q9nk83 drosophila
18	875	16.4	170	4 Q9UDL7	Q9udl7 homo sapien
19	832.5	15.6	1022	5 Q9V6T7	Q9v6t7 drosophila

20	738.5	13.8	519	4 Q9NY18	Q9ny18 homo sapien
21	589.5	10.7	1148	5 Q17517	Q17517 caenorhabdi
22	514.5	9.6	104	4 Q9UD81	Q9ud81 homo sapien
23	506	9.5	100	6 Q9GLH1	Q9gli1 bos taurus
24	498.5	9.3	121	4 Q9UD82	Q9ud82 homo sapien
25	482	9.0	98	4 Q9UDU5	Q9udu5 homo sapien
26	465	8.7	97	4 Q9UD80	Q9ud80 homo sapien
27	402	7.5	77	4 Q9S026	Q9s026 homo sapien
28	337.5	6.3	1185	4 Q9HCJ9	Q9hcj9 homo sapien
29	317.5	5.9	223	11 Q9RI42	Q9ri42 mus musculu
30	222	4.2	1449	5 Q9V917	Q9v917 drosophila
31	170.5	3.2	494	5 Q9U7P4	Q9u7p4 eufolliculi
32	167	3.1	796	1 Q9HJR0	Q9hjr0 thermoplas
33	161	3.0	2706	5 O15870	O15870 plasmodium
34	156.5	2.9	903	6 Q9GLY5	Q9gly5 orectolagus
35	155	2.9	1516	5 Q9GLY6	Q9gly6 orectolagus
36	155	2.9	2364	2 Q46342	Q46342 clostridium
37	154.5	2.9	1315	2 O86488	O86488 staphylococ
38	153	2.9	932	11 Q35802	Q35802 rattus norv
39	152.5	2.9	789	2 Q45793	Q45793 bacillus th
40	152	2.8	1105	14 Q9EMZ8	Q9emz8 ansacta moo
41	151.5	2.8	2867	5 Q9N2M3	Q9n2m3 plasmodium
42	150.5	2.8	2771	5 Q26216	Q26216 plasmodium
43	150	2.8	946	6 Q9GLY6	Q9gly6 orectolagus
44	149	2.8	459	2 Q25905	Q25905 helicobacte
45	149	2.8	930	4 Q9UQ54	Q9uq54 homo sapien

ALIGNMENTS

RESULT 1

Q9UIU0 Q9UIU0 PRELIMINARY; PRT; 1110 AA.
 ID Q9UIU0;
 AC Q9UIU0;
 DT 01-MAY-2000 (TREMREL. 13, Created)
 DT 01-MAY-2000 (TREMREL. 13, Last sequence update)
 DT 01-MAR-2001 (TREMREL. 16, Last annotation update)
 DE DIHYDROXYRIDINE RECEPTOR ALPHA 2 SUBUNIT.
 GN CACNA2D1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_taxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20005942; PubMed=10534405;
 RA Schleithoff L., Mehrke G., Reutlinger B., Lehmann-Horn F.;
 RT "Genomic structure and functional expression of a human alpha(2)/delta
 RL calcium channel subunit gene (CACNA2).";
 RL Genomics 61:201-209(1999).
 DR EMBL; AF083854; AAF03259.1; JOINED.
 DR EMBL; AF083817; AAF03259.1; JOINED.
 DR EMBL; AF083818; AAF03259.1; JOINED.
 DR EMBL; AF083819; AAF03259.1; JOINED.
 DR EMBL; AF083820; AAF03259.1; JOINED.
 DR EMBL; AF083821; AAF03259.1; JOINED.
 DR EMBL; AF083822; AAF03259.1; JOINED.
 DR EMBL; AF083823; AAF03259.1; JOINED.
 DR EMBL; AF083824; AAF03259.1; JOINED.
 DR EMBL; AF083825; AAF03259.1; JOINED.
 DR EMBL; AF083826; AAF03259.1; JOINED.
 DR EMBL; AF083827; AAF03259.1; JOINED.
 DR EMBL; AF083828; AAF03259.1; JOINED.
 DR EMBL; AF083829; AAF03259.1; JOINED.
 DR EMBL; AF083830; AAF03259.1; JOINED.
 DR EMBL; AF083831; AAF03259.1; JOINED.
 DR EMBL; AF083832; AAF03259.1; JOINED.
 DR EMBL; AF083833; AAF03259.1; JOINED.
 DR EMBL; AF083834; AAF03259.1; JOINED.
 DR EMBL; AF083835; AAF03259.1; JOINED.
 DR EMBL; AF083836; AAF03259.1; JOINED.
 DR EMBL; AF083837; AAF03259.1; JOINED.


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DR EMBL; AF083838; AAF03259.1; JOINED.
DR EMBL; AF083839; AAF03259.1; JOINED.
DR EMBL; AF083840; AAF03259.1; JOINED.
DR EMBL; AF083841; AAF03259.1; JOINED.
DR EMBL; AF083842; AAF03259.1; JOINED.
DR EMBL; AF083843; AAF03259.1; JOINED.
DR EMBL; AF083844; AAF03259.1; JOINED.
DR EMBL; AF083845; AAF03259.1; JOINED.
DR EMBL; AF083846; AAF03259.1; JOINED.
DR EMBL; AF083847; AAF03259.1; JOINED.
DR EMBL; AF083848; AAF03259.1; JOINED.
DR EMBL; AF083849; AAF03259.1; JOINED.
DR EMBL; AF083850; AAF03259.1; JOINED.
DR EMBL; AF083851; AAF03259.1; JOINED.
DR EMBL; AF083852; AAF03259.1; JOINED.
DR EMBL; AF083853; AAF03259.1; JOINED.
DR InterPro; IPR000885; -.
DR Pfam; PF00092; vwa; 1.
DR ProDom; PD002078; -. 1.
KW Receptor.
SQ SEQUENCE 1110 AA; 125307 MW; 8358DC6AD489C074 CRC64;

Query Match 99.4%; Score 5312.5; DB 4; Length 1110;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 1015; Conservative 1; Mismatches 2; Indels 19; Gaps 1;

QY 1 MAAGCLLALTTLTFLQSLLLIGPSSSEPPFPSSAVTIKSWDKMQEDLVTLAKTAGVNLVDI 60
DB 1 MAAGCLLALTTLTFLQSLLLIGPSSSEPPFPSSAVTIKSWDKMQEDLVTLAKTAGVNLVDI 60
QY 61 YEKYQDLYTVEPNNAQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRWEDFASN 120
DB 61 YEKYQDLYTVEPNNAQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRWEDFASN 120
QY 121 EYVYNAKDDLPENKNDSPGSGRIKPVFIEDANFGRIQSYQHAHVHIPTDIYEGSTIVL 180
DB 121 EYVYNAKDDLPENKNDSPGSGRIKPVFIEDANFGRIQSYQHAHVHIPTDIYEGSTIVL 180
QY 181 NELNWTLSALDEVFKKNREDDPSLLQVQGSATGLARIYPASPWVDNSRTPNKIDLYDVR 240
DB 181 NELNWTLSALDEVFKKNREDDPSLLQVQGSATGLARIYPASPWVDNSRTPNKIDLYDVR 240
QY 241 RPWYIQGAASPRDMLILDVDSVSGSLTKLIRTSVSEMLETSLDDDFNVNASFNSAQD 300
DB 241 RPWYIQGAASPRDMLILDVDSVSGSLTKLIRTSVSEMLETSLDDDFNVNASFNSAQD 300
QY 301 VSCFQHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSAFQQLLNYNVSRANCKNIIML 360
DB 301 VSCFQHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSAFQQLLNYNVSRANCKNIIML 360
QY 361 FTDGGEERAQAEYFNKYNDKKVRFVFSVQGHNYERGPQIWMACENKGYEYIPISGAIR 420
DB 361 FTDGGEERAQAEYFNKYNDKKVRFVFSVQGHNYERGPQIWMACENKGYEYIPISGAIR 420
QY 421 INTQYLDVLGRPMVLADGKAKQVQWNTVYLDALGLVITGLPVENTIGOFENKTNLK 480
DB 421 INTQYLDVLGRPMVLADGKAKQVQWNTVYLDALGLVITGLPVENTIGOFENKTNLK 480
QY 481 NOLIIGVGVDSVLSLEDKRLTPRFTLCPNGYFPAIDPNGYLLHPNLQPK----- 530
DB 481 NOLIIGVGVDSVLSLEDKRLTPRFTLCPNGYFPAIDPNGYLLHPNLQPK----- 530
QY 531 -----NPKSQEPVLDLDALENDIKVEINRKNKIDGESGKTFRTLVKSODERYI 581
DB 541 LKRRNPNTQNPQSQEPVLDLDALENDIKVEINRKNKIDGESGKTFRTLVKSODERYI 600
QY 582 DKGNTTYTTPVNGDYSLALVLPYTFYVYIKAKLEETITQARSKKKKMKKSETLKPDPNF 641
DB 601 DKGNTTYTTPVNGDYSLALVLPYTFYVYIKAKLEETITQARSKKKKMKKSETLKPDPNF 660
QY 642 EESGYTFIAPRDYCNLDKISDNNTFELLNFEFIDRKTPNPNPCNADLINRVLLDAGFTN 701

661 EESGYTFIAPRDYCNLDKISDNNTFELLNFEFIDRKTPNPNPCNADLINRVLLDAGFTN 720
702 ELVQVYWSKOKNIKGKRVFVTDGGITRVYPKAENQENPETYEDSFYKRSNDNY 761
721 ELVQVYWSKOKNIKGKRVFVTDGGITRVYPKAENQENPETYEDSFYKRSNDNY 780
762 VFTAPYFNKSGGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDP 821
781 VFTAPYFNKSGGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDP 840
822 CAGPVCDCRNSDVMDCVILDDGGFLLMANHDDYTQIOGRFCEIDPISLMRHLVNI SVYA 881
841 CAGPVCDCRNSDVMDCVILDDGGFLLMANHDDYTQIOGRFCEIDPISLMRHLVNI SVYA 900
882 FNKSYDYQVCEPGAAPKQAGHRSAYVPSVADILQIGMWATAAASWIILOQFLLSLTFPR 941
901 FNKSYDYQVCEPGAAPKQAGHRSAYVPSVADILQIGMWATAAASWIILOQFLLSLTFPR 960
942 LLEAVEMEDDDFTASLSKOSCITEQTQYFFDNDKSFSGVLDGCGNCSRIFFHGEKLMNTNL 1001
961 LLEAVEMEDDDFTASLSKOSCITEQTQYFFDNDKSFSGVLDGCGNCSRIFFHGEKLMNTNL 1020
1002 IFIMVESKGTCTPCDTRL 1018
1021 IFIMVESKGTCTPCDTRL 1037

RESULT 2
ID 077773 PRELIMINARY; PRT; 1091 AA.
AC 077773;
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DE VOLTAGE-DEPENDENT CALCIUM CHANNEL ALPHA-2 DELTA SUBUNIT PRECURSOR.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CEREBRAL CORTEX;
RX MEDLINE=98411353; PubMed=9738015;
RA Brown J.P., Gee N.S.;
RT "Cloning and deletion mutagenesis of the alpha2 delta calcium channel
RT subunit from porcine cerebral cortex. Expression of a soluble form of
RL the protein that retains [3H]gabapentin binding activity.";
RL J. Biol. Chem. 273:25458-25465(1998).
DR EMBL; AF077665; AAC36289.1; -.
DR InterPro; IPR002035; -.
DR Pfam; PF00092; vwa; 1.
DR Signal.
KW SIGNAL.
FT CHAIN 1 24
FT SIGNAL 25 1091
FT CHAIN 25 1091
SQ SEQUENCE 1091 AA; 123150 MW; 293DDC7EBE9EE60E CRC64;

Query Match 98.9%; Score 5288; DB 6; Length 1091;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1006; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 MAAGCLLALTTLTFLQSLLLIGPSSSEPPFPSSAVTIKSWDKMQEDLVTLAKTAGVNLVDI 60
DB 1 MAAGCLLALTTLTFLQSLLLIGPSSSEPPFPSSAVTIKSWDKMQEDLVTLAKTAGVNLVDI 60
QY 61 YEKYQDLYTVEPNNAQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRWEDFASN 120
DB 61 YEKYQDLYTVEPNNAQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRWEDFASN 120
QY 121 EYVYNAKDDLPENKNDSPGSGRIKPVFIEDANFGRIQSYQHAHVHIPTDIYEGSTIVL 180
DB 121 EYVYNAKDDLPENKNDSPGSGRIKPVFIEDANFGRIQSYQHAHVHIPTDIYEGSTIVL 180
```

RC STRAIN=SPRAGUE-DAWLEY; TISSUE=SUPERIOR CERVICAL GANGLIA;
 RA Lin Y. Lipscombe D.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF286488; AAG28164.1;
 FT VARIANT 209 212 GSAT -> AADR.
 FT VARIANT 338 338 S -> T.
 FT VARIANT 599 600 SL -> RY.
 FT VARIANT 869 869 S -> R.
 SQ SEQUENCE 1091 AA; 123467 MW; C155088971628E19 CRC64;

Query Match 97.3%; Score 5202; DB 11; Length 1091;
 Best Local Similarity 96.6%; Pred. No. 0;
 Matches 983; Conservative 20; Mismatches 15; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLLTQSLGSPSEPPSAVITKSWDKMQEDLVTLAKTASGVNOLVDI 60
 DB 1 MAAGCLLALTLLTQSLGSPSEPPSAVITKSWDKMQEDLVTLAKTASGVNOLVDI 60
 QY 61 YEKYQDLYVPEPNARQLVEIAARDIEKLSNRSKALVLAELAEKVAQAAHQWREFASN 120
 DB 61 YEKYQDLYVPEPNARQLVEIAARDIEKLSNRSKALVLAELAEKVAQAAHQWREFASN 120
 QY 121 EYVYNAKDDLDPEKNDSEPSQRIKPVFTEDANFGROISYQHAHVHPTDIYEGSTIVL 180
 DB 121 EYVYNAKDDLDPEKNDSEPSQRIKPVFTEDANFGROISYQHAHVHPTDIYEGSTIVL 180
 QY 181 NELNWTALDEVEFKKNEEDPSLLQWVFGSATGLARYYPASPVWDNSRTNPKIDLYDVR 240
 DB 181 NELNWTALDEVEFKKNEEDPSLLQWVFGSATGLARYYPASPVWDNSRTNPKIDLYDVR 240
 QY 241 RPWYIOGAASPDKMLILVDVSGVSGITLKLIRTSVSEMLETSDDDFVNVSFNSNAQD 300
 DB 241 RPWYIOGAASPDKMLILVDVSGVSGITLKLIRTSVSEMLETSDDDFVNVSFNSNAQD 300
 QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAEQLLNVSFNSNAQD 360
 DB 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAEQLLNVSFNSNAQD 360
 QY 361 FTDGGEERAQEIFAKYKNDKVRVFTSVGQHNDRGPIQWACENKGYEIPSGAIR 420
 DB 361 FTDGGEERAQEIFAKYKNDKVRVFTSVGQHNDRGPIQWACENKGYEIPSGAIR 420
 QY 421 INTQEYLDVLRPMVLGADKAKQVNTNVLDALEGLVITGTLVPFNITQGFENKTNLK 480
 DB 421 INTQEYLDVLRPMVLGADKAKQVNTNVLDALEGLVITGTLVPFNITQGFENKTNLK 480
 QY 481 NQILGVMGVDSLEDIKRLTPRTLCPCNGYFAIDPNGYVLLHNPLOKPKKSEPTVL 540
 DB 481 NQILGVMGVDSLEDIKRLTPRTLCPCNGYFAIDPNGYVLLHNPLOKPKKSEPTVL 540
 QY 541 DFLDALENDIKVEIRNKMIDGESKERTFLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600
 DB 541 DFLDALENDIKVEIRNKMIDGESKERTFLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600
 QY 601 ALVLPYTFYIIKAKLEETITQARSKGKMKDSETLKPDNFEESGYTFIAPRDYCNLKI 660
 DB 601 ALVLPYTFYIIKAKLEETITQARSKGKMKDSETLKPDNFEESGYTFIAPRDYCNLKI 660
 QY 661 SDNTEFLNNEFIDRKTTPNPNADLINRVLDAGFTNELVQVNSKQNKIKVKAR 720
 DB 661 SDNTEFLNNEFIDRKTTPNPNADLINRVLDAGFTNELVQVNSKQNKIKVKAR 720
 QY 721 FVYTDGGITRVYPKEAGENQENPETEYDSFYKRSIDNDNYVFTAPYFNKSGPGAYESGI 780
 DB 721 FVYTDGGITRVYPKEAGENQENPETEYDSFYKRSIDNDNYVFTAPYFNKSGPGAYESGI 780
 QY 781 MYSKAVEIYIQGKLLKPAVVGKIDVNSNIENFTKTSIRDPCAGPVCDCKRNSDMDCVI 840
 DB 781 MYSKAVEIYIQGKLLKPAVVGKIDVNSNIENFTKTSIRDPCAGPVCDCKRNSDMDCVI 840
 QY 841 LDDGGFLMANHDDYTNGIRFFGEIDPSLMRHLNINISVAFNKSIDYQSVCEPGAAPQ 900
 DB 841 LDDGGFLMANHDDYTNGIRFFGEIDPSLMRHLNINISVAFNKSIDYQSVCEPGAAPQ 900

Db 121 EYVYNAKDDLDPEKNDSEPSQRIKPVFIDANFGROISYQHAHVHPTDIYEGSTIVL 180
 QY 181 NELNWTALDEVEFKKNEEDPSLLQWVFGSATGLARYYPASPVWDNSRTNPKIDLYDVR 240
 Db 181 NELNWTALDEVEFKKNEEDPSLLQWVFGSATGLARYYPASPVWDNSRTNPKIDLYDVR 240
 QY 241 RPWYIOGAASPDKMLILVDVSGVSGITLKLIRTSVSEMLETSDDDFVNVSFNSNAQD 300
 Db 241 RPWYIOGAASPDKMLILVDVSGVSGITLKLIRTSVSEMLETSDDDFVNVSFNSNAQD 300
 QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAEQLLNVSFNSNAQD 360
 Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAEQLLNVSFNSNAQD 360
 QY 361 FTDGGEERAQEIFAKYKNDKVRVFTSVGQHNDRGPIQWACENKGYEIPSGAIR 420
 Db 361 FTDGGEERAQEIFAKYKNDKVRVFTSVGQHNDRGPIQWACENKGYEIPSGAIR 420
 QY 421 INTQEYLDVLRPMVLGADKAKQVNTNVLDALEGLVITGTLVPFNITQGFENKTNLK 480
 Db 421 INTQEYLDVLRPMVLGADKAKQVNTNVLDALEGLVITGTLVPFNITQGFENKTNLK 480
 QY 481 NQILGVMGVDSLEDIKRLTPRTLCPCNGYFAIDPNGYVLLHNPLOKPKKSEPTVL 540
 Db 481 NQILGVMGVDSLEDIKRLTPRTLCPCNGYFAIDPNGYVLLHNPLOKPKKSEPTVL 540
 QY 541 DFLDALENDIKVEIRNKMIDGESKERTFLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600
 Db 541 DFLDALENDIKVEIRNKMIDGESKERTFLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600
 QY 601 ALVLPYTFYIIKAKLEETITQARSKGKMKDSETLKPDNFEESGYTFIAPRDYCNLKI 660
 Db 601 ALVLPYTFYIIKAKLEETITQARSKGKMKDSETLKPDNFEESGYTFIAPRDYCNLKI 660
 QY 661 SDNTEFLNNEFIDRKTTPNPNADLINRVLDAGFTNELVQVNSKQNKIKVKAR 720
 Db 661 SDNTEFLNNEFIDRKTTPNPNADLINRVLDAGFTNELVQVNSKQNKIKVKAR 720
 QY 721 FVYTDGGITRVYPKEAGENQENPETEYDSFYKRSIDNDNYVFTAPYFNKSGPGAYESGI 780
 Db 721 FVYTDGGITRVYPKEAGENQENPETEYDSFYKRSIDNDNYVFTAPYFNKSGPGAYESGI 780
 QY 781 MYSKAVEIYIQGKLLKPAVVGKIDVNSNIENFTKTSIRDPCAGPVCDCKRNSDMDCVI 840
 Db 781 MYSKAVEIYIQGKLLKPAVVGKIDVNSNIENFTKTSIRDPCAGPVCDCKRNSDMDCVI 840
 QY 841 LDDGGFLMANHDDYTNGIRFFGEIDPSLMRHLNINISVAFNKSIDYQSVCEPGAAPQ 900
 Db 841 LDDGGFLMANHDDYTNGIRFFGEIDPSLMRHLNINISVAFNKSIDYQSVCEPGAAPQ 900
 QY 901 GAGHSAYVPVADILQIGWATAAASILQOFLSLFPRLLEAEMEDDDFTASLSQ 960
 Db 901 GAGHSAYVPVADILQIGWATAAASILQOFLSLFPRLLEAEMEDDDFTASLSQ 960
 QY 961 SCITEOTQYFFDNDSKPSGVLDGNCGRIFHVEKLMNTNLFIMVESKGTCPDCTRL 1018
 Db 961 SCITEOTQYFFDNDSKPSGVLDGNCGRIFHVEKLMNTNLFIMVESKGTCPDCTRL 1018
 RESULT 3
 Q9ERS3 PRELIMINARY; PRT: 1091 AA.
 ID Q9ERS3
 AC Q9ERS3;
 DT 01-MAR-2001 (Tremblrel..16, Created)
 DT 01-MAR-2001 (Tremblrel..16, Last sequence update)
 DT 01-MAR-2001 (Tremblrel..16, Last annotation update)
 DE VOLTAGE-GATED CALCIUM CHANNEL ALPHA2/DELTA-1 SUBUNIT.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.

Db 841 LDGGFLMANHDDYTNQIGRFFGEIDPSMRHLVNLISLYAFNKSVDYOSVCDPAAKQ 900

QY 901 GAGRSAYVPSVDILQIGWATAAASILQOFLLSITPRLLAEVEMEDDDFTASLSKQ 960

Db 901 GAGRSAYVPSVDILQIGWATAAASILQOFLLSITPRLLAEVEMEDDDFTASLSKQ 960

QY 961 SCITEQTFYFFDNDKSFSGVLDCGNCRSRIFHGEKLMNTNLIFIMVESKGTCPDTRL 1018

Db 961 SCITEQTFYFFKNDTKSFSGLLDCGNCRSRIFHVEKLMNTNLIFIMVESKGTCPDTRL 1018

RESULT 4

ID 008532 PRELIMINARY; PRT: 1103 AA.

AC 008532; 008533; 008534; 008536;

DT 01-JUN-1998 (IREMBLrel. 06, Created)

DT 01-JUN-1998 (IREMBLrel. 06, Last sequence update)

DT 01-JUN-2000 (IREMBLrel. 14, Last annotation update)

DE DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-2/DELTA

DE SUBUNITS PRECURSOR.

GN CACNA2D1 OR CACNA2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxId=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=BRAIN;

RX MEDLINE=97113514; PubMed=8955374;

RA Angelotti T., Hofmann F.;

RL FEBS Lett. 397:331-337(1996).

CC -!- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN EXCITATION-CONTRACTION COUPLING.

CC -!- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS: ALPHA-1, ALPHA-2, BETA AND GAMMA.

CC -!- SUBUNIT: ALPHA-2 AND DELTA FORM HETERODIMERS THAT ARE DISULFIDE-LINKED.

CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -!- ALTERNATIVE PRODUCTS: FIVE FORMS OF THE PROTEIN. ISOFORMS 2A-2E, ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THE SEQUENCE SHOWN HERE IS THAT OF ISOFORM 2A.

CC -!- TISSUE SPECIFICITY: ISOFORM 2A IS EXPRESSED IN SKELETAL MUSCLE AND AORTA, 2B IS EXPRESSED IN BRAIN, 2C IS EXPRESSED IN HEART, 2D IS EXPRESSED IN HEART AND SMOOTH MUSCLE, AND 2E IS EXPRESSED IN SMOOTH MUSCLE. ALL FIVE ISOFORMS ARE EXPRESSED IN THE CARDIOVASCULAR SYSTEM.

CC -!- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM A PRECURSOR FORM.

CC -!- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.

DR EMBL; U73484; AAB50139.1; -

DR EMBL; U73485; AAB50140.1; -

DR EMBL; U73483; AAB50138.1; -

DR EMBL; U73486; AAB50141.1; -

DR EMBL; U73487; AAB50142.1; -

DR MGI; MGI:88295; Cacna2d1.

DR InterPro; IPR002035; -

DR Pfam; PF00092; vwa; 1.

KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel; Calcium channel; Glycoprotein; Phosphorylation; Signal;

KW Alternative splicing.

FT SIGNAL 1 24

FT CHAIN 25 957

FT CHAIN 958 1103

FT TRANSMEM 446 469

FT TRANSMEM 918 942

FT TRANSMEM 1079 1098

FT MOD_RES 501 501

FT MOD_RES 845 845

FT CARBOHYD 92 92

FT CARBOHYD 136 136

FT CARBOHYD 184 184

FT CARBOHYD 324 324

FT CARBOHYD 348 348

FT CARBOHYD 348 348

FT CARBOHYD 475 475 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 604 604 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 675 675 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 781 781 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 824 824 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 888 888 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 895 895 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 985 985 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 998 998 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT VARSPLIC 531 549 MISSING (IN ISOFORMS 2B AND 2E).

FT VARSPLIC 531 554 MISSING (IN ISOFORMS 2C AND 2D).

FT VARSPLIC 644 644 Y -> SKGKKMD (IN ISOFORMS 2A, 2D AND 2E).

SQ SEQUENCE 1103 AA; 124629 MW; 103773BA735120D4 CRC64;

Query Match 96.0%; Score 5134; DB 11; Length 1103;

Best Local Similarity 94.2%; Pred. No. 0;

Matches 977; Conservative 20; Mismatches 14; Indels 26; Gaps 2;

QY 1 MAAGCLLALTTLFOSLLIGPSEEPFSAVTIKSWDKMQEDLVTLAKTAGVNLVDI 60

Db 1 MAAGCLLALTTLFOSLLIGPSEEPFSAVTIKSWDKMQEDLVTLAKTAGVTLADI 60

QY 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLAEAEKVAQAAHQWREDFASN 120

Db 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLAEAEKVAQAAHQWREDFASN 120

QY 121 EVVYVNAKDDLDPEKNDSEPGSQRIKPVIEDANFGQISQYQHAHVHPTDIYEGSTIVL 180

Db 121 EVVYVNAKDDLDPERNESEPGSQRIKPVIEDANFGQISQYQHAHVHPTDIYEGSTIVL 180

QY 181 NELNWTSALEDEVFKKNREEDPSLIMQVFGSATGLARYYPASWPVDNSRTPNKIDLYDVR 240

Db 181 NELNWTSALEDEVFKKNREEDPTLLMQVFGSATGLARYYPASWPVDNSRTPNKIDLYDVR 240

QY 241 RPYITQGAASPKDMLILVDVSGVSLTLKLTSTVSEMLETSLDSDDFNVASFNSNAOD 300

Db 241 RPYITQGAASPKDMLILVDVSGVSLTLKLTSTVSEMLETSLDSDDFNVASFNSNAOD 300

QY 301 VSCFOHLVQANVRNKKVLKDAVNNTAKGITYKKGFSAFQQLLNYNVSRANCKNIIML 360

Db 301 VSCFOHLVQANVRNKKVLKDAVNNTAKGITYKKGFSAFQQLLNYNVSRANCKNIIML 360

QY 361 FTDGGEERAQEIFNKYNKDKKVRVFRFSVQHNYPGRPIQWMACENKGYIYEIPSGAIR 420

Db 361 FTDGGEERAQEIFAKYNKDKKVRVFTFSVQHNYPGRPIQWMACENKGYIYEIPSGAIR 420

QY 421 INTQEYLDVLGRPMVLADGKAKOVQWTVNYLDALGLVITGTLVPFNTIGQFENKTNLK 480

Db 421 INTQEYLDVLGRPMVLADGKAKOVQWTVNYLDALGLVITGTLVPFNTIGQSENKTNLK 480

QY 481 NOLIILGVMGVDVSLIEDIKRLTPRFTLCPNGYFFADPNGYVLLHHPNLOPK ----- 530

Db 481 NOLIILGVMGVDVSLIEDIKRLTPRFTLCPNGYFFADPNGYVLLHHPNLOPKPGTGVGPIPTIN 540

QY 531 -----NPKSQEPVTLDFDAELENDIKVEIRNKMIDGESGEKTFRTLVKSDERYI 581

Db 531 -----NPKSQEPVTLDFDAELENDIKVEIRNKMIDGESGEKTFRTLVKSDERYI 600

QY 582 DKGNTYTWTPVNGTDYSIALVLPYSPYIIKAKLEETITQARSKKGMKDSKSETLKPONF 641

Db 601 DKGNTYTWTPVNGTDYSIALVLPYSPYIIKAKLEETITQARSKKGMKDSKSETLKPONF 653

QY 642 EESGYTFIAPRDYCNLDKISDNTEFLNFEFIDRKTPNPNPCNADLNRLVLLDAGFTN 701

Db 654 EESGYTFIAPREYCNLDKPSDNTTEFLNFEFIDRKTPNPNPCNADLNRLVLLDAGFTN 713

QY 702 ELVQYWSKQNKIKGVKARFVVVDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNY 761

Db 714 ELVQYWSKQNKIKGVKARFVVVDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNY 773

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QY 762 VFTAFYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIEFTKTSIRDP 821
DB 774 VFTAFYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIEFTKTSIRDP 833
QY 822 CAGPVCDCRNSDVMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNISVYA 881
DB 834 CAGPVCDCRNSDVMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNISVYA 893
QY 882 FNKSYDYOSVCEPGAAPKQAGHRSAYVPSVADIIQIGWATAAAWSILQOFLLSLTTPR 941
DB 894 FNKSYDYOSVCEPGAAPKQAGHRSAYVPSIADIQIGWATAAAWSILQOFLLSLTTPR 953
QY 942 LLEAVEMEDDDFTASLSKQSCITEQTQYFFDNDSKFSFSGVLDGCGNCSRFHGEKLMNTNL 1001
DB 954 LLEAVEMEDDDFTASLSKQSCITEQTQYFFDNDSKFSFSGVLDGCGNCSRFHGEKLMNTNL 1013
QY 1002 IFIMVESKTCPCDTRL 1018
DB 1014 VFIMVESKTCPCDTRL 1030

RESULT 5
ID Q9UDQ3 PRELIMINARY; PRT; 745 AA.
AC Q9UDQ3;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE WUGSC:HLJ056004.1 PROTEIN (FRAGMENT).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99063792; PubMed=9847074;
RA Sulston J.E., Waterston R.;
RT "Toward a complete human genome sequence.";
RL Genome Res. 8:1097-1108(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Mead K., Bauer C.;
RT "The sequence of Homo sapiens PAC clone RP4-560014.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Waterston R.H.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006145; A020938.1;
DR InterPro; IPR002035;
FT NON_TER;
SQ SEQUENCE 745 AA; 84396 MW; BC07B53484B71EA4 CRC64;

Query Match 66.88; Score 3570; DB 4; Length 745;
Best Local Similarity 99.7%; Pred. No. 7.1e-220;
Matches 670; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 347 YNVSFRANCKIIMLFTDGEERAQEIFNKYKNDKKVRVFRFSVGOHNYVERGPIQWACEN 406
DB 1 YNVSFRANCKIIMLFTDGEERAQEIFNKYKNDKKVRVFRFSVGOHNYDRGPIQWACEN 60
QY 407 KGYEYIPSGAIRINTQYLDVLRPMVLADGAKQVQWNTNVLDALEGLVITGLPV 466
DB 61 KGYEYIPSGAIRINTQYLDVLRPMVLADGAKQVQWNTNVLDALEGLVITGLPV 120
QY 467 FNITQFENKTNKQLILGVNGVDVSLIEDIKRLTPRTLCPNGYFFAIDPNGYVLLHPN 526
DB 121 FNITQFENKTNKQLILGVNGVDVSLIEDIKRLTPRTLCPNGYFFAIDPNGYVLLHPN 180

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QY 527 LQPNKPSQEPVTLDFDLDALENDIKVEIRNKMIDGSEKFTFTLVKSQDRIYDKGNR 586
DB 181 LQPNKPSQEPVTLDFDLDALENDIKVEIRNKMIDGSEKFTFTLVKSQDRIYDKGNR 240
QY 587 TYTWTVPVNGTDSLALVPTYSFYIKAKLEETITQAKSKGKMDSETLKPNDNEESY 646
DB 241 TYTWTVPVNGTDSLALVPTYSFYIKAKLEETITQAKSKGKMDSETLKPNDNEESY 300
QY 647 TFIAPRDYCNLDKISDNNTFEFLNNEFDRTKTPNPNPCNADLINRVLLDAGFTNELVN 706
DB 301 TFIAPRDYCNLDKISDNNTFEFLNNEFDRTKTPNPNPCNADLINRVLLDAGFTNELVN 360
QY 707 YWSKOKNIKGVKARFVVTGGITRVYPKEAGENWQENPETYEDSFYKRSILDNDNYVFTAP 766
DB 361 YWSKOKNIKGVKARFVVTGGITRVYPKEAGENWQENPETYEDSFYKRSILDNDNYVFTAP 420
QY 767 YFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIEFTKTSIRDP 826
DB 421 YFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIEFTKTSIRDP 480
QY 827 CDCKRNSDVMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNISVYAFNKSY 886
DB 481 CDCKRNSDVMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNISVYAFNKSY 540
QY 887 DYQSVCEPGAAPKQAGHRSAYVPSVADIIQIGWATAAAWSILQOFLLSLTTPRLEAV 946
DB 541 DYQSVCEPGAAPKQAGHRSAYVPSVADIIQIGWATAAAWSILQOFLLSLTTPRLEAV 600
QY 947 EMEDDDDFTASLSKQSCITEQTQYFFDNDSKFSFSGVLDGCGNCSRFHGEKLMNTNLIFIMV 1006
DB 601 EMEDDDDFTASLSKQSCITEQTQYFFDNDSKFSFSGVLDGCGNCSRFHGEKLMNTNLIFIMV 660
QY 1007 ESKGTCPCDTRL 1018
DB 661 ESKGTCPCDTRL 672

RESULT 6
ID Q9NY47 PRELIMINARY; PRT; 1150 AA.
AC Q9NY47;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE CALCIUM CHANNEL, ALPHA 2/DELTA SUBUNIT 2.
GN CACNA2D2.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYROID;
RA Klugbauer N.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=THYROID;
RA Hobom M., Dai S., Marats E., Lacinova L.;
RT "Neuronal distribution and functional characterization of the calcium channel alpha2delta-2 subunit.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ251368; CAB86193.1;
DR InterPro; IPR002035;
SQ SEQUENCE 1150 AA; 129875 MW; 37B75F687AFE573C CRC64;

Query Match 54.2%; Score 2900; DB 4; Length 1150;
Best Local Similarity 54.7%; Pred. No. 9.6e-177;
Matches 564; Conservative 164; Mismatches 273; Indels 30; Gaps 13;

QY 7 LALTLTFLQSLIGPSSPEPPFSAVTIKSWDKMQEDLVTLAKTAGVNLVIEKYQD 66

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Db 44 LWLLPPLPAAAPGASAYSPQOHTMQHARRLEQVDGWNIRFGVQOQLREIYKDRN 103
QY 67 LTVTPNARQULVEAARDIEKLLSNRSKALVSLALEAEKVAQAQHWREDFASNEVYIN 126
Db 104 LFEVQENEPQKLVKAVAGDIESLLDRKQVALKRLADAAENFKAHQWQDNKEEDIVYD 163
QY 127 AKDDL---DPEKNDSEPGSQ--RIKPVIEDANFGRQISYQAAHVIPTDIYEGSTIVLN 181
Db 164 AKADAELODPESEDVERGSKASTLRDLFIEDPNFNKNYNSYAAVQIPTDIYKGSTVLN 223
QY 182 ELNWTLSALDEYFKKREDDPSLLWQVFGSATGLARYYPASPWDNSRTPNKIDLYDVR 241
Db 224 ELNWTLEALNFVEMENRRQDPTLLAQVFSATGVTYYPATPW----RAPKKIDLYDVR 279
QY 242 PWYIOGASPKDMLILVDVSGVSLTLKLRISYSEMLETLSDDDFYNVASFNSAQDV 301
Db 280 PWYIOGASPKDMLILVDVSGVSLTLKLRISYSEMLETLSDDDFYNVASFNEKAQPV 339
QY 302 SCFOHLVQANRNKKVLKADANNITAKGITDYKKGFSFAFQOLLNLYNVRANCNKIIMLF 361
Db 340 SCFTHLVQANRNKKVKEAVQGVMAKGTGKAGFYAFDQOLQNSNITRANCNKIMMF 399
QY 362 TDGGEERAQEIFNKN--KDKKVRFRFSVGOHNYERGPIONMACENKGYIYEPSIGAIR 420
Db 400 TDGGEDRVQDVFYKYNPNRTVRVFTSVGOHNYDYTPLOWMACANKGYIYEPSIGAIR 459
QY 421 INTQEYLDVGRPMVLGADKAKQVQWNTNVDLDALEGLVITGTLVPFNITGQFENKTLK 480
Db 460 INTQEYLDVGRPMVLGADKAKQVQWNTNVDLDALEGLVITGTLVPFNITGQFENKTLK 517
QY 481 NOLLILGVGVDVSLDKRLTPRTLCPCNGYFAIDPNGYVLLHPNLOPKNPKSQEPVTL 540
Db 518 NOLLILGVGVDVSLDKRLTPRTLCPCNGYFAIDPNGYVLLHPNLOPKNPKSQEPVTL 577
QY 541 DFLDAELENDIKVIRNKMDGEGEKTFTLVKSODERYIDKGNRTYTWTPYNGTDYSL 600
Db 578 DFLDAELENDIKVIRNKMDGEGEKTFTLVKSODERYIDKGNRTYTWTPYNGTDYSL 637
QY 601 ALVLPYTSFYIAKLEETITQARKKGMKDSITLKPDMFESGYTFIAPRYCNDLKI 660
Db 638 GLVLPYTSFYIAKLEETITQARKKGMKDSITLKPDMFESGYTFIAPRYCNDLKI 697
QY 661 SDNTEFLANFEDIRKTPNPNPCNADLNRLVLLDAGTNELVQNVWSKQK--NIKGVKA 719
Db 698 SDNTEFLANFEDIRKTPNPNPCNADLNRLVLLDAGTNELVQNVWSKQK--NIKGVKA 757
QY 720 RFVVTGGITRVPKPEAGENQENPTYEDSFYKRSLDNDNVYFAPYFNK--SGPGAYES 778
Db 758 RFVVTGGITRVPKPEAGENQENPTYEDSFYKRSLDNDNVYFAPYFNK--SGPGAYES 817
QY 779 ---GIMYSKAVEIYIOGKLLKPAVVGKIDVNSWIEF-----TKTSIRDP--CAGP--- 825
Db 818 DTGVLVSTAVELSLGRTRLPRAVVGKLDLEAWAEKFKVLASNRTHQDQPKC--GPNSH 876
QY 826 -VDCRNSVDMCVLDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNI-SVAFNK 884
Db 877 CEMDCVNNEDLCLVLDGGFLVLSQNHQWQVGRFFSEVDANLMLALYNNSFYTRKE 936
QY 885 SYDQSVCEPGAAPKAGHRSAYSVADILQIGWATAAHSILQOFLSLTFFRLLE 944
Db 937 SYDQSVCEPGAAPKAGHRSAYSVADILQIGWATAAHSILQOFLSLTFFRLLE 996
QY 945 AVEMEDDDFTASLSKOSCTEQTOYFFDNDKSKFSGLVDCGNCGRIFPHGKLMNTLIFI 1004
Db 997 ADPAEAG--SPETRESSCVMKQTYFGSVNASYALIDCGNCSRLFHAQRLTNLTLLFV 1055
QY 1005 MWESKTCPCD 1015
Db 1056 VAEKPLCSQCE 1066
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RESULT 7

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Q9EQG2
ID Q9EQG2 PRELIMINARY; PRT; 1156 AA.
AC Q9EQG2;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE VOLTAGE-DEPENDENT CALCIUM CHANNEL ALPHA-2-DELTA-2 SUBUNIT.
GN CACNA2D2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TKDU;
RX MEDLINE=21015416; PubMed=11130987;
RA Barclay J., Rees M.;
RT "Genomic organization of the mouse and human alpha2delta2 voltage-
RT dependent calcium channel subunit genes.";
RL Mamm. Genome 11:1142-1144(2000).
DR EMBL; AF247139; AAC47846.1;
SQ SEQUENCE 1156 AA; 130611 MW; A732545A2B302A52 CRC64;

Query Match 53.9%; Score 2883.5; DB 11; Length 1156;
Best Local Similarity 54.2%; Pred. No. 1.1e-175;
Matches 560; Conservative 168; Mismatches 274; Indels 31; Gaps 14;

QY 6 LLALTLLFOSLLIGP--SSEPPFSAVTIKSWDKMEDLVLTAKTAGVGNQLVDIYEKY 64
Db 45 LLLPPLPPLPPTAPGASAYSPQOHTMQHARRLEQVDGWNIRFGVQOQLREIYKDN 104
QY 65 QDLYTPNARQULVEAARDIEKLLSNRSKALVSLALEAEKVAQAQHWREDFASNEVY 124
Db 105 RNFEVQENEPQKLVKAVAGDIESLLDRKQVALKRLADAAENFKAHQWQDNKEEDIMY 164
QY 125 YNAKDDL---DPEKNDSEPGSQ--RIKPVIEDANFGRQISYQAAHVIPTDIYEGSTIV 179
Db 165 YDAKADAELODPESEDVERGSKASTLRDLFIEDPNFNKNYNSYTAQVQIPTDIYKGSTVI 224
QY 180 LNELNWTLSALDEYFKKREDDPSLLWQVFGSATGLARYYPASPWDNSRTPNKIDLYDVR 239
Db 225 LNELNWTLEALNFVEMENRRQDPTLLAQVFSATGVTYYPATPW----RAPKKIDLYDVR 280
QY 240 RRPWYIOGASPKDMLILVDVSGVSLTLKLRISYSEMLETLSDDDFYNVASFNSAQ 299
Db 281 RRPWYIOGASPKDMLILVDVSGVSLTLKLRISYSEMLETLSDDDFYNVASFNSAQ 340
QY 300 DVSCFOHLVQANRNKKVLKADANNITAKGITDYKKGFSFAFQOLLNLYNVRANCNKIIM 359
Db 341 PVSCFTHLVQANRNKKVKEAVQGVMAKGTGKAGFYAFDQOLQNSNITRANCNKIM 400
QY 360 LFTDGGEEERAQEIFNKN--KDKKVRFRFSVGOHNYERGPIONMACENKGYIYEPSIGA 418
Db 401 MFTDGGEDRVQDVFYKYNPNRTVRVFTSVGOHNYDYTPLOWMACNKGYIYEPSIGA 460
QY 419 IRINTQEYLDVGRPMVLGADKAKQVQWNTNVDLDALEGLVITGTLVPFNITGQFENKTN 478
Db 461 IRINTQEYLDVGRPMVLGADKAKQVQWNTNVDLDALEGLVITGTLVPFNITGQFENKTN 518
QY 479 LKNQLILGVGVDVSLDKRLTPRTLCPCNGYFAIDPNGYVLLHPNLOPKNPKSQEPV 538
Db 519 KKNQLILGVGVDVSLDKRLTPNTLTPNTLTPNTLTPNTLTPNTLTPNTLTPNTLTPNT 578
QY 539 TLDLDAELENDIKVIRNKMDGEGEKTFTLVKSODERYIDKGNRTYTWTPYNGTDY 598
Db 579 TLDLDAELENDIKVIRNKMDGEGEKTFTLVKSODERYIDKGNRTYTWTPYNGTDY 638
QY 599 SLALVLPYTSFYIAKLEETITQARKKGMKDSITLKPDMFESGYTFIAPRYCNDL 658
Db 639 SLGLVLPYTSFYIAKLEETITQARKKGMKDSITLKPDMFESGYTFIAPRYCNDL 698
QY 659 KISDNNTPELLNFNEFIDRKTPNPNPCNADLNRLVLLDAGTNELVQNVWSKQK--NIKGV 717
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Db 699 NASDNSTFLKDFTELMEKVTYPSKQCNFFLLHNLILDGTQOLVERVWRDQDLNTYSL 758
Qy 718 KARFVVDGGTRVYKPEAGENWOENETEDSYFKRSLDNDNVTFAPYFNK-SGPGAY 776
Db 759 LAVFAADGGITRVFPNKAEDWTENPEFNASFYRSLDNHGVIFKPPHODSLRLPLEL 818
Qy 777 ES---GIMWSKAVEIYTOGKLLKPAVVGIIKIDVNSWTENF-----TKTSIRDP--CAGP- 825
Db 819 ENDTVGLVSTAVELSGLRTRLPVAVGVKLDLEAWAEKFKVLASNRTHODQPKC-GPS 877
Qy 826 ---VCDCKRNSDVMDCVILDDGGFLMANHDDYTNQIGREFGEIDPSLMRHLNIVSYAF 882
Db 878 SHCMECEVNNEDLILCVIDDDGGFLVLSNQNHQDQVGRFFSEVDANLMLALYNNSYTR 937
Qy 883 NKSYDYSQVCEPGAAPKQAGHRSAYVPSVADIQIGWATAAAWSILQOFLSLTTPRL 942
Db 938 KESYDYQAACAPOPPGNLGAAPRGVFTTADFLNLAWTSAAAWSLFQQLLYGLIYHSW 997
Qy 943 LEAVEMEDDDFTASLSKOSCIOTQYFFDNDKSFSGVLDCGNCRSIFRHEGKLMNTNLI 1002
Db 998 FOADPAEAG-SPTRESSCMKQTYFGSVNASYNAIIDCGNCSRLFHAQRLTNTNLL 1056
Qy 1003 FIMVESKGTCPD 1015
Db 1057 FVAEKLCSQCE 1069

RESULT 8
Q9N48 PRELIMINARY; PRT; 1143 AA.
AC Q9N48;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE CALCIUM CHANNEL, ALPHA 2/Delta SUBUNIT 2.
GN CACNA2D2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART;
RA Klugbauer N.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART;
RA Hobom M., Dai S., Marais E., Lacinova L.;
RT "Neuronal distribution and functional characterization of the calcium channel alpha2delta-2 subunit.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ251367; CAB86192.1; -.
DR InterPro; IPR02035; -.
SQ SEQUENCE 1143 AA; 129084 MW; 492556C9919A0CE5 CRC64;

Query Match 53.78; Score 2872.5; DB 4; Length 1143;
Best Local Similarity 54.58; Pred. No. 5.4e-175;
Matches 562; Conservative 162; Mismatches 270; Indels 37; Gaps 14;

Qy 7 LALTLTQSLIGSPSEPPSAVTIKSWDKMDELVTLAKTASGVNQLVDIYKQD 66
Db 44 LWLLPLPLAALPACASAYSFPQHTMGHARRLEQGVGWRIFGGVQQLREIYKDRN 103
Qy 67 LYTVPNNARQLVETIARDIEKLSNRKALVSLALEAKVQAQAHQWRDFASNEVYYN 126
Db 104 LFEVQENEPKLVKAVAGDIESLLDRKYALKRLADAAENFQKAHRWQDNKEEDIVYD 163
Qy 127 AKDDL---DPEKNDSEPGS--RIKPVTEIDANFORQISYQAHHVHPTDIYEGSTIVLN 181
Db 164 AKADAEALDDPESEDVERGSKASTLRDIEDFNFKNKNYSYAAVQIPTDIYKGSTIVLN 223
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Qy 182 ELNWTSLADVEFKNREDDPSLLQVFGSATGLARYYPASPWVDSRTPNKIDLYDVRRR 241
Db 224 ELNWTALENVFENFENRRODPTLLQVFGSATGLARYYPATPW----RAPKIDLYDVRRR 279
Qy 242 PWYOGAASPKMDLILVDVSGSVGLTKLIRTSVSEMLETSLDDDFNVNVSFNSAODY 301
Db 280 PWYIQGASSPKDVIIVDVSGSVGLTKLTKTSVCEMLDTLSDDDYNVNVSFNEKAQPV 339
Qy 302 SCFOHLVQANVRNKKVLKDAVNNTAKGIDYDKGFSFAFEQLLNVNVSFNSAODY 361
Db 340 SCFTHLVQANVRNKKVKEAVQGVAKGTTGKAGFEYAFDQLQNSITRANCNKMTMF 399
Qy 362 TDGGEBAQAELEFNKN-KDKKRVRFRESVGOHNYERGIOWMACENKGYEIEISIGAIR 420
Db 400 TDGGEEDVQDVFKEKYNPNRTVRFTFSVGOHNYDVTPLQMACANKGYEIEISIGAIR 459
Qy 421 INTOEYDLVLRPMAVLADKAKQVQWNTNVYLDALGLVITGTLPVFNITQGFENKTLK 480
Db 460 INTOEYDLVLRPMAVLADKAKQVQWNTNVYLDALGLVITGTLPVFNITQ--DGPGEKK 517
Qy 481 NQLILGVMDVDSLEDIKRLTPRTLPNGYFAIDPNGYVLLHPNLPKPKSQEPVTL 540
Db 518 NQLILGVMDVDSLEDIKRLTPRTLPNGYFAIDPNGYVLLHPNLPKPKSQEPVTL 577
Qy 541 DFLDAELENDIKVEIRNKMIDGESGEKTRFLVKSQDERYDKGNRTVYTWTPVNGTDYSL 600
Db 578 DFLDAELENDIKVEIRNKMIDGESGEKTRFLVKSQDERYDKGNRTVYTWTPVNGTDYSL 637
Qy 601 ALVLPTSYFYIKAKLETITQARSKKMKDSETLPKDPNFDESGYTFIAPDRYCNLDKI 660
Db 638 GLVLPPTSTFYLQANLSQILQ-----VKYFEFLPSSSESEGHVFIAPREYCKDLNA 690
Qy 661 SDNTEFLNENEFIDRKTPNNPCNADLINRVLLDAGFTNELVQVYWSKQK-NIKGVKA 719
Db 691 SDNTEFLNENEFIDRKTPNNPCNADLINRVLLDAGFTNELVQVYWSKQK-NIKGVKA 750
Qy 720 RFVYTDGTRVYKPEAGENWOENETEDSYFKRSLDNDNVTFAPYFNK-SGPGAYES 778
Db 751 VFAATDGGITRVFPNKAEDWTENPEFNASFYRSLDNHGVIFKPPHODSLRLPLELN 810
Qy 779 ---GIMWSKAVEIYTOGKLLKPAVVGIIKIDVNSWTENF-----TKTSIRDP--CAGP--- 825
Db 811 DTGVLVSTAVELSGLRTRLPVAVGVKLDLEAWAEKFKVLASNRTHODQPKC-GPNSH 869
Qy 826 -VCDCKRNSDVMDCVILDDGGFLMANHDDYTNQIGREFGEIDPSLMRHLNIVSYAFNK 884
Db 870 CEMDEVNEDLILCVIDDDGGFLVLSNQNHQDQVGRFFSEVDANLMLALYNNSYTRKE 929
Qy 885 SYDYSQVCEPGAAPKQAGHRSAYVPSVADIQIGWATAAAWSILQOFLSLTTPRLLE 944
Db 930 SYDYQAACAPOPPGNLGAAPRGVFTTADFLNLAWTSAAAWSLFQQLLYGLIYHSWFO 989
Qy 945 AVEMEDDDFTASLSKOSCIOTQYFFDNDKSFSGVLDCGNCRSIFRHEGKLMNTNLI 1004
Db 990 ADPAEAG-SPTRESSCMKQTYFGSVNASYNAIIDCGNCSRLFHAQRLTNTNLLFV 1048
Qy 1005 MVESKGTCPD 1015
Db 1049 VAEKPLCSQCE 1059

RESULT 9
Q9Y268 PRELIMINARY; PRT; 1145 AA.
AC Q9Y268;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE KIAA0558 PROTEIN.
GN KIAA0558.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Db 61 KYQALKLADAEAFQKHAHQNIKEEDIVYDADKADAELEDPESDVERGSKASTLRL 120
QY 148 VFTEDANFGROISQOAHVHIPTDIYEGSTIVLNELNWTLSALDEVPFKKNEEDPSLLQV 207
Db 121 DFDENPKKNVNSYAQVPTDIYKGSIVLNELNWTLEALENVFENRRQDPTLLQV 180
QY 208 FGSATGLARYYPASPVNDNRTPNKIDLYVRRRPWTIOGAASPKMDLILVDVSGVSG 267
Db 181 FGSATGTRYYPATP-----RAPKKIDLYVRRRPWTIOGASPKMDVIVVDVSGVSG 236
QY 268 TLKLRISVSEMLETSDDDFVNVASFNASNAQVSCFOHLVQANVRNKKVLDKAVNNITA 327
Db 237 TLKMKTSVCEMLDTSDDDIYVNVASFNASKAPVSCFTHLVQANVRNKKVFEKAVQKVA 296
QY 328 KGITDYKGFSAFAPQLLNYSRANCKIMLFTDGGEEARQIFNKN-KDKKRVFR 386
Db 297 KGITGYKAGFEYAFDQLNSNITRANCKIMLFTDGGEDRVQDVFENKPNWTRVFT 356
QY 387 FSVGQHNRYERPTIOWACENKGYIYEPSIGAIRINTQEVLDVLRPMVLGAKQVOW 446
Db 357 FSVGQHNRYERPTIOWACENKGYIYEPSIGAIRINTQEVLDVLRPMVLGAKQVOW 416
QY 447 TNYVLDALGLVITGTPVFNITGQENKTNLKNOLILGVMGVDSLEDKRLTPRFTL 506
Db 417 TNYVEDALGLVITGTPVFNITGQENKTNLKNOLILGVMGVDSLEDKRLTPRFTL 474
QY 507 CPNGYFAIDPNGVYLLHPLNLPKNPKSQEPVTLDFDAELENDIKVEIRNKNMIDGESSE 566
Db 475 GANGVFAIDNGVYLLHPLNLPKNPKSQEPVTLDFDAELENDIKVEIRNKNMIDGESSE 534
QY 567 KTFRLVKSODERYDKGNRYTTPVNGTDYSLALVPTYSFYIYAKLEETIQARSK 626
Db 535 KQIRTLVKSODERYDKGNRYTTPVNGTDYSLALVPTYSFYIYAKLEETIQARSK 590
QY 627 KGMKDSLETPDNFESGYFIAPRDYCNLKIISDNNTEFLNFEIDRKTNPNSCN 686
Db 591 ---VKYFEFLPSFESGHHVFIAPREYCKOLNADNNTEFLNFEIDRKTNPNSCN 647
QY 687 ADLNRVLDAAGFYNELVQNSKQK-NIKGVKARFVVTGGITRVYKPEAGENQENPE 745
Db 648 NELLNLIDTGIQQLVERWRQDLNYSLLAVFAATDGGITRVYKPEAGENQENPE 707
QY 746 TYEDSFYKRSLDNDNYFTAFYFNK-SGPAYES---GIMVSKAVEIYQKLLKPAVVG 801
Db 708 PFNASFYRRSLDNHGYVFKPPHODALLRPLENDTGVILYSTAVELSLGRTRLPVVG 767
QY 802 IKIDVNSWIEF-----TKTSIRDP--CAGP-----VCDCKRNSVMDCVILDDGGFLMA 850
Db 768 VKLDLEAWAEKFKVLAASRTHQDQPKC-GPNSHCMDCEVNNEDLLCVLDDGGFLVLS 826
QY 851 NHDDYTNIGRFFGIDPDLMLHNLVNSYAFNKSQYQVCEPAAKQAGHRSAYVP 910
Db 827 NONHQWDQVGRFFSVSDANLMLALYNNFYRKESYDYQAACAPPPGNLGAAPGVFP 886
QY 911 SVADTLOIGMWATAAASILQOFLSLTFPRLLEAVEMEDDDFTASLKQSCITEQTQYF 970
Db 887 TVADPLNLAWTSAASLSLQQLLYGLYHSWFQADPAEAG-SPEPRESSCMVQTOY 945
QY 971 FDNDSKFSVGLDCNCSRIHGEKMLNTLIFIVWESKGICPCD 1015
Db 946 FGSVNASYNIAIDCNCRLFAORLTNTNLLFVVAEKPLCSQCE 990

RESULT 11
QNSA6 PRELIMINARY: PRT: 975 AA.
ID QNSA6
AC QNSA6;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE LUAC11.1 (CALCIUM CHANNEL, VOLTAGE-DEPENDENT, L TYPE, ALPHA 2D SUBUNIT
DE (KIAA0558)). (FRAGMENT).
GN LUAC11.1.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Barlow K.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z84492; CAB41767.2; -.
DR InterPro: IPR02035; -.
FT NON_TER 1
SQ SEQUENCE 975 AA; 110192 MW; C7874D46B88242BF CRC64;

Query Match 50.2%; Score 2682; DB 4; Length 975;
Best Local Similarity 57.4%; Pred. No. 6.3e-163;
Matches 518; Conservative 134; Mismatches 217; Indels 34; Gaps 13;

QY 132 DPEKNDSEPGSO--RIKPVFTEDANFGROISQOAHVHIPTDIYEGSTIVLNELNWTSL 189
Db 2 DPESEDVERGSKASTLRLDFIEDFNKNVNSYAQVPTDIYKGSIVLNELNWTAL 61
QY 190 DEVFKKNEEDPSLLQVFGSATGLARYYPASPVNDNRTPNKIDLYVRRRPWTIOGA 249
Db 62 ENVMENRRQDPTLLQVFGSATGTRYYPATP-----RAPKKIDLYVRRRPWTIOGAS 117
QY 250 SPKMDLILVDVSGVSGITLKLIRTSVSEMLETSDDDFVNVASFNASNAQVSCFOHLVQ 309
Db 118 SPKMDVIVVDVSGVSGITLKLIRTSVSEMLETSDDDFVNVASFNASKAPVSCFTHLVQ 177
QY 310 ANVRNKKVLDKAVNNITAKGITDYKGFSAFAPQLLNYSRANCKIMLFTDGGEEAR 369
Db 178 ANVRNKKVFEKAVQKVAQVGTGKAGFEYAFDQLNSNITRANCKIMLFTDGGEDRV 237
QY 370 QEIFENKYN-KDKKRVKRSFQHNRYERPTIOWACENKGYIYEPSIGAIRINTQEVLD 428
Db 238 QDVEKYNWPNRTVRVFTSVGQHNRYERPTIOWACENKGYIYEPSIGAIRINTQEVLD 297
QY 429 VLGRPMVLGAKQVOWTNYVLDALGLVITGTPVFNITGQENKTNLKNOLILGV 488
Db 238 VLGRPMVLGAKQVOWTNYVEDALGLVITGTPVFNITGQENKTNLKNOLILGV 355
QY 489 GVDVSLDILKRLTPFTLCPNGYFAIDPNGVYLLHPLNLPKNPKSQEPVTLDFDAELE 548
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QY 609 FYYIKAKLEETITQARSKKGMKDSLETPDNFESGYFIAPRDYCNLKIISDNNTEFL 668
Db 476 TFYLANLSQILQ-----VKYFEFLPSFESGHHVFIAPREYCKOLNADNNTEFL 528
QY 669 LNFNEDIRKTPNPNFSCNADLNLNVLDAAGFYNELVQNSKQK-NIKGVKARFVVTGG 727
Db 529 KNFIELMEKVTDPDSKOCNLLHNLIDTGIQQLVERWRQDLNYSLLAVFAATDGG 588
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Db 649 TAVELSLGRTRLPVVGKIDVNSWIEF-----TKTSIRDP--CAGP-----VCDCKR 707
QY 833 SDVMDCVILDDGGFLMLANHHDDYTNIGRFFGIDPDLMLHNLVNSYAFNKSQYQV 892
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QY 893 EFGAAPKQAGHRSAYVPVADILQIGMWATAAASILQOFLSLTFPRLLEAVEMEDDD 952
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58 FI---LAPNDHFNLPVNISSLDVQVPTNNYNDPAIVNGVYVWSESLNKYFVDFNDRDPS 114
203 LLWQVGSATGLARYYPASVPWNSRTPNPKIDLYDVRPRWYIQAASPKDMLILVDVSG 262
115 LIWQVGSAGFRQYPIGWEDPE---NGVIAFDCNRKRYIQAATSPKDVILLVDVSG 171
263 SVSGLTLKLIARTSVSEMLETSDDDDFNVASFNNAQDVS-CFQ-HLVQANVRNKKVYLD 320
172 SMKGLRLTIKQIVSSILDTLGGDDFFNIAYNEELHYVEPCLNGTLVQADRNKHEFRE 231
321 AVNITAKGIDYKKGSPFAFQLLNVRAN--CNKIIMLTFDGGEEAQAELFNKYN- 377
232 HLDKLFAGICMLDIALNEAFNLSLDNHTGQGSICQAIMLITDGAVDYDITFAIKNW 291
378 KDKVRVFRSVGHNRYERGIOWMACENKGYVEISGAIRINTOEYLDVLRPVMVLA 437
292 PDKRVITFLYIGREAAFAADNLKMACANKGFFQIOTSLADVQENVMEYLHLVSRPKVI- 350
438 GDKAKOVQWNTVYLDAL-----ELG--LVITGTLPVNITGQFENKTNLKNQILG 486
351 -DQEHVWVTEAYIDSPLQAQKLTDDGQVLMTTVAMPVFS-----KONETRSKG-ILLG 404
487 VMGVDSLEDKRTPRTPLCPNGYYPFAIDPNGYVLLHNPLO---PKNPKSQEP--VTLG 541
405 VVGTDVPVKELLTPKYKLGIGHYAFATNNGYILTHPELRLLYEEGKKRKNPSVSD 464
542 FLDALENDIKVETRNKMDIGESKEKFTLVKSQDERYIDKGNRT-----YTWTPVNG 595
465 LSEVWEEDRDDV-URNAMVNRKTK--FSMEVK-----KTVDKGRVLVMTWYDITDKG 517
596 TDYSLALVLPY-YSFYIKAKLEETITQARSKKGKMDSETLKPDNFEEGYTTIAPRKY 654
518 TPFSLGVALSRGKGYF-----RGNTTIEGL--HDLHPDVSGLADENSY 561
655 CN-DLKISDNTEFLLNFEIDRTPNPNPCNADLNRVLLDAGFTNELVQNTWS----- 709
562 CNTDLHPHRLHSQLEAIKLYLKGEP-LLOCDKELIQEVLFDV-VWSAPTEAYWTSIAL 619
710 --KQNKIGVKARFVTDGGITRVYP-----KEAGENWQENPEYEDSFYKRS 755
620 NKSENSDKGVEAFVIGTGTGSRNLNFGVABQLTNQDFLAKGDKENIENADHFFPLWYRA 679
756 LDN--DNYVFTAPYFNKSPGAYESGIMVSKAVEYIYQGLKLPVAVGKIDVNSWIENF 813
680 AEQIPGSFVYSIPF--STGVPKNSVNTASTSIQLLDERKSPVVAAGIQMKLEFFQKRF 737
814 TKTSIRDPACGVPCKKNSVMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRH 873
738 WTASRQCASLDGKCSISCDDETVCYLIDNNGFILVS--EDYT-OTGDDFFGEGIEGAVNK 794
874 LVNISVYAENKSYDYQVCEPAAPKQGA-GHRSVAVPSVADILQIGWATAAASILQQ 932
795 LVTMGSKRITLYDQAMCRANKESSDGAHGLDPI-----NAFLSAVKIMIMEL 844
933 FLTLSTFPRLLEAVEMEDDDFTASLSK-----QSCITEQTOFFDNDKSKFSGLVDCGNC 987
845 VLFLVEF-----NLCSSWHSMDTAKAQLKQTLPECDTEYPAFVSERTIKETGNIACEDC 900
988 SRIFFGEKIMLNTLFIYVESKGTCPDCT 1016
901 SKSFVQIQIPSSNLFMWVYDS--SCLCES 927
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AC Q9NK64;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE HYPOTHETICAL 249.8 KDA PROTEIN.
GN BG:DS07473.1 OR CG12455.

OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
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RP SEQUENCE FROM N.A.
RC STRAIN-Y, CN BW SP;
RX MEDLINE=99403001; PubMed=10471707;
RA Ashburner M., Misra S., Rotee J., Lewis S.E., Blazej R., Davis T.,
Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,
Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.,
Cealiker S., Rubin G.M.;
RA "An exploration of the sequence of a 2.9-Mb region of the genome of
RT Drosophila melanogaster: the Adh region.";
RL Genetics 153:179-219(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Y, CN BW SP;
RA Cealiker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,
Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequelira A.,
Sethi H., Snir E., Svirska R.R., Wan K.H., Weinburg T., Zhang R.,
Zieran L.L., Rubin G.M.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL: AE003415; AAF4988.1;
DR FlyBase: FBgn0028859; BG:DS07473.1.
DR InterPro: IPR002035;
KW Hypothetical protein.
SQ SEQUENCE 2190 AA; 249754 MW; B8C657A2F80F226E CRC64;

Query Match 17.4%; Score 929.5; DB 5; Length 2190;
Best Local Similarity 25.1%; Pred. No. 2.4e-50;
Matches 276; Conservative 213; Mismatches 387; Indels 225; Gaps 42;

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DB 13 SKATVQKWATQGDLEFALQKITKSQBIKEYN--ARVELKNGTELKSIKTNVGR 70
QY 89 LLSNRKALVSLALEAEKVAHQHREDFASNEVVY-----NAKDDLDPEKNDSE 139
DB 71 MLARKMDAVRCIOERAEYVNFENLTYALQNFYFSKYSTFNNGNSELEP--NEAE 128
QY 140 PG----SQRKIPVFTEDANF--GROIYQAAVHIPTDIYEGSTIVLNLNMTSALDEVFK 194
DB 129 FAWMYRNNELNP----DTHFYNTPYDTEHSSVHVPSNIWDRSERVLKTIWSEHLDEVR 184
QY 195 KNREEDPSLLWQVFGSATGLARYYPASVPWNSRTPNPKIDLYDVRPRWYIQAASPKDM 254
DB 195 QNYQSDPALSMQYFCGSDTGILRHYPAAQWTDPRNRDDADTYDCRKRWSYIETATCSKI 244
QY 255 LILVDVSGVSGLTLLKIRTSVSEMLETSDDDDFNVASFNNAQD--VSCFQ-HLVQANV 312
DB 245 VILLDHSGSMTGFRHHVAKFTIRSIDLTFNSNDDFTILRYSEVNDIIPCFNGALVQATP 304
QY 313 RNKKVYLDVAVNNI--TAKGITDYKKGFSAPFAEQLLVNYSR-----ANCNKIIMLTFDGE 366
DB 305 ENIEFVNOQIEQLDDPEGYANLTLAYETAFQLLRKYDSRHCVTNSTCQAIMLYTDGVA 364
QY 367 ERAQETFNKYN-----KDKKRVYFRFSVGHNRYERGIOWMACENKGYVEISGA 418
DB 365 GNTVEFQKYNNGENGSTQSDTRVFTYLLGKEVTKVREIQMACNLNGYSHVQTLDE 424
QY 419 IRIQTQYLDVLRPVMVLAGDKAKQVQWNTVYLDAL-----ELGLVITGTLPVFNI 469
DB 425 VHEEVLKYVDVIATPLVLQNEQHPPT--WTHAFTDKTYDPKTSNEKRPRLMISVGVPAFOR 483
QY 470 TQGFENKTNLKNQILGVMGVDVSLEDIKRLTPRTPLCPNGYYPFAIDPNGYVLLHNPLO 529

484 FYRHANSTNPRARL-LGVAGTDPVEDIDKLTLPYKLGNGYSFVVSNNGYVLLHPLRLP 542
QY 530 -----KNPKSQEPTVTLDFLDAE-LENDIK-----VEIRNKMIDGESG-KTFRTLV 573
DB 543 IGTNGKMNPNYN---SIDPTEVHLFDQSPREPESILHIRNANVMRHEANEFKSISVKF 599
QY 574 KQSDERYIDKGNRTTWPVNGTDSYALVLT-YSFYIKAKLEETITQARSKKGKKD 632
DB 600 HYDKMRVSEKQDIFAPLPNPTFTGLVMPSEYKWKVGEVD-----KNKHKINI 655
QY 633 SETLAPDNPEE-----SGYTFIAP-----RDYC-----NDLKISDNNTPELLNFN 672
DB 656 SDFEIGENKVVHPDVYKYHLEGEHEKTPAEALREFLAKQNDKWSEQVAEDSDWD 715
QY 673 EFID-----AKTNPNPS--CNADLNRLVDAGFTNELVQNYH-----SKQKNIKGVKA-- 719
DB 716 DKDDLNCGRKTLGDDAYYCNKELNLLIFDAKVTNS-SYGVWRFESDEERQOLIERFRADL 774
QY 720 RFVVTGDTTTRYVPREAGENWO-----ENPETYEDSFYKRSI-----D 757
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QY 758 NDNYFTAPYFNKSPGAYESGIMVSKAVEIYIQGLLKPAAVVGKIDVNSWIENTFTIS 817
DB 826 AESFVYSKYVD-----DPMEDSE 844
QY 818 IRDPCAGPVCDCKRNSDVMDVLDGDFLLMANHDDYTNQIGRFEIGEDPSLMRLHVINI 877
DB 845 VRCNHLCPIC-----TDDDDVDCVVDNNAYIVIGQN---INTTKGFEFGHDGVMYAMVER 897
QY 878 SYVAFNKSVDYOSVC--EPGAAPKQAGHRSAYVPSVAD-ILQIGWATAAAWSILQOFL 934
DB 898 GIFLSTEVYDYOQKEEPAKYN-----YTDEIDEYVAVGGGKSSA----- 941
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DB 942 -----SKPKDSDSDENAMFDEPEPPDIYKACDKRSTLAL--QPSALVGINDFVEA 990
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DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)
DE CG12455 PROTEIN.
GN BG:DS07473.1 OR CG12455.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN NCBI_Taxid=7227;
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RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=107311132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Prankoch C., Baldwin D.,
RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova K.D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
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RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector R., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao X., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000).
DR EMBL; AE003650; AAF53505.1.
DR Flybase; FBgn0028859; BG:DS07473.1.
DR InterPro; IPR003035;
SQ SEQUENCE 2172 AA; 247574 MW; 39AA7BCB470DIA39 CRC64;

Query Match 17.1%; Score 912.5; DB 5; Length 2172;

Best Local Similarity 25.1%; Pred. No. 2.9e-48;

Matches 275; Conservative 207; Mismatches 383; Indels 229; Gaps 42;

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QY 89 LLSNRSKALVSLAEAEKQVAAHWRDFA--SNEVYVYNKDDLDPEKNDSERG--S 142
DB 71 ML-----ARKMDAVRCIQEHFTYFSKYSTFNGNSSELEPEAEFAWMYRN 117
QY 143 QRIKPVFTIEDANF-QRQISYQHAHVHPTDIYEGTIVLNLNWTLSALDEVEKKREEDP 201
DB 118 MELNP---DTHFYTPVDTESSVHVPSNIWDRSERVLKTMWSEHLDEVERQYQSDP 173
QY 202 SLLWQVFGSAGTLARYYPASPMVONSRTPNKIDLYDVRPWPYIOGAASPKDMLILVDVS 261
DB 174 ALSWQYFGSDTGILRHYPAAQWTDTRPNKDDADTDCKRARSWIETATCSKDIVILLDS 233
QY 262 GSVSGLTLKIRTSVSEMLETSLDDDFVNVASFNSNAQD-VSCFO-HLVQANVRNKKVLK 319
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QY 374 NKNY-----KDKKVRVRESVGOHNVERGPIONMACENKGYIYEIPISGAIRINTOE 425
DB 354 QKYNNGNGENGTSQMDTRVFTVLLGKVTKEVRIOWMACINRGYTSHVOTLDEVEHVLK 413
QY 426 YLDVLGRPVLAKGAKAQVQWNTNVIDAL-----ELGLVITGTLPFVFNITQGFENK 476
DB 414 YVDVATPLVQLNEQHPPT-WTHAFTDKTYDTPKTSNEKRPRLMISVGVPAFDFRYHANS 472
QY 477 TNLKNQILGVNGVDVSLIEDIKRLPRFTLPCNGYFYAIDPNGYVLLHPNLQOP-----K 530
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Job time: 593 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 23, 2001, 07:36:25 ; Search time 92.97 Seconds

(without alignments)
675,556 Million cell updates/sec

Title: US-09-397-548-16

Perfect score: 5443

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Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	5443	100.0	1091	19	AA1981
3	5443	100.0	1091	21	AA1982
4	5439	99.9	1091	19	AA1983
5	5437	99.9	1091	14	AA1984
6	5423.5	99.6	1110	19	AA1985
7	5403.5	99.3	1086	16	AA1986
8	5403.5	99.3	1086	21	AA1987
9	5403.5	99.3	1086	21	AA1988
10	5386.5	99.0	1084	16	AA1989
11	5386.5	99.0	1084	19	AA1990

12	5386.5	99.0	1084	21	AA1989	Human calcium chan
13	5367	98.6	1103	16	AA1990	Human neuronal cal
14	5367	98.6	1103	19	AA1991	Human calcium chan
15	5367	98.6	1103	21	AA1992	Human calcium chan
16	5347	98.2	1079	19	AA1993	Human calcium chan
17	5347	98.2	1079	21	AA1994	Human calcium chan
18	5341	98.1	1079	16	AA1995	Human neuronal cal
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20	5229.5	96.1	1106	18	AA1997	Rabbit skeletal ca
21	5229.5	96.1	1106	21	AA1998	Rabbit skeletal ca
22	5208.5	95.7	1106	16	AA1999	Rabbit skeletal ca
23	5101.5	93.7	1100	10	AA2000	Rabbit skeletal mus
24	2907.5	53.4	1145	21	AA2001	Human alpha-2-delt
25	2581.5	47.4	508	19	AA2002	(Alpha)-2 subunit
26	2581.5	47.4	508	21	AA2003	Human skeletal cal
27	1087	20.0	1085	21	AA2004	Human alpha-2-delt
28	1067	19.6	1120	21	AA2005	Human alpha-2-delt
29	1037	19.1	1096	21	AA2006	Human alpha-2-delt
30	992.5	18.2	1096	21	AA2007	Human alpha-2-delt
31	733.5	13.5	519	21	AA2008	Human membrane cha
32	161	3.0	1829	18	AA2009	DNA polymerase wit
33	158.5	2.9	894	20	AA2010	Enterococcus faeca
34	158.5	2.9	962	20	AA2011	Enterococcus faeca
35	158.5	2.9	962	20	AA2012	Enterococcus faeca
36	158.5	2.9	962	20	AA2013	Enterococcus faeca
37	158.5	2.9	962	20	AA2014	Enterococcus faeca
38	158.5	2.9	962	20	AA2015	Enterococcus faeca
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40	155	2.8	1516	21	AA2017	Plasmodium falcipa
41	154.5	2.8	946	21	AA2018	Human inter-alpha-
42	154.5	2.8	1315	20	AA2019	S. aureus SdrD pro
43	154	2.8	903	15	AA2020	PA(1-725)----Huma
44	152.5	2.8	789	17	AA2021	B. thuringiensis V
45	152.5	2.8	789	18	AA2022	B. cereus VIP3A(b)

ALIGNMENTS

RESULT

1
AA1980
ID AA1980 standard; Protein; 1091 AA.
XX
AC AA1980;
XX
DT 01-DEC-1995 (first entry)
XX
DE Human neuronal calcium channel subunit alpha 2b.
XX
KW Calcium channel subunit; antagonist; agonist; diagnosis;
KW Lambert Eaton Syndrome.
XX
OS Homo sapiens.
XX
PN WO9504822-A.
XX
PD 16-FEB-1995.
XX
PF 11-AUG-1994; 94WO-US09230.
XX
PR 11-AUG-1993; 93US-0105536.
PR 05-NOV-1993; 93US-0149097.
(SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
Ellis SB, Gillespie A, Harpold WM, McCue AF, Williams ME;
WPI, 1995-090900/12.
N-PSDB; AAQ84664.
DNA encoding human calcium channel sub-unit(s) - used for
developing prods. for studying calcium channels, e.g. for
obtaining agonists and antagonists

XX Disclosure; Page 166-171; 285pp; English.

XX Human neuronal alpha 2 coding sequence (AA084664) transcript is

CC differentially processed in skeletal muscle, aorta, and CNS in

CC the region corresp. to nt 1595-1942 of AA084664 in each of the

CC tissues. Five alternatively spliced variant transcripts that differ

CC in the presence or absence of one to three different portions of

CC this region. There are three sequences involved (see AA084664 FT

CC and AA084665 FT), sequence 1, sequence 2 and sequence 3. The five

CC alpha 2 encoding transcripts from the different tissues include

CC different combinations of the three sequences, except for one of

CC the alpha 2 transcripts expressed in aorta which lacks all three

CC sequences. The five alpha 2 forms identified are (1) a form that

CC lacks sequence 3 called alpha 2a, expressed in skeletal muscle

CC (2) one that lacks sequence 1 called alpha 2b, expressed in CNS

CC (3) one that lacks sequences 1 and 2 called alpha 2c, expressed in

CC aorta (4) one that lacks sequences 1, 2 and 3 called alpha 2d,

CC expressed in aorta and (5) one that lacks sequences 1 and 3

CC called alpha 2e.

XX SQ Sequence 1091 AA;

Query Match 100.0%; Score 5443; DB 16; Length 1091;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCIIATLTTLFQSLIGSPSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNOLVDI 60

DB 1 maagcIIatlttlfqslligspseepfseavtikswdkmqedlvltaktasgvnlvdi 60

QY 61 YEKYQDLYTVEPNAROLVBIARDIEKLSNRSKALVSLALEAEKVQAHOHREDFASN 120

DB 61 yekyqDlytvepnaRqlveIardieklSnrSkalvslaleaekvqaahqwedfasn 120

QY 121 EVVYNAKDLDPKNDSEPSGRIKPVFTEDANFGROISYQHAHVHPDIVEGSTIVL 180

DB 121 evvYnAKdlDpKndsePsgRikPvfTedaNfGRoiSyqHAvhPdpIvegstIvL 180

QY 181 NEIWNLSALDEVFKKREEDPSLLWVFGSATGLARYYPASPVWDSRTPNKKIDLYDVR 240

DB 181 neiwnlsaldevfkKreEdpsllwVfgsatglaryypasPwdsrtpnKkIdlydvr 240

QY 241 RPWYIQAASPKDMLILVDVSGVSGITLKITRVSSEMLETISDDDFVNVASFNSNAQD 300

DB 241 rpywiqaasPkDmlilvdvsgvsgitlkitrVssEmletIsdddfvNvasfnsnaqd 300

QY 301 VSCFOHLVQANVRNKKVLDVANNITAKGTDYKGFSAFEOLLNYSRANCNKIIML 360

DB 301 vscfqlhvqanvrnkkvldvannitakgtdyKgfSafEOLLnysrancnkiImL 360

QY 361 FTDGGERAQEIFNKYKDKVRFRFSVGHVNERGPIOWMACENKGYEYIPIPSIGAIR 420

DB 361 ftdgGerageifnkykdkVrfrfsVghvnergpiowMacenkgyeyeiPipsigair 420

QY 421 INTOEYLDVZGRPMVLADGAKAQVQMTNVYLDALGLVITGTLPVFNITGQFENKTNL 480

DB 421 intqeyldvZgrpmvLadgAkAQvQmtNvYldALglvItgtlpvfnItgQfEnktnL 480

QY 481 NQLILGVMGVDVSLIEDIKRLTPFTLCPNGYFYFAIDPNGYVLLHPNLQPNKPSQEPVIL 540

DB 481 nqlilgvmgvdvslieDikrltpftlcpngyfyfaIdpNgYvllhPnlqPnkpsqepvIl 540

QY 541 DFLDAELNDIKVEIRNKMIDGSEGTFTFLVKSOBERYIDKGNRTYTTPVNGTDYSL 600

DB 541 dflDAelndIkveirNkmIdgsegtftflvKsoBerYidKgnrtYtTPvngtdySl 600

QY 601 ALVLPYTSFYIKAKLEETITQARSKGKMKDSETLKPDNFEESGYTFIAPRDYCNLDKI 660

DB 601 alvlpYtsfyiKaKleetiTqarsKgkMkdseTLkPdNfEEsgyTfiAPrdyCnldki 660

QY 661 SDNTEFLNFEZIDKRTNNPNSCNADLNRVLLDAGFTNELVQNWSKQNIKGVKAR 720

DB 661 sDnteFlNfEzIdKrtNnPnScNadLnrVllDagftNeLvQnwSkqNikgVkar 720

QY 721 FVYTDGGITRVYPKEAGENWQENPETYEDSFYKRSILDNDNYFTAPYFNKSGPGAYESGI 780

DB 721 fvtDggitrVypkeagenwqenpetyedsfYkrsIldndnyftaPyfnKsgpgayesgi 780

QY 781 MYSKAVEIYIQGLKLPVAVGKIDVNSHIEFTKTSIRDPGAGVCDCKRNSDVMDCVI 840

DB 781 mYskaveiyigkllkpavvgkIdvnsHieftKtsirDpGagvcdCKrnsdvmDcvi 840

QY 841 LDGCGFLLMANHDDYTNOIGREFGEIDPSLMRHLNIVSYAFNKNKSYDYOSVCEPGAAPKQ 900

DB 841 ldgGfllmanhddytNoiGrEfgEidpSlmRhlNivsyafNknKsydyosVcePgAapKq 900

QY 901 GAGHRSAYVPSVADILQIGWATAAASWLSLOQLSLTPRLLLEAVEMEDDDFTASLSKQ 960

DB 901 gagh-rsayvpsvadilqigwataaawslqllfllsttfrlleavemedddftaslskq 960

QY 961 SCITQTQYFFPDNDKSPSGVLDGNCNCRIFHGEKLMNTNLIFIMVESKGTCPDTRLLI 1020

DB 961 scitqtgyffDndksfsgvldGncnCrifhgeKlmntnlifimvesKgtcpDtrllI 1020

QY 1021 QAEQTSDBGPNPCDMVK 1036

DB 1021 qaeqtsdgnpncdmvk 1036

RESULT 2

AAW63145

ID AAW63145 standard; Protein; 1091 AA.

XX AAW63145;

XX 12-OCT-1998 (first entry)

XX Human calcium channel alpha-2 subunit.

DE Alpha-2 subunit; human; calcium channel; assay; detection;

XX characterisation; Lambert Eaton Syndrome; LES; diagnosis.

OS Homo sapiens.

XX US5792846-A.

XX 11-AUG-1998.

XX 31-MAY-1995; 95US-0455543.

XX 04-APR-1994; 94US-0223305.

PR 04-APR-1988; 88US-0176899.

PR 04-APR-1989; 89US-0603751.

PR 04-APR-1989; 89WO-US01408.

PR 20-FEB-1990; 90US-0482384.

PR 30-NOV-1990; 90US-0620250.

PR 15-AUG-1991; 91US-0745206.

PR 31-MAY-1995; 95US-0455543.

XX (SIBI-) SIBIA NEUROSCIENCES INC.

XX Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;

PI Williams ME;

XX WPI; 1998-456192/39.

DR N-PSDB; AAV42689.

XX DNA encoding human calcium channel alpha 1B subunit protein -

PT useful for recombinant production of the channel for screening of

PT its modulators, and diagnosis of Lambert Eaton Syndrome

PS Claim 4; Columns 283-288; 166pp; English.

XX The present sequence represents the alpha-2 subunit of a human calcium

CC channel. Calcium channels are membrane-spanning, multi-subunit proteins
 CC that allow controlled entry of calcium ions into cells. This leads
 CC to depolarisation events required for muscle contraction. The recombinant
 CC subunit, when expressed with nucleic acids encoding the complete calcium
 CC channel, can be used in assays for the detection and characterisation of
 CC compounds that modulate the channel. The DNA encoding the subunits can
 CC be alternatively spliced when transcribed, giving more than one form of
 CC the protein from the same transcript, each having slightly different
 CC properties. In addition, the reactivity of the alpha 1 subunit with IgG
 CC molecules from the serum of an individual with Lambert Eaton Syndrome
 CC (LES) can be used as a diagnostic for the disease.

XX Sequence 1091 AA;

Query Match 100.0%; Score 5443; DB 19; Length 1091;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLTFLQSLIIGPSSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
 Db 1 maagcillaltlflqslilgspseepfapsavtikswdkmqedlvtlaktasgvnqlvdi 60
 QY 61 YEKYQDLYTVEPNARQVLAARDIEKLNSRKSALVSLALEAEKVQAAHQHREDPASN 120
 Db 61 yekyqdytvepnarqvlvaardieklnsrksalvslaleaekvqaahqwhredfasn 120
 QY 121 EVVYNAKDLDPEKNDSEPSGRIRKPVFIEDANFRQISQVQAAVHIPDIYEGSVIL 180
 Db 121 evvyinakddlpekdndsepsgrirkpvfiedanfrqisqyqaaahvipdiyegstivl 180
 QY 181 NELNWSALDEVKKNREEDPSLLMQVFGSATGLARYYPASPWWDSRTPNKIDLYDVR 240
 Db 181 nelnwsaldevkknreepdpsllmqvfgsatglaryypaspwwdsrtpnkidlydvr 240
 QY 241 RPYVIOGAASPKDMLIVDVGSGVGLTLIRTSVSEMLETSLDDDFNVASFNSNAQD 300
 Db 241 rpyviogaaspkdmlilvdvgsgvgtlklrtsvsemlletlstddfnvafnsnaqd 300
 QY 301 VSCFQHLVQANRKNKVLDAVNNTAKGITDYKKGFSFAFEOILLNYSRANCNKIIML 360
 Db 301 vscfqlhvanrnkknvldavnnitakgitdykkgfsfafelnllynsrancnkiiml 360
 QY 361 FTGGEERAQEIFKNYKDKKRVFRFSGVGHYERGIQWACENKGYIYEIPISGAIR 420
 Db 361 ftggeeraqeifknynkdkkrrvfrfsgvghyergiqwacenkgyiyeipisgair 420
 QY 421 INTQEYLDVLGRPMVLADGAKQVQWNTNVDLAELGLVITGLPVPNTGQFENKTNLK 480
 Db 421 intqeyldvlgrpmvladgakqvqwnvnyldalelglvitglpvpntgqfenktnlk 480
 QY 481 NQILGVMGVDVSLIEDIKRLTFRFTLCPNGYYFAIDPNGVYLLHPNLQPNKPSQEPVTL 540
 Db 481 nqilgvmgvdvsliedikrltfrftlcpngyyfaidpngvylhpnlpknpsqepvtl 540
 QY 541 DFLDAELENDIKVEIRNMKTGDSGEKFTFLVKSDERYIDKGNRTYTPVNGTDYSL 600
 Db 541 dfldaeendikveirnmktgdsgektftflvksqderidkgnrtytvpvngtdysl 600
 QY 601 ALVLPYFYFYIAKLEETIQARSKKGMKDSKSETLKPDPNFESGYTFIAPRYCNDLKI 660
 Db 601 alvlpysfyfyiakleetiqarskkgmksksetlkdndfesytyfiaprycndlki 660
 QY 661 SDNNTFLLNFEDIRKTPNPNPSCNADLNRLVLLDAGFTNELVQYNSKOKIKGVKAR 720
 Db 661 sdntefllnfnedirktpnnpncnadlnrvlldagftnelvqywsqknikgvkar 720
 QY 721 FVYTDGTRVYKPEAGENQENPEYEDSFYKRSRLDNDNYFTAPYFNKSGPAYESGI 780
 Db 721 fvytdgtrvypkeagenqenpeyedsfykrslndndnyftapyfnksppayesgi 780
 QY 781 MVSKAVEIYIQGLLPVAVGIIKIDVNSWJENTTKTSIRDPACGVCDCRNSDVMDCVI 840

Db 781 mvskaveiyiqgllkpvavvgikidvnswnienftktairdpcagpvcckrnsdvmcvi 840
 QY 841 LDGGFLLMANHDDYTNQIGRFFGEIDPCLMRHLVNTSVYAFNKSXYDSVCEPGAAPKQ 900
 Db 841 ldggfllmanhddytngirffgeidpclrhlvntsvyafnksxydsqvcepgaapkq 900
 QY 901 GAGHRSAYVPSVADILQIGHWATAAASIIQQFLLSLTFFRLLLEAVEMEDDFTASLSKQ 960
 Db 901 gaghrsayvpsvadilqigwataaawsilqqfllsltfprlleavemeddftaslskq 960
 QY 961 SCTEQOYQYFDDNDSKFSFGLDCGNCGRIFPHGKLMNTNLIFFIMVESKGTCPDCTRLII 1020
 Db 961 sciteqoyqyffddndskfsfvgldcgcncsrifhgeklmntnlifimveskgtcpdctrlli 1020
 QY 1021 QAEQTSQGNPCDMVK 1036
 Db 1021 qaeqtsqgnpcdmvk 1036
 RESULT 3
 AAB10576
 ID AAB10576 standard; Protein; 1091 AA.
 XX
 AC AAB10576;
 XX
 DT 22-DEC-2000 (first entry)
 XX
 DE Human calcium channel alpha-2 subunit protein.
 XX
 KW Human; calcium channel; calcium channel subunit; diagnosis;
 KW Lambert Eaton Syndrome; calcium channel subunit alpha-2.
 XX
 OS Homo sapiens.
 XX
 PN US6096514-A.
 XX
 PD 01-AUG-2000.
 XX
 PF 25-MAY-1995; 95US-0450562.
 XX
 PR 04-APR-1988; 88US-0176899.
 PR 02-FEB-1990; 90US-0482384.
 PR 08-NOV-1990; 90US-0603751.
 PR 30-NOV-1990; 90US-0620250.
 PR 15-AUG-1991; 91US-0745206.
 PR 10-APR-1992; 92US-0868354.
 PR 13-JUL-1992; 92US-0914231.
 PR 11-AUG-1993; 93US-0105536.
 PR 05-NOV-1993; 93US-0149097.
 PR 07-FEB-1994; 94US-0193078.
 PR 04-APR-1994; 94US-0223305.
 PR 11-AUG-1994; 94US-0290012.
 PR 23-SEP-1994; 94US-0311363.
 PR 28-SEP-1994; 94US-0314083.
 PR 07-NOV-1994; 94US-0336257.
 PR 13-MAR-1995; 95US-0404950.
 XX
 (SIBI-) SIBIA NEUROSCIENCES INC.
 XX
 PI Ellis SB, Williams ME, McCue AF, Harpold MW;
 XX
 DR WPI; 2000-548230/50.
 DR N-PSDB; AAA71707.
 XX
 PT Human calcium channel beta subunit polynucleotides, useful for
 PT producing recombinant eukaryotic cells and for diagnosing Lambert Eaton
 Syndrome
 XX
 PS Example IV; Column 135-144; 153pp; English.
 CC This invention describes a novel isolated DNA molecule (I) comprising a
 CC sequence encoding a beta3-1 subunit of a human calcium channel.
 CC Nucleic acid probes comprising 14-30 contiguous nucleotides of

CC beta_3 subunit encoding DNA are useful for isolation and cloning of
CC calcium channel subunit-encoding DNA. Recombinant eukaryotic cells that
CC express heterologous calcium channel are useful for identifying compounds
CC that modulate calcium channel activity and in assays for identifying
CC agonists and antagonists of calcium channel activity in humans. Human
CC calcium channel subunit or eukaryotic cells expressing the channel are
CC useful for diagnosing Lambert Eaton Syndrome (LES) in a human. This
CC sequence represents the human calcium channel alpha-2 subunit which is
CC described in the method of the invention.
XX
SQ Sequence 1091 AA;

Query Match 100.0%; Score 5443; DB 21; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLFOSLLIGPSSPEPPSAVTKSWDKMQEDLYTLAKTAGSVNQLVDI 60
Db 1 maagcllaltlclfgslilgppsseepfssavtikswdkmqedlvtlaktasgvnqlvdi 60

QY 61 YEKYQDLYVEPNARQVLEIAARDIEKLLSNRSKALVSLALEAEKVQAAHOWREDFASN 120
Db 61 yekyqdytvepnarqlveiaardieklslsrskalvslaleaeekvqaahqwedrfasn 120

QY 121 EYVYNAKDDLPKNDSPGQRKIPVFIEDANFGROISYQHAHVHPTDIYEGSTIVL 180
Db 121 evvynakddlpkndspgqgrkvpfiedanfgroisyaahvhtdiyegstivl 180

QY 181 NELNWTSADEVFKKNEEDPSLLQVFGSATGLARYYPASVPWDSNRTPNKKIDLYVRR 240
Db 181 nelnwtalsaldevfkknreedsllqvfgsatglaryypasvpwdsnrtpnkkidlyvrr 240

QY 241 RPYWQGAASPKDMLILVDVSGVSLIKLIRTSVSEMLETLSDDDFVNVSFNSAQD 300
Db 241 rpywqgaaspkdmlilvdvsgvsgltiklirtsvsemletlstdddfvnvasfnsnaqd 300

QY 301 VSCFQHLVQANVRNKKVLKADAVNNITAKITDYKKGFSAFQQLNLYNVSRANCKIIML 360
Db 301 vscfqlhvanvrnkvkldavnnitakitdykkgfsafqqlnlynvsranckiiiml 360

QY 361 FTDGGEERAQEIFNKNYKDKVYRFRFSVQGHNYERGPQIWMACENKGYIYIPIGAIK 420
Db 361 ftdggeeraqeifnknkdkvyrfrfsvqghnyergpqiwmacenkgyyiyeipsigair 420

QY 421 INTOEYLDVLRPMVLGAKQVQWTVNYLDLLEGLVITGTLVFNITGOFENKTNLK 480
Db 421 intqeyldvlgrpmvlgakqvwtnvnyldalleglvitgtlvpfnitgofenktnlk 480

QY 481 NOLILGVMGVDVSLIEDIKRLTPRFTLCPNGYFAIDPNGYVLLHNPLOPKPKSOEPTVL 540
Db 481 nqililgvmgvdvsliekrltprftlcpngyfaidpngyvllhnplopkpksoepvtl 540

QY 541 DFLDAELENDIKVEINRNMIDGSEKFTRTLKVSQDERYIDKGNRTYTWTVPNGTDYSL 600
Db 541 dfldaelendikveinrnmidgsektftrtlvksqderiyidkgnrtytwtvtpngtdysl 600

QY 601 ALVLPYSPYIKALEEITITQARSKGKMKOSEFLKPDNFESGYTFTAPRDYCNDLKI 660
Db 601 alvlpyspyikaleeittitqarskkgmkdsetlkpndfnesgytftiaprdocndlki 660

QY 661 SDNTEFLNFEIDRKPNNPSCNADLINRVLLDAGFTNELVQNSKQKNIGVKAR 720
Db 661 sdnteflnfeidrkpnnpscnadlinrvllldagftnelvqnskqknigvkarkar 720

QY 721 FVYTDGGITRVYPKEAGENQENPETEDSFYKSLDNDNYVFTAPYFNKSGPGAYESGI 780
Db 721 fvytdggitrvyypkeagenqenpetyedsfykrslndnyvftapyfnkspggayesgi 780

QY 781 MYSKAVEIYIQGLKLPVAVGKIDVNSHENTFTKTSIRDPAGVPVCDCKRNSDMDCVI 840
Db 781 mvskaveyiqgkllkpavvgkldvnsnientftktsirdpcagvpvcdckrnsdmdcvi 840

QY 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNIISVYAFNKSVDYQSVCEPGAAPKQ 900
Db 841 lddggflmanhddytntqigrfgeidpslmrhlvnisvafnksydyqsvcepgaapqk 900

QY 901 GAGHRSATVPSVADILQIGWATATAAASILQOFLLSLTFPRLEAVEDEDDFTASLSKQ 960
Db 901 gaghrsavypsavadilqigwataaasilqgflsltfprlleavedddftaslskq 960

QY 961 SCITEOTQYFDDNSKSPSGVLDGNCGRIFPHGEKLMNTNLIIFIMVESKGTCPDCTRLLI 1020
Db 961 sciteotqyffddnsksfsgvldcncsrifhgeklmntnliifimveskgtpcdctrlli 1020

QY 1021 QAEQTSDDGNPCDMVK 1036
Db 1021 qaeqtsdgnpcdmvk 1036

RESULT 4
AAW37879
ID AAW37879 standard; Protein; 1091 AA.

XX AC AAW37879;
XX DT 28-AUG-1998 (first entry)
XX DE Human calcium channel a2d subunit.
XX KW Calcium channel; human; central nervous system disorder;
XX KW Lambert-Eaton syndrome; diagnosis; therapy.
XX OS Homo sapiens.
XX PN W09811131-A2.
XX PD 19-MAR-1998.
XX PF 11-SEP-1997; 97WO-US16146.
XX PR 16-SEP-1996; 96US-0713118.
XX PA (AMHP) AMERICAN HOME PROD CORP.
XX PI Chen ARS, Franco R, Shuey DJ;
XX DR WPI: 1998-207325/18.
XX DR N-PSDB; AAV29060.
XX PT DNA encoding human neuronal calcium channel subunit(s) - useful for
XX PT diagnosis of and treatment of central nervous system disorders, e.g.
XX PS Lambert-Eaton syndrome
XX PS Disclosure; Fig 2; 89pp; English.

XX This polypeptide comprises the a2d subunit of the human neuronal
XX calcium channel. cDNA clones (see AAV29059-61) encoding the a1b
XX subunit (see AAW37878), the a2d subunit and a b3 subunit (see AAW37880)
XX have been isolated. These have been inserted into expression
XX vectors and are stably expressed in transformed cell lines. The
XX transformed cells show omega-conotoxin GVIA binding activity,
XX and omega-conotoxin GVIA toxin sensitive potassium-stimulated
XX calcium uptake, indicating that the proteins expressed by the
XX clones are capable of forming a functioning calcium channel.
XX Nucleic acids encoding the 3 subunits, as well as vectors, host
XX cells and methods of isolating nucleic acids encoding related
XX calcium channels are disclosed. Fusion proteins incorporating the
XX subunit proteins, antibodies, and assays for identifying agents
XX that modulate calcium channel activity are also provided. Such
XX agents can be used to treat certain central nervous system
XX disorders by altering calcium channel activity. Methods of
XX diagnosing diseases associated with particular calcium channels,
XX such as Lambert-Eaton syndrome, are disclosed.

SQ Sequence 1091 AA;

Query Match		99.9%; Score 5439; DB 19; Length 1091;	
Best Local Similarity		99.9%; Pred. No. 0;	
Matches 1035; Conservative		0; Mismatches 1; Indels 0; Gaps 0;	
QY	1	MAAGCLLALTLTFSQLLIGPSSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI	60
Db	1	maagcllaltltfsglligpsseepfsvavtikswdkmqedlvtlaktasgvnqlvdi	60
QY	61	YERYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDEFASN	120
Db	61	yekyqdltyvepnarqlveiaardieklslsnrskalvslaleaekvqaahqwrdefasn	120
QY	121	EVVYNKDDLDPEKNDSEPGSRQIKPVFIEDANFGQISYQHAHVHIPTDIYEGSTIVL	180
Db	121	evvynakddldpekndsepgsrqikpvfiedanfgqisyqhaavhiptdiyegstivl	180
QY	181	NELNWTSAIDVEPKKREDEPSLLQVFGSATGLARYYPASPWDNSRTNPKIDLIDVRR	240
Db	181	nelnwtasaldevfkreedepsllwvfgsatglaryypaspwvdsrtpkidlydrr	240
QY	241	RPWTIOGAASPDKMLIIVDVGSGVGLTLKIRTSVSEMLETISDDDFNVASFNSNAQD	300
Db	241	rpwyigaaspdkmllivdvsgsvgltklirtsvsemlletisdddfnvafnsnaqd	300
QY	301	VSCFQHLVQANVRNKKVLDVANNITAKGITYDKKGFSAFEOQLLNVSRANCKIIML	360
Db	301	vscfqlhivqanvrnkylkdavnnitakgitdykkgfafeqllnvsvrancnkliiml	360
QY	361	FTDGGERRAQEIENKYNKDKVRFRPSVQCHNVERGPIQWACENKGYIYEIPSGAIR	420
Db	361	ftdggerraeieinkynkdkvfrfsvqghnyergpiqwmacenkgyyiyeipsigair	420
QY	421	INTQEYLDVLRPMVLADGAKOVQNTVYLDALGLVITGLPVFNITGQFNKTNLK	480
Db	421	intqeyldvlgpmvladgakovqntvnyldalelgvltglpvfnitgqfnktnlk	480
QY	481	NQILGVMGVDVLSLEDKRITPRTLCPNGYIFAIDPNGVYLLHNPONPKNSQEPVTL	540
Db	481	nqilgvmgvdsledikritpftlcpngyifaidpngyallhnpnlqpnkpsqepvtl	540
QY	541	DELDAELENDIKVEIRNKMTDGESEKFTFLYKSDQERYIDKGNRTYTWTPVNGTDYSL	600
Db	541	dldaeldendikveirnkmtidesgektftrlvksqderydkgnrtytwtpvngtdysl	600
QY	601	ALVLPYSFYIYAKLETITQARSKGKMKDSETLKPDNFEESGYTFIAPRDYCNDLKI	660
Db	601	alvlpysfyiyakleetitqarskgkmdsetlkdndfeesgytfiaprdywndlki	660
QY	661	SDNTEFLNFEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQNTWSKOKNKGVKAR	720
Db	661	sdntefllnfeidrktpnpncnadlinrvlldagftnelvqnvyskqknkgvkar	720
QY	721	FVYTDGTRIVYKEAGENQENPETYEDSFYKRSNDNDNVFTAPYFNKSGCAYESGI	780
Db	721	fvtydgtrivypkeagenqenpetyedsfyrslndndnyvftapyfnsksgayesgi	780
QY	781	MVSKAVEIYIQGLLKPVAVGIKIDVNSWIENFTKTSIRDPACGVCDCRNSDVMDCVI	840
Db	781	mvskaveiyiqgllkpavvgikidvnswieenftktsirdpacgvpdcckrnsdvmdcvi	840
QY	841	LDGGFLLMANHDDYTHQIGRFGEEIDPDSLMRHLVNTSVAFNKSQYDQVCEPGAAPKQ	900
Db	841	ldggfllmanhddytqigrfgelidpslmrhlvntsvafnksydyqvscepgaapqk	900
QY	901	GAGHSAYVSVADILQIGWATAAANSILQQFLLSTLTFPRLLAEVEMEDDDFTASLSKQ	960
Db	901	gaghsayvsvadilqigwataaansilqqfllstltpfrrlleavemedddftaslskq	960
QY	961	SCITEQYQYFFDNDKSFSGVLDGNCGRIFPHGKLMNTNLIIFIMVSKGTCPCDTRILLI	1020
Db	961	sciteqcyqyffndksfsgvldcncsrifphgklmntnlifimveskgtcpcdtrilli	1020

Query Match		99.9%; Score 5437; DB 14; Length 1091;	
Best Local Similarity		99.9%; Pred. No. 0;	
Matches 1035; Conservative		0; Mismatches 1; Indels 0; Gaps 0;	
QY	1	MAAGCLLALTLTFSQLLIGPSSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI	60
Db	1	maagcllaltltfsglligpsseepfsvavtikswdkmqedlvtlaktasgvnqlvdi	60
QY	61	YERYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDEFASN	120
Db	61	yekyqdltyvepnarqlveiaardieklslsnrskalvslaleaekvqaahqwrdefasn	120

RESULT 5

AAAR33553	1021	QAEQTSQSDGNPCDMVK	1036
ID	AAAR33553	standard; Protein; 1091 AA.	
XX	AAAR33553;		
XX	AC		
XX	30-JUN-1993	(first entry)	
XX		Sequence of the alpha 2 human calcium channel subunit.	
XX		Human calcium channel subunit; diagnosis; agonist; antagonist;	
XX		Lambert Eaton syndrome.	
XX		Homo sapiens.	
XX		WO9304083-A.	
XX	04-MAR-1993.		
XX	14-AUG-1992;	92WO-US06903.	
XX	15-AUG-1991;	91US-0745206.	
XX	10-APR-1992;	92US-0868354.	
XX		(SALK) SALK INST BIOTECHNOLOGY IND ASSOC.	
XX		Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;	
XX		Williams ME;	
XX		WPI: 1993-093936/11.	
XX		N-PSDB; AAQ37821.	
XX		DNA encoding specific human calcium channel sub-units - used for	
XX		identifying calcium channel agonists and antagonists and	
XX		diagnosing Lambert Eaton syndrome	
XX		Disclosure; Page 134-138; 150pp; English.	
XX		DNA encoding a human neuronal calcium channel alpha 2 subunit was	
XX		isolated from a human genomic DNA library probed under low and high	
XX		stringency conditions with a fragment of DNA encoding the rabbit	
XX		skeletal muscle calcium channel alpha 2 subunit. The fragment	
XX		included nucleotides having a sequence corresponding to the	
XX		nucleotide sequence between nucleotides 43 and 272 inclusive of	
XX		rabbit back skeletal muscle calcium channel alpha 2 subunit cDNA.	
XX		PCR analysis identified splice variants of the human calcium alpha	
XX		2 subunit transcript. In particularly preferred embodiments, the	
XX		DNA encoding the alpha 2 subunit is produced by alternative	
XX		processing of a primary transcript that includes DNA encoding the	
XX		amino acids set forth in AAR33553 and the DNA of AAQ37823 inserted	
XX		between nucleotides 1624 and 1625 of AAQ37821.	
XX		Sequence 1091 AA;	

QY 121 EVVYNAKDDLDPEKNDSPGSGRIKPVIEDANFGRIQISYQHAHVHIPTDIYEGSTIVL 180
DB 121 evvynakddldpekndspgsgrikpviedanfgriqisyaahvhiptdiyegstivl 180
QY 181 NELNWTSAIDVEFKKNEEDPSLLWQVFGSATGLARYYPASFWVDSNRTPNPKIDLYDVR 240
DB 181 nelnwtalsidevfkknreedpsllwqvfgsatglaryypasfwvdsnrtpnkdilydvrr 240
QY 241 RPWYIQAASPKDMLILVDVSGVSGLTLEKLRISVSEMLETSDDDFNVASFNSNAQD 300
DB 241 rpwyiqaaSPKdMLILVDVSGVSGLTLEKLRISVSEMLETSDDDFNVASFNSNAQD 300
QY 301 VSCFQLVQANVRNKKVLDKADANNITAKGIDYKKGFSAFEPQLLNINVSANCNKIIML 360
DB 301 vscfqlvqanvrnkklvdannitakgidtykkgfsafepqllnynvsrncnkiiML 360
QY 361 FDTGGEERAQEIFENKYNKDKKVRVFRFSVQGNHYERGPQIOWACENKGYIYIPSGAIR 420
DB 361 ftdggeeraqeifENKYNKDKKVRVFRFSVQGNHYERGPQIOWACENKGYIYIPSGAIR 420
QY 421 INTQEVLDVLRPMVLGAKQOVQWTVNYLDALGLVITCTLPVFNITGOFENKTNLK 480
DB 421 intqevldvLRPMVLGAKQOVQWTVNYLDALGLVITCTLPVFNITGOFENKTNLK 480
QY 481 NQILGVMGVDSLEIDIKRLTPRFTLPCPNYYFAIDPNGYVLLHPLNLPKNKSPQEPVTL 540
DB 481 nqilgvmgvdsleidIKRLTPRFTLPCPNYYFAIDPNGYVLLHPLNLPKNKSPQEPVTL 540
QY 541 DFLDALENDIKVEIKNKMIDGESGEKTRTLVKSDODERYIDKGNRTYTWVNGTDYSL 600
DB 541 dfldaelendikveiknkmidgesgektRtlvksdoderyidkgnrtytwtvngtdysl 600
QY 601 ALVLPYSYVYIKAKLEETITQARSKGKMDSETLKPONFEESGVTFTAPRDXCNDLKI 660
DB 601 alvlpysyvyikakleetitqARSKGKMDSETLKPONFEESGVTFTAPRDXCNDLKI 660
QY 661 SDNTEFLNLFNEFIDRKTNNPNSCNADILNRVLLDAGFTNELVQWYKQNIKGVKAR 720
DB 661 sdnteflnlfnefidrktNNPNSCNADILNRVLLDAGFTNELVQWYKQNIKGVKAR 720
QY 721 FVYTDGGITRVYPKEAGENQENPEYEDSFYKRSJLDNDNYVFTAPYFNKSGPGAYESGI 780
DB 721 fvtytdggitrvypkeagenqenpeyedSFYKRSJLDNDNYVFTAPYFNKSGPGAYESGI 780
QY 781 MYSKAVEIYIQGLKLPVAVGKIDVNSHNIENFTKTSIRDPCAGPVCDCRNSDVMDCVI 840
DB 781 mvsKaveiyiqglkLPVAVGKIDVNSHNIENFTKTSIRDPCAGPVCDCRNSDVMDCVI 840
QY 841 LDGQGLLANHDDYNTQIRFPFGEIDPSLMRLHVNISVYAFNKSVDYQSVCEPGAAPKQ 900
DB 841 ldgqglLANHDDYNTQIRFPFGEIDPSLMRLHVNISVYAFNKSVDYQSVCEPGAAPKQ 900
QY 901 GAGHRSAYVPSVADILQIGWATAAAMSILQOFLSLTTPRLLAEVEMEDDDFTASLSKQ 960
DB 901 gaghrsAYVPSVADILQIGWATAAAMSILQOFLSLTTPRLLAEVEMEDDDFTASLSKQ 960
QY 961 SCITEOTQFFDNDKSFSGVLDGCNCSIFRCEKLMNLFIFIMVESKGTCPCDTRLII 1020
DB 961 sciteotqffDNDKSFSGVLDGCNCSIFRCEKLMNLFIFIMVESKGTCPCDTRLII 1020
QY 1021 QAEQTSDDGPNPCDMVK 1036
DB 1021 qaeqtsddgPNPCDMVK 1036
RESULT 6
ID AAW63148
XX AAW63148 standard; Protein; 1110 AA.
AC AAW63148;
XX AAW63148;
DT 12-OCT-1998 (first entry)
XX

DE Human calcium channel alpha-2 subunit.
XX Alpha-2 subunit; human; calcium channel; assay; detection;
KW characterisation; Lambert Eaton Syndrome; LES; diagnosis.
XX Homo sapiens.
XX US5792846-A.
XX 11-AUG-1998.
XX 31-MAY-1995; 95US-0455543.
XX 04-APR-1994; 94US-0223305.
PR 04-APR-1988; 88US-0176899.
PR 04-APR-1989; 89US-0603751.
PR 04-APR-1989; 89WO-US01408.
PR 20-FEB-1990; 90US-0482384.
PR 30-NOV-1990; 90US-0620250.
PR 15-AUG-1991; 91US-0745206.
PR 31-MAY-1995; 95US-0455543.
XX (STBI-) STBIA NEUROSCIENCES INC.
PA Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AP;
PI Williams ME;
XX WPI: 1998-456192/39.
DR N-FSDB; AAV42694.
XX DNA encoding human calcium channel alpha 1B sub:unit protein -
PT useful for recombinant production of the channel for screening of
PT its modulators, and diagnosis of Lambert Eaton Syndrome
XX Disclosure: Columns 131-138; 166pp; English..
PS The present sequence represents the alpha-2 subunit of a human calcium
CC channel. Calcium channels are membrane-spanning, multi-subunit proteins
CC that allow controlled entry of calcium ions into cells. This leads
CC to depolarisation events required for muscle contraction. The recombinant
CC subunit, when expressed with nucleic acids encoding the complete calcium
CC channel, can be used in assays for the detection and characterisation of
CC compounds that modulate the channel. The DNA encoding the subunits can
CC be alternatively spliced when transcribed, giving more than one form of
CC the protein from the same transcript, each having slightly different
CC properties. In addition, the reactivity of the alpha 1 subunit with IgG
CC molecules from the serum of an individual with Lambert Eaton Syndrome
CC (LES) can be used as a diagnostic for the disease.
XX Sequence 1110 AA;
SQ
Query Match 99.6%; Score 5423.5; DB 19; Length 1110;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 1036; Conservative 0; Mismatches 0; Indels 19; Gaps 1;
QY 1 MAAGCLLATLTLFQSLILGPSSEEPFSAVTIKSVWDMQEDLVTLAKTASGNOLVDI 60
DB 1 maagcllatlTLfQSLilGPSSEEPfSAvtIKSVWDMQEDLVtlAKtASGNOLVDI 60
QY 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRKSALVSLALEAEKVQAHHQWREDFASN 120
DB 61 yekyqdlytvepnaRqlVEIAARDIEKllSNRKSALVslALEAEKVQAHHQwREdfasn 120
QY 121 EVVYNAKDDLDPEKNDSEPGSGRIKPVIEDANFGRIQISYQHAHVHIPTDIYEGSTIVL 180
DB 121 evvynakddldpekndsepgsgrikpviedanfgriqisyaahvhiptdiyegstivl 180
QY 181 NELNWTSAIDVEFKKNEEDPSLLWQVFGSATGLARYYPASFWVDSNRTPNPKIDLYDVR 240
DB 181 nelnwtalsidevfkknreedpsllwqvfgsatglaryypasfwvdsnrtpnkdilydvrr 240
QY 241 RPWYIQAASPKDMLILVDVSGVSGLTLEKLRISVSEMLETSDDDFNVASFNSNAQD 300
DB 241 rpwyiqaaSPKdMLILVDVSGVSGLTLEKLRISVSEMLETSDDDFNVASFNSNAQD 300

|||||
Db 241 rpwyiqgaaspkdmllilvdvsgsvglklkirtssemlctisdddfvnvasfnsgd 300
Qy 301 VSCFOHLVQAVNRNKKVLKDAVNNTAKGIDYKKGFSFAFQQLNYSRANCNKIIML 360
Db 301 vscfghlvqanvrnkvlkdavnntakgldkdykkgfsfafqqlnynvsrancnkiiiml 360
Qy 361 FTDGGEERAQEIFNKYNDKKVRFPSVGOHNYERGIOWMACENKGYEYIPEISGAIR 420
Db 361 ftdggeeraqefinkyndkkvrfvsvgqnyergplqwmacenkgyyeipsigair 420
Qy 421 INTOBYLDVLRPMVLADGKAKQVQWTVYLDALGLVITGLTFVFNITGOFENKTNLK 480
Db 421 intqeyldvlgprpmvladgkakqvwtvnyldalelgvltgtlpvfnitgqfenktnlk 480
Qy 481 NQILGVNGVDVSLIEDIKRLPRFTLCPNGYFFAIDPNGYLLHPNLQPK----- 530
Db 481 nqililgvngvdsledikrlprftlcpngyffaidpnygvyllhpnlpkpgvgiptin 540
Qy 531 -----NPKSQBPVTLDFDAELENDIKVEIRNKMIDGESGEKTRTLVKSQDERYI 581
Db 541 lrkrpnlqnpksgpvtldfldaelendikveirnkmidgesgektfirtlvksqderyi 600
Qy 582 DKGRTYTWTPVNGDYSLALVLPYSFYIKAKLEETITQARSKKGKMKDSETLKPDNF 641
Db 601 dkgntytwtpvngtdyslalvlpysfyikakleetitgarskkgmksdsetlkpdnf 660
Qy 642 EESGYTFIAPDYCNLDKISDNNTFLNFEFIDRKPNNPNSCNADLTNRVLIDAGFTN 701
Db 661 eesgytfiaprdycondlkisdnteflnfeidrktpnpscnadlnrvllidagftn 720
Qy 702 ELVQYNSQKNIKGVKARFVVTVGGITRVYPKEAGENQENPETYDSFYKRSLDNDNY 761
Db 721 elvqnywskqnikgvkarfvvtvggitrvypkeagenqenpetyedsfykrsldndny 780
Qy 762 VFTAPYFNKSGPGAYESIMVSKAVEYIIOGKLKPAVVGKIDYNSWIENFTKSIDRP 821
Db 781 vftapyfnksgpgayesimvskaveyiqgklkpaavgkldvnswnienftktsirdp 840
Qy 822 CAGPVCDCKRNSDMVDCVILDDGGFLMANHDDYTNQIRFFGEIDPSLMRHLNVSIVA 881
Db 841 cagpvcdckrnsdmvdcvildggflmanhddytncqirffgeidpslmrhlvnsviva 900
Qy 882 FNKSYDYOSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAASWISLQOFLSLTPPR 941
Db 901 fnksydyosvcepgaapkgaghrsayvpsvadilqigwataaawsilqgflsltppr 960
Qy 942 LLEAVEMEDDDFTASLSKQSCITETQTYFFDNDSKFSVLDGCGNCSRFHGEKLMNTNL 1001
Db 961 lleavemedddftaslskqsciteqtgyffdnkskfsvldcgncsrfhgekilmntnl 1020
Qy 1002 IFIMVESKGTCPDTRLLIOAEQTSQSDGNPCDMVK 1036
Db 1021 ifimveskgtcpdtrlliqaeqtsdgnpcdmvk 1055

RESULT 7

ID AAR71013 standard; Protein; 1086 AA.

XX AAR71013;

XX AAR71013;

DT 01-DEC-1995 (first entry)

DE Human neuronal calcium channel subunit alpha 2c.

XX Calcium channel subunit; agonist; diagnosis;
KW Lambert Eaton Syndrome.

XX Homo sapiens.

XX W09504822-A.

PN

16-FEB-1995.
XX 11-AUG-1994; 94WO-US09230.
XX 11-AUG-1993; 93US-0105536.
PR 05-NOV-1993; 93US-0149097.
XX (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
XX Ellis SB, Gillespie A, Harpold MM, McCue AF, Williams ME;
PI WPI; 1995-090900/12.
XX N-PSDB; AAQ84667.
XX DNA encoding human calcium channel sub-unit(s) - used for
PT developing prods. for studying calcium channels, e.g. for
PT obtaining agonists and antagonists
XX
PS Disclosure; Page 237-242; 285pp; English.
XX Human neuronal alpha 2 coding sequence (AAQ84664) transcript is
CC differentially processed in skeletal muscle, aorta, and CNS in
CC the region corresp. to nt 1595-1942 of AAQ84664 in each of the
CC tissues. Five alternatively spliced variant transcripts that differ
CC in the presence or absence of one to three different portions of
CC this region. There are three sequences involved (see AAQ84664 FT
CC and AAQ84665 FT), sequence 1, sequence 2 and sequence 3. The five
CC alpha 2 encoding transcripts from the different tissues include
CC different combinations of the three sequences, except for one of
CC the alpha 2 transcripts expressed in aorta which lacks all three
CC sequences. The five alpha 2 forms identified are (1) a form that
CC lacks sequence 3 called alpha 2a, expressed in skeletal muscle
CC (2) one that lacks sequence 1 called alpha 2b, expressed in CNS
CC (3) one that lacks sequences 1 and 2 called alpha 2c, expressed in
CC aorta (4) one that lacks sequences 1, 2 and 3 called alpha 2d,
CC expressed in aorta and (5) one that lacks sequences 1 and 3
CC called alpha 2e. The DNA and AA sequences of alpha 2a - alpha 2e
CC are set forth in AAQ84666-084669 and AAR71012-R71015 respectively.
XX
SQ Sequence 1086 AA;

Query Match 99.3%; Score 5403.5; DB 16; Length 1086;

Best Local Similarity 99.5%; Pred. No. 0;

Matches 1031; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

Qy 1 MAAGCLLALTTLTFLFOSLLIGPSSPEPPPSAVTIKSWVDKMOEDLVTLAKTAGVNLVDI 60

Db 1 maagcllaltltlfgslilgspseepfpfsavtikswvdkmqedlvclaktasgvnqlvdi 60

Qy 61 YEKYQDLYTVEPNARQLVEIARAARDIEKLLNSRKALVSLALEAEKVQAAHQRDFASN 120

Db 61 yekyqdytvepnnarqlveiaardieklkllnsrkalsvslaleaeqvqaahqrdfasn 120

Qy 121 EVVYVNAKDDLDPEKNDEPQSQRKPKVFIEDANFGROIHQHAAVHIPTDIYEGSTVL 180

Db 121 evvyvnaakddldpekndepgsqrikpvfiedanfgrlsyqhaavhiptdiyegstvl 180

Qy 181 NELNWTSSALDEVFKKNREEDPSLLWQVFGSATGLARYYPASPPWVDSRTPNKIDLYDVR 240

Db 181 nelnwtssaldevfkknreedpsllwqvfgsatglaryypasppwvdsrtpnkidlydvr 240

Qy 241 RPWYIQGAASPKDMLILVDVSGSVSGLTKLIRTSVSEMLETSLDSDDFVNVASFNSAQD 300

Db 241 rpwyiqgaaspkdmililvdvsgsvgltklirtsvsemlletlsdddfvnvasfnsgd 300

Qy 301 VSCFOHLVQAVNRNKKVLKDAVNNTAKGIDYKKGFSFAFQQLNYSRANCNKIIML 360

Db 301 vscfghlvqanvrnkvlkdavnntakgldkdykkgfsfafqqlnynvsrancnkiiiml 360

Qy 361 FTDGGEERAQEIFNKYNDKKVRFPSVGOHNYERGIOWMACENKGYEYIPEISGAIR 420

Db 361 ftdggeeraqefinkyndkkvrfvsvgqnyergplqwmacenkgyyeipsigair 420

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QY 421 INTQEVLDVLRPMVLADGKAKQVQWTVNYLDALGLVITGLTPVENITGQFENKTLK 480
DB 421 intqeyldvlgpvmvladgkqkvqwnvldalelgvltgltpvfnitgqfentknlk 480
QY 481 NQLILGVMGVDSLEDEIKRLTPRFTLCPNGYFFAIDPNGYVLLHPNLOPKPKSQEPVTL 540
DB 481 nqlilgvmgvdvsledikrltprftlcpcngyffaidpnyvllhpnlpk-----epvtl 535
QY 541 DFLDAELENDIKVEIRNKMIDGSEKFTRLVKSQDRIYIDKGNRTYTWTPVNGTDSL 600
DB 536 dfldaelendikveirnmidgesekftrtlvksqderiyidkgnrtwtwtpvngtdysl 595
QY 601 ALVLPYISYIIKALEEITQARSKGKMDSETLKPDNFEESGYTFIAPRDYCNDLKI 660
DB 596 alvlpysyiyikaleetitqarskkgkmdsetlkdnpnfesgytffiaprdychnlki 655
QY 661 SNNTEFLNFEIDRTPNPNPSCNADLINRVLLDAGFTNELVQYWSKQKNIKGVKAR 720
DB 656 sdnntefllnfnedrtpnpnpncnadlinrvllldagftnelvqywsqknikgvkar 715
QY 721 FVYTDGGITRVYPKEAGENWQENPETEYDFYKRLDNDNYVFTAPYFNKSGPGAYESGI 780
DB 716 fvytdggitrvyypkeagenwqenpeteasfykrlndndnyvftapyfnksgpgayesgi 775
QY 781 MYSKAVEIYIQKLLKPAVVGKIDVNSWNIENFTKTSIRDPGAGVPCDKRNSDVMDCVI 840
DB 776 mvskaveyiqkllkpvavvgikidvnswnienftktsirdpcagpvcckrnsvmdcvi 835
QY 841 LDGGFLLMANHDDVTNQIGRFFGEIDPSLMRLHVNISVYAFNKSVDYQSVCEPGAAPKQ 900
DB 836 ldggfllmanhddvtngqgrffgeidpslmrhlvnisvyafrnksydyqsvcepgaapq 895
QY 901 GAGHRSAYVPSVADILQIGWATAAAMSTLQOFLSLNFPRLLEAVEMEDDFTASLSKQ 960
DB 896 gaghrsayvpsvadilqgwataaawstlqofllslnfprrlleavemeddftaslskq 955
QY 961 SCITEQTQYFFONDSPKSGVLDGNCRSRIFHGEKLMNTNLIIFIMVESKGTGCPDTRLII 1020
DB 956 sciteqtqyffondsksfsgvldgncrsrifhgeklmntnlifimveskgtpcdtrlli 1015
QY 1021 QAEQTSQDGNPCDMVK 1036
DB 1016 qaeqtsdgnpcdmvk 1031

RESULT 8
AAW63153
ID AAW63153 standard; Protein; 1086 AA.
AC AAW63153;
XX AAW63153;
DT 12-OCT-1998 (first entry)
DE Human calcium channel alpha-2c subunit.
XX Alpha-2 subunit; human; calcium channel; assay: detection;
KW Characterisation; Lambert Eaton Syndrome; LES; diagnosis.
XX Homo sapiens.
XX US5792846-A.
PN 11-AUG-1998.
PD 31-MAY-1995; 95US-0455543.
XX 04-APR-1994; 94US-0223305.
PR 04-APR-1988; 88US-0176889.
PR 04-APR-1989; 89US-0603751.
PR 04-APR-1989; 89WO-US01408.
PR 20-FEB-1990; 90US-0482384.
PR 30-NOV-1990; 90US-0620250.
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PR 15-AUG-1991; 91US-0745206.
PR 31-MAY-1995; 95US-0455543.
XX (SIBI-) SIBIA NEUROSCIENCES INC.
XX Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;
PI Williams ME;
XX WPI; 1998-456192/39.
DR N-PSDB; AAV42702.
XX DNA encoding human calcium channel alpha 1B subunit protein -
PT useful for recombinant production of the channel for screening of
PT its modulators, and diagnosis of Lambert Eaton Syndrome
XX Claim 3; Columns 293-300; 166pp; English.
XX The present sequence represents the alpha-2c subunit of a human calcium
CC channel. Calcium channels are membrane-spanning, multi-subunit proteins
CC that allow controlled entry of calcium ions into cells. This leads
CC to depolarisation events required for muscle contraction. The recombinant
CC subunit, when expressed with nucleic acids encoding the complete calcium
CC channel, can be used in assays for the detection and characterisation of
CC compounds that modulate the channel. The DNA encoding the subunits can
CC be alternatively spliced when transcribed, giving more than one form of
CC the protein from the same transcript, each having slightly different
CC properties. In addition, the reactivity of the alpha 1 subunit with IgG
CC molecules from the serum of an individual with Lambert Eaton Syndrome
CC (LES) can be used as a diagnostic for the disease.
XX Sequence 1086 AA;
SQ
Query Match 99.3%; Score 5403.5; DB 19; Length 1086;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1031; Conservative 0; Mismatches 0; Indels 5; Gaps 1;
QY 1 MAAGCLLALTITLFLSLLIGPSSEPPFPSSAVTIKSWDKMQEDLVTLAKTAGVNLVDI 60
DB 1 maagcllaaltitlflslligpsseepfpssavtikswdkmgdvltlaktasgvnqlvdi 60
QY 61 YEKYQDLYTVEPNNAQOLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRREDFASN 120
DB 61 yekyqdlytvepnnaqolvelaardieklslsrskalvslaleaeekvqaahqwrdfasn 120
QY 121 EVVYINAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRQISQHOAAVHIPTDIYEGSTIVL 180
DB 121 evvyinakddldpekndsepgsqrikpvfiedanfgrqisqhaavhiptdiyegstivl 180
QY 181 NELNWTSAALDEVFKKNREEDPSLLMQVFGSATGLARYYPASPVDNSRTPNKIDLYDVRR 240
DB 181 nelnwtasaldevfkknreedpsllmqvfgsatglaryypaspvwnsrtpnkidlydvrr 240
QY 241 RPWYIQGAASPKDMLILVDVSGSVSGLTKLIRTSVSEMLETSLDDDFNVNASFNSNAQD 300
DB 241 rpwyiqgaaspkdmlilvdvsgsvsgltklirtsvsemletlsdddfnvvasfnsnaqd 300
QY 301 VSCFOHLVQAVNRNKKVLKDAVNNTAKGIDYKKGFSFAFEPQLLNYNVSRANCNKIIML 360
DB 301 vscfhlvqanvrnkvlkdavnnitakgidtykkgfsfafepqllnynvsrancnkiiml 360
QY 361 FTDGGEERAQEIFNKYNDKKVRFVRFVSGOHNVERGPQIOWMACENKGYIYIPSTGATR 420
DB 361 ftdggeeraqeilfnkynkdkkvrfrfvrfvsgvgnqyergpqiowmacenkgyiypstgatr 420
QY 421 INTQEVLDVLRPMVLADGKAKQVQWTVNYLDALGLVITGLTPVENITGQFENKTLK 480
DB 421 intqeyldvlgpvmvladgkqkvqwnvldalelgvltgltpvfnitgqfentknlk 480
QY 481 NQLILGVMGVDSLEDEIKRLTPRFTLCPNGYFFAIDPNGYVLLHPNLOPKPKSQEPVTL 540
DB 481 nqlilgvmgvdvsledikrltprftlcpcngyffaidpnyvllhpnlpk-----epvtl 535
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QY 541 DFLDAELENDIKVEIRKMKIDGESGKTFRTLVKSODERYIDKGNRTYTWTPVNGTDYSL 600
DB 536 dfldaelendikveirkmkidgesgkftlrvksqderidkgnrtwtvpngtdysl 595
QY 601 ALVLPYSYIYKAKLEETITQARSKKGMKDETLKPDNFESGTYFFIAPRDCYNDLKI 660
DB 596 alvlpysyikakleetitqarskkgmkdsetlkpdnfeesgyffiaprdcndlki 655
QY 661 SDNTEFLNFNFIDRKTPNPNPCNADLNIRVLLDAGFTNELVQNYWSKQKNIKGVKAR 720
DB 656 sdntefllnfnefidrktppnpsncadlnirvlldagftnelvqnywskqnikgvkar 715
QY 721 FVYTDGIRVYPKEAGENKQENPEYERYSFYKRSIDNDNIVTAPYFNKSGPGAYESGI 780
DB 716 fvytdgirtvypkesagenkqenpeyedyfkyrsidndnyvtapyfnksgpgayesi 775
QY 781 MVSKEVEIYIOGKLLPAPVVGIIKIDVNSWTENTFTKSIRDPACGPPVCDCKRNSDVMDCVI 840
DB 776 mvskaveiyiogkllpavvgiikidvnswtentftksirpcagppvcdckrnsdvmdcvi 835
QY 841 LDGSGFLMANHDDYTNQIGRFFGEIDPISLMRHLVNIISVYAFNKSYDYQSVCEPGAAPKQ 900
DB 836 ldgsgflmanhdynqnggrffgeidpslmrhlvnisvyafnkdyqsvcepgaapkq 895
QY 901 GAGHRAYVPSVADIIQIGWATAAASWIIQQFLSLTTPPRLLEAVEMEDDDFTASLSKQ 960
DB 896 gaghrayvpsvadliqigwataaaswiiqqflsltpprlleavemedddftaslskq 955
QY 961 SCITEGTOYFFDNDKSFSGVLDGCGNSRIFHGEKLMNTNLIIFIMVESKGTCPDTRLLI 1020
DB 956 scitegtqyffndksfsgvldcgncsrifhgeklmntnliifimveskgtcpdtrlli 1015
QY 1021 QABQTSQGNPCDMVK 1036
DB 1016 qaeqtsdggnpcdmvk 1031

RESULT 9
AAB10587
ID AAB10587 standard; Protein; 1086 AA.
AC AAB10587;
XX
XX
DT 22-DEC-2000 (first entry)
DE Human calcium channel alpha-2c subunit; protein.
KW Human; calcium channel; calcium channel subunit; diagnosis;
KW Lambert Eaton Syndrome; calcium channel subunit alpha-2c.
XX Homo sapiens.
OS
PN US6096514-A.
PD
PF 01-AUG-2000.
XX
XX 25-MAY-1995; 95US-0450562.
XX
XX 04-APR-1988; 88US-0176899.
PR 02-FEB-1990; 90US-0482384.
PR 08-NOV-1990; 90US-0603751.
PR 30-NOV-1990; 90US-0620250.
PR 15-AUG-1991; 91US-0745206.
PR 10-APR-1992; 92US-0868354.
PR 13-JUL-1992; 92US-0914231.
PR 11-AUG-1993; 93US-0105536.
PR 05-NOV-1993; 93US-0149097.
PR 07-FEB-1994; 94US-0193078.
PR 11-AUG-1994; 94US-0223305.
PR 23-SEP-1994; 94US-0290012.
PR 28-SEP-1994; 94US-0311363.
PR 07-NOV-1994; 94US-0336257.
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PR 13-MAR-1995; 95US-0404950.
XX (SIBI-) SIBIA NEUROSCIENCES INC.
PA Ellis SB, Williams MB, McCue AF, Harpold MM;
PI WPI; 2000-548230/50.
XX N-PSDB; AAA711725.
PT Human calcium channel beta subunit polynucleotides, useful for
PT producing recombinant eukaryotic cells and for diagnosing Lambert Eaton
PT Syndrome
XX
XX Disclosure; Column 237-244; 153pp; English.
XX
CC This invention describes a novel isolated DNA molecule (I) comprising a
CC sequence encoding a beta3-1 subunit of a human calcium channel.
CC Nucleic acid probes comprising 14-30 contiguous nucleotides of
CC beta3 subunit encoding DNA are useful for isolation and cloning of
CC calcium channel subunit-encoding DNA. Recombinant eukaryotic cells that
CC express heterologous calcium channel are useful for identifying compounds
CC that modulate calcium channel activity and in assays for identifying
CC agonists and antagonists of calcium channel activity in humans. Human
CC calcium channel subunit or eukaryotic cells expressing the channel are
CC useful for diagnosing Lambert Eaton Syndrome (LES) in a human. This
CC sequence represents the human calcium channel alpha-2c subunit which is
CC described in the method of the invention.
XX
SQ Sequence 1086 AA;

Query Match 99.3%; Score 5403.5; DB 21; Length 1086;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1031; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 1 MAAGCLLALTLTFLQSLIGPSSSEPPSAVTIKSWDKQEDLVTLAKTAGSVNQVLVDI 60
DB 1 maagcllaltltlfqslilgspseepfsavtikswdkmqedlvtlaktasgvnqlvdi 60
QY 61 YEKYQDLYTVEPNNAQOLVETIARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120
DB 61 yekyqdltyvepnnaqlveiaardieklisnrskalvslaleaeekvqaahqwrdfasn 120
QY 121 EYVYNAKDDLPEKNDSEPGSORIKPVFIEDANFGQISYQHAHVHPTDIYEGSTIVL 180
DB 121 evvyynakddldpekndsepgsgrikpvfiedanfgqisvqhaavhiptdiyegstivl 180
QY 181 NELNWTSALEDEVFKKNEEDPSLLWQVFGSATGLARYYPASPWVDNSRTNPKIDLYDVR 240
DB 181 nelnwtasaldevfkknreedpsllwqvgatglaryypaspwvdnsrtnpkidiydvrr 240
QY 241 RPWYIOGAASPDKMLILVDYSGVSGLTALKLIRTSVSEMLETSDDDFVNVSFNSNAQD 300
DB 241 rpwyiogaaspkdmllilvdvsgsvsgltklirtsvsemletisdddfvnvasfnnaqd 300
QY 301 VSCFQHLVQANVRNKKVYLKDAVNNITAKGITYDKKGSFAFEQLLLNYSRANCKNIML 360
DB 301 vscfqlhvqanvrnkkvylkdavnnitakgitdykkgfsafeqllnysrancknkiml 360
QY 361 FTDGGERAQEIENKYNKDKKRVFRFESVGHNYVERGPIQWACENKGYEYIEPSIGAIR 420
DB 361 ftdggeeraqeiefnkynkdkkrrvfrfsvghnyerpgiqwacenkgyyieipsigair 420
QY 421 INTQEYLDVLGRPMVLAGDRAKQVQMTNVYLDALGLVITGTLPVFNITGQFENKYNLK 480
DB 421 intqeyldvlgrpmvlagdkakqvqmtcnvyldalelglvitgtlpvfnitgqfenkntlk 480
QY 481 NQLILGYMVDVSLIEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHPNLQPNKPSQEPVTL 540
DB 481 nqlilgvmgvdvsledikrltprftlcpngyyfaidpnyvllhpnlpknpsqepvttl 540
QY 541 DFLDAELENDIKVEIRKMKIDGESGKTFRTLVKSODERYIDKGNRTYTWTPVNGTDYSL 600
DB 536 dfldaelendikveirkmkidgesgkftlrvksqderidkgnrtwtvpngtdysl 595
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Db 536 dflaelendikveirnmkidgesgektfrtlvksqderyldkgnrtvtwtpvngtdysl 595
 QY 601 ALVLPYFYIYKAKLEETITQARSKKGMKMDSETPKPDNFEESGYTFIAPRDYCNLDKI 660
 Db 596 alvlpysfyikakleetitqarskkgmkmdsetlkdndfeesgytfiaprdyandlki 655
 QY 661 SDNTEFLINNEFDRTKTPNPNPCNADLINRVLLDAGFTNELVONYSKOKNIKGVKAR 720
 Db 656 sdntefllnnefidrktpnpscnadlinrvlldagftnelvgnyskqknikgvkar 715
 QY 721 FVTDGGITRVPKPEAGENWQENPETYEDSFYKRSKLDNDNVFTAPYFNKSGPGAYESGI 780
 Db 716 fvtddggitrvpkeagenwgenpetyedsfykrsldndnvyftapyfnksgpgayesgi 775
 QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPCAGPVCDCRKNSDVMDCVI 840
 Db 776 mvskaveiyigkllkpvvgikidvnswieenftktsirdpcagpvcdccknsdvmdcvi 835
 QY 841 LDGSGFLMANHDDYTQIGRFFGEIDPSLMRHLNLSVAFNKSVDYQSVCEPGAAPKQ 900
 Db 836 ldgggflmanhddytqigrffgeidpslmrhlvnsvafnksydyqsvcepgaapqk 895
 QY 901 GAGHRSAYVPSVADILQIGMWATAAASILQOFLLSLTFEPRLLEAVEMEDDDFTASLSKQ 960
 Db 896 gaghrsayvpsvadilqigwataaasilqqlfllstfprlleavemedddftaslskq 955
 QY 961 SCITEQYQYFDDNSKFSGVLDGCGNSRIFPHGKLMNTNLIFIMVESKGTCTPCDTRLLI 1020
 Db 956 sciteqyqyfdndskfsgvldcgncsrifhgeklmntnlifimveskgtctpcdtrlli 1015
 QY 1021 QAETSQGPNPCDMVK 1036
 Db 1016 qaeqtsqgpnpcdmvk 1031
 RESULT 10
 AAR71015
 ID AAR71015 standard; Protein; 1084 AA.
 XX
 AC AAR71015;
 XX
 DT 01-DEC-1995 (first entry)
 XX
 DE Human neuronal calcium channel subunit alpha 2e.
 XX
 KW Calcium channel subunit; antagonist; agonist; diagnosis;
 KW Lambert Eaton Syndrome.
 XX
 OS Homo sapiens.
 XX
 PN W09504822-A.
 XX
 PD 16-FEB-1995.
 XX
 PF 11-AUG-1994; 94WO-0509230.
 XX
 PR 11-AUG-1993; 93US-0105536.
 PR 05-NOV-1993; 93US-0149097.
 XX
 PA (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
 XX
 PI Ellis SB, Gillespie A, Harpold MM, Mccue AF, Williams ME;
 XX
 DR WPI; 1995-090900/12.
 DR N-PSDB; AAQ84669.
 XX
 PT DNA encoding human calcium channel sub-unit(s) - used for
 PT developing prods. for studying calcium channels, e.g. for
 PT obtaining agonists and antagonists
 XX
 PS Disclosure; Page 248-253; 285pp; English.
 XX
 XX Human neuronal alpha 2 coding sequence (AAQ84664) transcript is

CC differentially processed in skeletal muscle, aorta, and CNS in
 CC the region corresp. to nt 1595-1942 of AAQ84664 in each of the
 CC tissues. Five alternatively spliced variant transcripts that differ
 CC in the presence or absence of one to three different portions of
 CC this region. There are three sequences involved (see AAQ84664 FT
 CC and AAQ84665 FT), sequence 1, sequence 2 and sequence 3. The five
 CC alpha 2 encoding transcripts from the different tissues include
 CC different combinations of the three sequences, except for one of
 CC the alpha 2 transcripts expressed in aorta which lacks all three
 CC sequences. The five alpha 2 forms identified are (1) a form that
 CC lacks sequence 3 called alpha 2a, expressed in skeletal muscle
 CC (2) one that lacks sequence 1 called alpha 2b, expressed in CNS
 CC (3) one that lacks sequences 1 and 2 called alpha 2c, expressed in
 CC aorta (4) one that lacks sequences 1, 2 and 3 called alpha 2d,
 CC expressed in aorta and (5) one that lacks sequences 1 and 3
 CC called alpha 2e. The DNA and AA sequences of alpha 2a - alpha 2e
 CC are set forth in AAQ84666-Q84669 and AAR71012-R71015 respectively.
 XX
 SQ Sequence 1084 AA;

Query Match 99.08; Score 5386.5; DB 16; Length 1084;
 Best Local Similarity 99.24; Pred. No. 0;
 Matches 1028; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY 1 MAAGCILLALTTLTFLFOSLLIGPSSPEPPSAVTIKSWDKQEDLVTLAKTAGVGNQLVDI 60
 Db 1 maagcillalttlfqlslligpsseepfpavtikswdkmedlvtlaktasgvnqlvdi 60
 QY 61 YEKYQDLYTEPNNAQRLVEIARDAIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120
 Db 61 yekyqdyltepnnarqlvelaardieklksnrskalvslaleaeqvaaahqwredfasn 120
 QY 121 EVVYNNAKDDLDPKENDSEPGSQRIKPVFTEDANFGKQISTQHAHVHPTDIYEGSTIVL 180
 Db 121 evvynnakddl dpkndsepgsqrikpvftedanfgkqistqhaavhptdiyegstivl 180
 QY 181 NELNWTSAIDVFKKNEEDPSLLQVFGSATGLARYYPASPWDNSRTPNKIDLYDVR 240
 Db 181 nelnwtaldevfkneedpsllwqvgfatglaryypaspwdnsrtpnkidlydvr 240
 QY 241 RPWYIOGAAPKMDMLILVDVSGVSGITLKITSVSEMLETSLDDDFVNVASFNSNAQD 300
 Db 241 rpwyiggaapkdmlilvdvsgvsgitlkitrvseemletisdddfvnvasfnnaqd 300
 QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGTDYKKGSPAFQQLNNTNVRANCNKIML 360
 Db 301 vscfqlhvqanvrnkkvldavnnitakgtdykggspafegqlnynvarancnkiml 360
 QY 361 FTDGGEEAQEIEFNKNDKKVRFRFVSQHNVERGPIOMACENKGYEYEPSIGAIR 420
 Db 361 ftdgggeeraqeiefnkndkkvrfrfvsqghnyergpiqwmacenkgyyeyepsigair 420
 QY 421 INTQEYLDVLGRPMVLGAKQVQWNTNVLDALELGLVITGLTPVFNITQGFENKTNLK 480
 Db 421 intqeyldvlgrpmvlgakqvgwntnvyldalelglvitgltpvfnitqgfenktnlk 480
 QY 481 NQLILGVMGVDSLEDIKRLTPRTFICPNGYIFAIDPNGYVLLHPNLQPKNPKSQEPVTL 540
 Db 481 nqlilgvmgvdsledikrltprfticpngyyifaidpngyvlhpnalqknpsqepvtl 540
 QY 541 DFLDALENDIKVEIRNKMIDGSGEKTFTLVKSODERYIDKGNRTYTWTPVNGTDYSL 600
 Db 541 dfldaelendikveirnkmidsgektftlvksoderyidkgnrtytwtpvngtdysl 600
 QY 601 ALVLPYFYIYKAKLEETITQARSKKGMKMDSETLKPDNFEESGYTFIAPRDYCNLDKI 660
 Db 601 alvlpysfyikakleetitqary-----setlkpndfeesgytfiaprdyandlki 653
 QY 661 SDNTEFLINNEFDRTKTPNPNPCNADLINRVLLDAGFTNELVONYSKOKNIKGVKAR 720
 Db 654 sdntefllnnefidrktpnpscnadlinrvlldagftnelvgnyskqknikgvkar 713

Mon Jul 23 08:36:22 2001

721 FVVDGGITRVYTPKEGKNGWQENPETYEDSEYKRSIDNDNYVFTAPYFNKSGPGAYESGI 780
 714 fvtvdggitrvypkeagenwqenpetyedfkyrsidndnyvftapyfnksgpgayesgi 773
 781 MYSKAVEIYIQGLKLPVAVGKIDVNSWIENFTKTSIRDPKAGPVCDCRNSDVMDCVI 840
 774 mvskaaveiyiqgklkpavvgikidvnswiensfktksirdpkagpvcdcrknsdvmdevi 833
 841 LDGCGFLMANHDDYTNOIGRFGEDIPSLMRHLVNSVYAFNKSIDYQSVCEPGAAPKQ 900
 834 lddggfllmanhddytngirfgedipslmrhlvnsyafnksdyqsvcepgaapqk 893
 901 GAGHRSAYVPSVADILQIGWATAAASIIQQFLLSLTFPRLLLEAVEMEDDDFTASLSKQ 960
 894 gaghrsayvpsvadilqigwataaasillqqfllsltfprlleavemedddftaslskq 953
 961 SCITEQTOYFFDNDKSGFSGVLDGNCGRIFPHGEKLMNTNLIFFIMVESKGTCPDTRLLI 1020
 954 sciteqtgyffndksksfsgvldgncsrifhgeklmntnliffimveskgtpcdtrlll 1013
 1021 QAEQTSQGNPCDMVK 1036
 1014 qaeqtsdgnpcdmvk 1029

RESULT 11
 AAW63155
 ID AAW63155 standard; Protein; 1084 AA.
 AC AAW63155;
 XX
 XX 12-OCT-1998 (first entry)
 XX Human calcium channel alpha-2e subunit.
 DE
 XX Alpha-2 subunit; human; calcium channel; assay; detection;
 KW characterisation; Lambert Eaton Syndrome; LES; diagnosis.
 KW
 XX Homo sapiens.
 OS
 XX US5792846-A.
 XX
 XX 11-AUG-1998.
 XX
 XX 31-MAY-1995; 95US-0455543.
 XX
 XX 04-APR-1994; 94US-0223305.
 XX 04-APR-1988; 88US-0176899.
 XX 04-APR-1989; 89US-0603751.
 XX 04-APR-1989; 89WO-US01408.
 XX 20-FEB-1990; 90US-0482384.
 XX 30-NOV-1990; 90US-0620250.
 XX 15-AUG-1991; 91US-0745206.
 XX 31-MAY-1995; 95US-0455543.
 XX (SIBI-) SIBIA NEUROSCIENCES INC.
 XX Brenner R, Ellis SB, Feldman DH, Harpold MW, McCue AF;
 PI Williams ME;
 XX WPI; 1998-456192/39.
 XX N-PSDB; AAV42704.
 XX
 XX DNA encoding human calcium channel alpha 1B subunit protein -
 PT useful for recombinant production of the channel for screening of
 PT its modulators, and diagnosis of Lambert Eaton Syndrome
 XX
 XX Claim 3; Columns 305-310; 166pp; English.
 XX
 XX The present sequence represents the alpha-2e subunit of a human calcium
 CC channel. Calcium channels are membrane-spanning, multi-subunit proteins
 CC that allow controlled entry of calcium ions into cells. This leads
 CC to depolarisation events required for muscle contraction. The recombinant

CC subunit, when expressed with nucleic acids encoding the complete calcium
 CC channel, can be used in assays for the detection and characterisation of
 CC compounds that modulate the channel. The DNA encoding the subunits can
 CC be alternatively spliced when transcribed, giving more than one form of
 CC the protein from the same transcript, each having slightly different
 CC properties. In addition, the reactivity of the alpha 1 subunit with IgG
 CC molecules from the serum of an individual with Lambert Eaton Syndrome
 CC (LES) can be used as a diagnostic for the disease.

XX Sequence 1084 AA;

Query Match 99.0%; Score 5386.5; DB 19; Length 1084;
 Best Local Similarity 99.2%; Pred. No. 0;
 Matches 1028; Conservative 0; Mismatches 1; Indels 7; Gaps 1;
 QY 1 MAAGCLLATLTTLFOSLLIGPSSEPPFPSPATYKSWDKMQEDLVTLAKTAGVGNQLVDI 60
 DB 1 maagcllatlttlfoslilgppsseepfpssavtikswdkmqedlvtlaktasvgnqlvdi 60
 QY 61 YEKYQDLYTVEPNNAQOLVEIAARDIEKLLSNRSKALVSLALEAEKVAQAHHQWREDFASN 120
 DB 61 yekyqdlytvepnnaqlveiaardieklksnrskalvslaleaeakvqaahqwfedfasn 120
 QY 121 EYVYNKADDLPEKNDSEPGSORIKPVFTEDANFGRIQISYQHAHVHPTDIYEGSTIVL 180
 DB 121 evvynakaddlpeknsepgsgrikpvfiedanfgriqisyqhaavhptdiyegstivl 180
 QY 181 NELNWTSAIDVEPKNREDEPSLLIQQVFGSATGLARYYPASPVWDSRTNPKIDLYDVR 240
 DB 181 nelnwtalsaidvefknredepsslllqqvfgsatglaryypaspvwdsrtnpkidlydvr 240
 QY 181 nelnwtalsaidvefknredepsslllqqvfgsatglaryypaspvwdsrtnpkidlydvr 240
 QY 241 RPWYIQGAASPDKMLILVDVSGSVSGITLIRTSVSEMLETSDDDDFNVASFNNAQD 300
 DB 241 rpwyiqgaaspdkmlilvdvsgsvsgitlirtsvsemlletlssdddfnvasfnnaqd 300
 DB 241 rpwyiqgaaspdkmlilvdvsgsvsgitlirtsvsemlletlssdddfnvasfnnaqd 300
 QY 301 VSCFHLVQANVRNKKVYLKDAVNNTAKGITDYKKGFSFAFEQLLNNVSRANCKIIML 360
 QY 301 vscfhlvqanvrnkvvylkdavnntakgitdykkgfsfafelqllnnvsrancnkiiiml 360
 QY 361 FTDGGEERAQELFNKYNKDKKRVFRFVSQHNYPGRPIQWACENKGYEYIPEISGAIR 420
 DB 361 ftdggeeraqelfnkynkdkkrrvfrfvsqghnygrpiqwmacenkgyyeipaisga 420
 DB 361 ftdggeeraqelfnkynkdkkrrvfrfvsqghnygrpiqwmacenkgyyeipaisga 420
 QY 421 INTOEYLDVIGRPMVLGAKAKOVQNTVYLDALGLVITGTLPVFNITGOFENKTNLK 480
 DB 421 intoeyldvigrpvmvlgakakovqntvyldaleglvitgtlpvfnitgofenkt 480
 DB 421 intoeyldvigrpvmvlgakakovqntvyldaleglvitgtlpvfnitgofenkt 480
 QY 481 NQILGVMGVDVSLDIKRLTPFTLCPNGYFAIDPNGYVLLHPLNQPNKPSQEPVTL 540
 DB 481 nqilgvmgvdsledikrltpftlcpngyfaidpngyvllhplnqpnpksqepvtl 540
 DB 481 nqilgvmgvdsledikrltpftlcpngyfaidpngyvllhplnqpnpksqepvtl 540
 QY 541 DFIDAELENDIKVEIRNKMIDGESGKFTFTLVKSQDERYIDKNGRNYTWTVPNGTDYSL 600
 DB 541 dfidaelendikveirnkmidgesgkftftlvksqderydngnyttwtvpngtdysl 600
 DB 541 dfidaelendikveirnkmidgesgkftftlvksqderydngnyttwtvpngtdysl 600
 QY 601 ALVLPYTSFYIIRAKLEETITQARSKKGKMKDSETLKPDPNFEEGSGYTFIAPRDYCN 660
 DB 601 alvlptysfyirakleetitqarskkgkmdsetlkdpnfnfeesgytfiaprdy 660
 DB 601 alvlptysfyirakleetitqarskkgkmdsetlkdpnfnfeesgytfiaprdy 660
 QY 661 SDNTEFLLNFEIDRKTNNPCNADLINRVLIDAGFTNELVQNVYWSKOKNKGKVKAR 720
 DB 661 sdnfefllnfeidrktnnpcnadlinrvlidagftnelvqnvyskknkgkvvkar 720
 DB 661 sdnfefllnfeidrktnnpcnadlinrvlidagftnelvqnvyskknkgkvvkar 720
 QY 721 FVVDGGITRVYTPKEGKNGWQENPETYEDSEYKRSIDNDNYVFTAPYFNKSGPGAYESGI 780
 DB 714 fvtvdggitrvypkeagenwqenpetyedfkyrsidndnyvftapyfnksgpgayesgi 773
 QY 781 MYSKAVEIYIQGLKLPVAVGKIDVNSWIENFTKTSIRDPKAGPVCDCRNSDVMDCVI 840
 DB 774 mvskaaveiyiqgklkpavvgikidvnswiensfktksirdpkagpvcdcrknsdvmdevi 833
 QY 841 LDGCGFLMANHDDYTNOIGRFGEDIPSLMRHLVNSVYAFNKSIDYQSVCEPGAAPKQ 900

Db 834 lddgfillmanhdytnqigrfgeidpslmrhlvnisvafnksydyqsvcepgaaapk 893
 QY 901 GAGHSAVPSVADILQIGWATAAASILQOFLLSLTFPRLLEAVENEDDDFTASLSKQ 960
 Db 894 gaghhsayvpsvaddilqigwataaawilqgflsltfprlleaveneddftaslskq 953
 QY 961 SCITPQTOYFFDNDKSPSGVLDGNCNCSRIFFHGEKLMNTNLIFFIMVESKGCPCDTRLLI 1020
 Db 954 sciteqtqyffondsksfsgvldcncsriffhgeklmtnliffimveskgcpcdtrlli 1013
 QY 1021 QAEQTSQGNPCDMVK 1036
 Db 1014 qaeqtsdgnpcdmvk 1029

RESULT 12

AAB10589
 ID AAB10589 standard; Protein; 1084 AA.

XX AC AAB10589;

XX DT 22-DEC-2000 (first entry)

XX Human calcium channel alpha-2e subunit protein.

XX Human; calcium channel; calcium channel subunit; diagnosis;
 KW Lambert Eaton Syndrome; calcium channel subunit alpha-2e.

XX OS Homo sapiens.

XX PN US6096514-A.

XX PD 01-AUG-2000.

XX PF 25-MAY-1995; 95US-04505052.

XX PR 04-APR-1988; 88US-0176899.

XX PR 02-FEB-1990; 90US-0482384.

XX PR 08-NOV-1990; 90US-0603751.

XX PR 30-NOV-1990; 90US-0620250.

XX PR 15-AUG-1991; 91US-0745206.

XX PR 10-APR-1992; 92US-0868354.

XX PR 13-JUL-1992; 92US-0914231.

XX PR 11-AUG-1993; 93US-0105536.

XX PR 05-NOV-1993; 93US-0149097.

XX PR 07-FEB-1994; 94US-0193078.

XX PR 04-APR-1994; 94US-0223305.

XX PR 11-AUG-1994; 94US-0290012.

XX PR 23-SEP-1994; 94US-0311363.

XX PR 28-SEP-1994; 94US-0314083.

XX PR 07-NOV-1994; 94US-0336257.

XX PR 13-MAR-1995; 95US-0404950.

XX (SIBI-) SIBIA NEUROSCIENCES INC.

XX PA Ellis SB, Williams ME, McCue AF, Harpold MM;

XX PI WPI; 2000-548230/50.

XX DR N-PSDB; AAA1727.

XX Human calcium channel beta subunit polynucleotides, useful for
 PT producing recombinant eukaryotic cells and for diagnosing Lambert Eaton
 PT Syndrome

XX Disclosure; Column 253-260; 153pp; English.

CC that modulate calcium channel activity and in assays for identifying
 CC agonists and antagonists of calcium channel activity in humans. Human
 CC calcium channel subunit or eukaryotic cells expressing the channel are
 CC useful for diagnosing Lambert Eaton Syndrome (LES) in a human. This
 CC sequence represents the human calcium channel alpha-2e subunit which is
 CC described in the method of the invention.

XX SQ Sequence 1084 AA;

Query Match 99.0%; Score 5386.5; DB 21; Length 1084;
 Best Local Similarity 99.2%; Pred. No. 0;
 Matches 1028; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY 1 MAAGCLLALTLTFLQSLLIGPSSSEPPPSAVTIISWVDKMOEDLVTLAKTASGVNQLVDI 60
 Db 1 maagcllaltltlfgslligpsseepfapsavtikswvdkmedlvtlaktasgvnqlvdi 60
 QY 61 YEKYQDLYTVPEPNAROLVEIAARDIEKLLSNRSKALVSLAEAEKVQAAHQWRDFAFN 120
 Db 61 yekyqdlytvepnnaqlveiaardieklksnrskalvslaeaeqvqaahqwrdfasn 120
 QY 121 EYVYNKADLDLPEKNDSEPGSQRIKPVFIEDANFGROIYSYQHAHVHIPTDIYEGSTIVL 180
 Db 121 evvynakddlpekdndsepgsqrikpvfiedanfgroisysyghaavhiptdiyegstivl 180
 QY 181 NELNWTLSALDEVFKKNEEDPSLLWQVFGSATGLARYYPASPFWVDNSRTPNKIDLYDVR 240
 Db 181 nelnwtlsaldevfkknreedpsllwqvfgsatglaryypaspfwvdnsrtpnkidlydvr 240
 QY 241 RPWYIQGAASPDKMLILVDVSGVSGLTCLKIRTSVSEMLETSLDDDFNVASFNQAQD 300
 Db 241 rpwyiqgaaspdkmlilvdvsgvsgltclkirtssemlletloddvfnvasfnasqd 300
 QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITYDKKGSFAFEQLLNVNVRANCKNIIML 360
 Db 301 vscfqlhvqanvrnkvlkdavnnitakgitydkkgsfafeqllnvnvrancnkilml 360
 QY 361 FTDCGEERAQEIFNKYKDKKRVFRSVGOHNERGPIOMACENKGYVYEISIGAIR 420
 Db 361 ftdggeeraqeifnknkdkkrrvfrsvgqnyergpiqmaceknkgyyieipsigair 420
 QY 421 INTQEYLDVLGRPMVLADGAKAQVQWTVNYLDALGLVITGLPVFNITQGFENKTLK 480
 Db 421 intqeyldvlgrpmvlagdakavqwtvnyldaleglvitgltpvfnitqgfekntlk 480
 QY 481 NQLILGVMGVDVSLIEDIKRLTPRTFLCPNGYFFAIDPNGYVLLHPNLQPKNPKSOEPTL 540
 Db 481 nqlilgvmgvdvsledikrltprftlcpngyffaidpnygvllhpnlpkpkpsqepvtl 540
 QY 541 DFLDAELENDIKVEIRNKMIDGESGEKTFRTLKSDERYIDKGNRYTWTVPVNGTDYSL 600
 Db 541 dfldaeelendikveirnkmidgesgektftrlvksqderiyidkgnrtywtvpvngtdysl 600
 QY 601 ALVLPYSFYVIRAKLETTIQAARKKMDSETLKPDPNEESGYTFIAPRDCNDLKI 660
 Db 601 alvlptsfyvirkaleettitqary-----setlkdneesgytfiaprdcndlki 653
 QY 661 SDNNTEFLNFEIDRKTNNPNSCNADLINRVLLDAGFTNELVQNTWSKQKNTKGVKAR 720
 Db 661 sdnteflnfnefidrktnpnpscnadlinrvlldagftnelvqnywskqknkgykar 713
 QY 721 FVYTDGGITRVYKPEAGENQWENPETVEDSFYKSLDNDNYVFTAPYFNKSGPGAYESGI 780
 Db 714 fvvtddggitrvypkeagenqwenpetyedsfyrslndndnyvftapyfnksgpgayesgi 773
 QY 781 MVSXAVIYIQQGLLKPAVVGKIDVNSWIENFTKTSIRDPACGVPDCKRNSDVMDCVI 840
 Db 774 mvsxaveiyiqgllkpaavgikidvnswiefktksirpdcagvpdcckrnsdvmdevi 833
 QY 841 LDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNTSVYAFNKSVDYQSVCEPGAAPKQ 900
 Db 834 ldggfllmanhddytngigrffgeidpslmrhlvnisvafnksydyqsvcepgaaapk 893

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Query Match	98.68;	Score 5367;	DB 16;	Length 1103;
Best Local Similarity	97.48;	Pred. No. 0;		
Matches 1028;	Conservative	0;	Mismatches	1;
				Indels 26;
				Gaps 2;
QY	1	MAACLLATLTTLQSLIGPSSEPPFPAYTIKSWDKMEDLVTLAKTAGVNLVDI	60	
Db	1	maagcilaaltlilqslilgspseepfipavtikawdkmedlvtlaktagvnlvdi	60	
QY	61	YKYOQDLYTVPNNARQVETAAARDIEKLLNRSKALYSALAEKVAQAHHQWREDFASN	120	
Db	61	yekyqdlytvepnnaqlveetaardiekllnsrskalsalsaleakvqaahqwrdfasn	120	
QY	121	EYVYNNAKDDLPKNDSEPGSQRIPKPIEDANFGRQISYQHAHVHPTDIYESTIVL	180	
Db	121	evvynnakddlpeknndsepgsqrirkpvfiedanfgqisyqhaavhptdiyegstivl	180	
QY	181	NELNWTSAIDDEVFKKNREDDPSLLQVFGSATGLARYYPASPVWDSRPNKIDLYDVR	240	
Db	181	nelnwtalsaiddevfkknreedpsllqvfgsatglaryypaspvwdsrpnkidlvdvrr	240	
QY	241	RPWYIQAASPKDMLILVDVSGVSGITLKIITSVSEMLETSLDDDFVNVASFNSNAQD	300	
Db	241	rpwyiqgaaspkdmlilvdvsgvsgitlkiirtsvsemlletlssdddfvnvasfnasnaq	300	
QY	301	VSCFQHLVQANVRNKKVLDVNNITAKGTDYKKGFSFAFEQLLNYNVSRANCNKIIML	360	
Db	301	vscfqlhvlqanvrnkklvldvnnitakgtdykgkfsfafeqllnynvsrancnkliiml	360	
QY	361	FTDGEERAQEIFPNKYNKDKRVFRFVSGOHNTERGPIQMACENKGYEYIEPSIGAIR	420	
Db	361	ftdgeeraqeifpnkynkdkrvfrfsvgohntergpigmacenkgyyeypsigaair	420	
QY	421	INTQEYLDVLGRPMVLADGKAKQVOWTNVYLDALGLVITGTLFPVNITQGFENKTLK	480	
Db	421	intqeyldvlgrpmvlagdkakqvowtnvyldaleglvitgtlfpvnitqgfenktnlk	480	
QY	481	NOLILGVMGVDSLEDIKRLTPFTLCPNGYFAIDPNGYVLLHNLHPNLPK	530	
Db	481	nqllilgvmgvdsledikrltpftlcpngyfaidpngyvlhpnlpkpiqvlgptin	540	
QY	531	-----NPKSQEPVTLDFDAELNDIKVEIRNKMIDGESGEKFTFLVKSQDERYI	581	
Db	541	lrrkrrpnigpnksqepvltldfaelndikveirnkmidgesgektfltlvksqderyl	600	
QY	582	DKGNRTYTWTPVNGTDYSIALVLPTYSFYIRAKLEETITQARSKKGMKDSSETLKP	641	
Db	601	dkgnrtwtvngtdysialvlpysfyirakleetitqarskkgmksdsetlkdndf	653	
QY	642	EESGYTFIAPRDYCNLDKISDNTEFLNFEIDRKTNNPCNADLINRVLLDAGFTN	701	
Db	654	eesgytfiaprdycndlkisdnteflnfneidrktnpncnadlinrvlldagftn	713	
QY	702	ELVQNTVWSKOKNIKGKARFVVTDDGTRVYKPEAGENWQENPETVEDSFYKSLDNDNY	761	
Db	714	elvqnvwsknknlkgvkarfvtdggtrvypkeagenwqenpetvedsfykrslndny	773	
QY	762	VFTAPYFNKSGPGAYESGIMVSKAVEIYIQGLKLKPAVVGKIDVNSWIENFTKTSIRDP	821	
Db	774	vftapyfnkspggayesgimvskaveiyigglklkpvvggikidvnswiensienftksirdp	833	
QY	822	CAGPVCDCKRNSDVMDCVILDDGGFLMANHDDYTQIGRFFGEIDPSLMHRLHVNISYA	881	
Db	834	cagpvcdckrnsdvmcdvildggfllmanhddytqigrffgeidpslmhrlhvnisyva	893	
QY	882	FNKSYDYQSVCEPGAAPKOGAGHRSAYVPSVADIQIGWATATAAASWILQOFLSLTFFR	941	
Db	894	fnksydyqsvcepgaapkgagghrsayvpsvadilqigwataataaawilqofllstfpr	953	
QY	942	LLEAVEMEDDDFTASLSKQSCITEQTYEFDNDKSFSGVLDGNCGRIFHGEKLMNTNL	1001	
Db	954	lleavemedddftaslskscitedqtyefdndksfsgvldgncsrifhgeklmntnl	1013	
QY	1002	IFIMVESKGTCPDCTELLIIQAQETSDGPNPCDMVK	1036	

QY	901	GAGHRSAYVPSVADILQIGWATATAAASWILQOFLSLTFFRLLLEAVEMEDDDFTASLSKQ	960	
Db	894	gaghrsavpsvadilqigwataataaawilqofllstfprllleavemedddftaslskq	953	
QY	961	SCITEQTYEFDNDKSFSGVLDGNCGRIFHGEKLMNTNLIFIMVESKGTCPDCTRLII	1020	
Db	954	sciteqtyefdndksfsgvldgncsrifhgeklmntnlifimveskgtpcdctrilli	1013	
QY	1021	QAEQTSQDGNPCDMVK	1036	
Db	1014	qaeqtsdgnpcdmvk	1029	
RESULT 13				
AAR71012				
ID	AAR71012 standard; Protein; 1103 AA.			
AC	AAR71012;			
DT	01-DEC-1995 (first entry)			
DE	Human neuronal calcium channel subunit alpha 2a.			
XX	Calcium channel subunit; antagonist; agonist; diagnosis;			
KW	Lambert Eaton Syndrome.			
OS	Homo sapiens.			
PN	W09504822-A.			
PD	16-FEB-1995.			
PF	11-AUG-1994; 94WO-US09230.			
PR	11-AUG-1993; 93US-0105536.			
PR	05-NOV-1993; 93US-0149097.			
PA	(SALK) SALK INST BIOTECHNOLOGY IND ASSOC.			
PI	Ellis SB, Gillespie A, Harpold MM, McCue AF, Williams ME;			
DR	WPI; 1995-090900/12.			
DR	N-PSDB; AAQ84666.			
PT	DNA encoding human calcium channel sub-unit(s) - used for			
PT	developing prods. for studying calcium channels, e.g. for			
PT	obtaining agonists and antagonists			
PS	Disclosure; Page 231-236; 285pp; English.			
CC	Human neuronal alpha 2 coding sequence (AAQ84664) transcript is			
CC	differentially processed in skeletal muscle, aorta, and CNS in			
CC	the region corresp. to nt 1595-1942 of AAQ84664 in each of the			
CC	tissues. Five alternatively spliced variant transcripts that differ			
CC	in the presence or absence of one to three different portions of			
CC	this region. There are three sequences involved (see AAQ84664 FT			
CC	and AAQ84665 FT), sequence 1, sequence 2, and sequence 3. The five			
CC	alpha 2 encoding transcripts from the different tissues include			
CC	the alpha 2 transcripts expressed in aorta which lacks all three			
CC	sequences. The five alpha 2 forms identified are (1) a form that			
CC	lacks sequence 3 called alpha 2a, expressed in skeletal muscle			
CC	(2) one that lacks sequences 1 and 2 called alpha 2b, expressed in			
CC	aorta (4) one that lacks sequences 1, 2 and 3 called alpha 2d,			
CC	expressed in aorta and (5) one that lacks sequences 1 and 3			
CC	called alpha 2e. The DNA and AA sequences of alpha 2a - alpha 2e			
CC	are set forth in AAQ84666-Q84669 and AAR71012-R71015 respectively.			
XX	Sequence 1103 AA;			
SQ				

Db 1014 ifimveskgtcpcdrllliqaeqtsdgnpcdmvk 1048
|||||

RESULT 14
AAW63151
ID AAW63151 standard; Protein; 1103 AA.

XX AC AAW63151;
XX DT 12-OCT-1998 (first entry)
XX Human calcium channel alpha-2a subunit.
XX DE Alpha-2 subunit; human; calcium channel; assay; detection;
XX KW characterisation; Lambert Eaton Syndrome; LES; diagnosis.
XX OS Homo sapiens.

XX FN US5792846-A.
XX PD 11-AUG-1998.
XX PF 31-MAY-1995; 95US-0455543.
XX PR 04-APR-1994; 94US-0223305.
XX PR 04-APR-1988; 88US-0176899.
XX PR 04-APR-1989; 89US-0603751.
XX PR 04-APR-1989; 89WO-US01408.
XX PR 20-FEB-1990; 90US-0482384.
XX PR 30-NOV-1990; 90US-0620250.
XX PR 15-AUG-1991; 91US-0745206.
XX PR 31-MAY-1995; 95US-0455543.

XX PA (SIBI-) SIBIA NEUROSCIENCES INC.
XX PI Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;
XX PI Williams ME;
XX WPI; 1998-456192/39.
XX N-PSDB; AAW42700.
XX DNA encoding human calcium channel alpha 1B subunit protein -
XX useful for recombinant production of the channel for screening of
XX its modulators, and diagnosis of Lambert Eaton Syndrome
XX Claim 3; Columns 287-294; 166pp; English.

XX The present sequence represents the alpha-2a subunit of a human calcium
XX channel. Calcium channels are membrane-spanning, multi-subunit proteins
XX that allow controlled entry of calcium ions into cells. This leads
XX to depolarisation events required for muscle contraction. The recombinant
XX subunit, when expressed with nucleic acids encoding the complete calcium
XX channel, can be used in assays for the detection and characterisation of
XX compounds that modulate the channel. The DNA encoding the subunits can
XX be alternatively spliced when transcribed, giving more than one form of
XX the protein from the same transcript, each having slightly different
XX properties. In addition, the reactivity of the alpha 1 subunit with IgG
XX molecules from the serum of an individual with Lambert Eaton Syndrome
XX (LES) can be used as a diagnostic for the disease.

XX Sequence 1103 AA;

Query Match 98.6%; Score 5367; DB 19; Length 1103;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 1028; Conservative 0; Mismatches 1; Indels 26; Gaps 2;

QY 1 MAAGCLLATLTTLFQSLTGPSSEEPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
Db |||||||
1 maagcllatltlfgallgppssepfpsavtikswdkmqedlvtlaktasgvnqlvdi 60
QY 61 YEKYQDLYTVEPNARQLVEIARDEIKLLSNRSKALVSLAEAEKVQAQHWREDFASN 120

Db 61 yekyqdytvepnarqlveiaardieklisnrskalvslaeaeqvaaahqwrdfasn 120
QY 121 EVYYNAKDDLDPEKNDSEPGSRIKPVFTEDANFGQISVQHAHVHPTDIIYEGSGIVL 180
Db |||||||
121 evyyanakddldpekndsepgsrikpvftedanfgqisyqhaavhlpdciyegstivl 180
QY 181 NELNWTSAALDEVFKKREEDPSLLMQVFGSATGLARYYPASPWWDSRTPNKIDLYDVR 240
Db |||||||
181 nelnwtasaldevfkknreedpsllmqvfgsatglaryypaspwwdsrtpnkdldyvr 240
QY 241 RPWYIOGAASPDKMLILVDYSGVSGTLKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300
Db |||||||
241 rpyiigaaaspdkmliilvdysgvgstlklirtsvsemletsldddfvvnasfnasqd 300
QY 301 VSCFOHLVQANVRNKKVLDVANNITAKGTDYKKGFSFAFEOILLNYSRANCNKIIML 360
Db |||||||
301 vscfqlhvanvrnkkvldavnnitakgtdykkgsfafefoillnysrancnkliiml 360
QY 361 FTDGGEERAQEIFNKYNKDKKRVFRFSVGOHNYERPIQWACENKGYEYIEIPSGAIR 420
Db |||||||
361 ftdggeeraqeifnknkdkkrrvfrfsvgohnyerpiqwmacenkgyyeipsigair 420
QY 421 INTQEYLDVLGRPMVLAKGAKQVQNTNMYLDALGLVITGTLPVFNITGQFENKTNLK 480
Db |||||||
421 intqeyldvlgrpmvlagkakqvqntnmyldaleglvitgtlvpfnitgqfentknlk 480
QY 481 NQILGVMGVDSLEIDIKRLTPFTLCPNGYYPADPNGVYLLHPNLQPK----- 530
Db |||||||
481 nqilgvmgvdsleidikrltpftlcpngyypadpnpvylhpnlpk----- 530
QY 531 -----NPKSOEPVTLDFDAELENDIKVEIRNMKIDGESGEKTFRLVKSQDERYI 581
Db |||||||
531 lkrtrpniqnpskqepvtldfdaelendikveirnmkidgesgektfrtlvksqderi 600
QY 582 DKGNRRTYTWTPVNGTDYSLALVPTYFYIYKAKLEETITQARSKGKMKDSETLKPDNF 641
Db |||||||
601 dkgnrtytwtpvngtdyslalvptyfyiykakleetitqary-----setlkpndf 653
QY 642 EESGYTFIAPROYCNDLKISDNNTEFLNFEFIDRKTNNPSCNADLINRVLLDAGFTN 701
Db |||||||
654 eesgytfiaproycndlkisdnnfeflnfnefidrktnpnpscnadlinrvlldagftn 713
QY 702 ELVQNTWSQKNIKGVKARFVWTDGGITRVYPKEAGENQENPETVEDSFYKRSLDNDY 761
Db |||||||
714 elvqnywsqkniqgvkarfvvtdggitrvykpeagenqenpetyedsfykrsldndy 773
QY 762 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRD 821
Db |||||||
774 vftapyfnksgpgayesgimvskaveiyioqkllkpavvgikidvnswiensfctksirdp 833
QY 822 CAGPYCDCKRNSDVMDCVTLDDGGFLMANHDDYTNQIGRFGFGEIDPSLMRHLVNI SVYA 881
Db |||||||
834 cagpycdckrnsdvmcdvtilddggflmanhddytnqigrffgeidpslmrhlvnisvya 893
QY 882 FNKSYDYQVSCVCPGAAPKOGAGHRSAYVPSVADILQIGWATAAAWSILQOFLSLTFFR 941
Db |||||||
894 fnksydyqsvcpaggaapkgaghsayvpsvadilqigwataaawslilqffllstftr 953
QY 942 LLEAVEMEDDDFTASLSKQSCITEQTQYFFDNDKSFSGVLDCGNCGRIFHGKLMNTNL 1001
Db |||||||
954 lleavemedddftaslskqsciteqtqyffndnskfsfgvldcgncsrifhgkclmntnl 1013
QY 1002 IFIMVESKGTCPCDTLLIQAQTSDDGNPCDMVK 1036
Db |||||||
1014 ifimveskgtcpcdrllliqaeqtsdgnpcdmvk 1048

RESULT 15
AAB10586
ID AAB10586 standard; Protein; 1103 AA.
XX
AC AAB10586;

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XX 22-DEC-2000 (first entry)
 XX Human calcium channel alpha-2a subunit protein.
 DE Human; calcium channel; calcium channel subunit; diagnosis;
 KW Human; calcium channel; calcium channel subunit alpha-2a.
 KW Lambert Eaton Syndrome; calcium channel subunit alpha-2a.
 XX Homo sapiens.
 OS US6096514-A.
 PN 01-AUG-2000.
 PD 01-AUG-2000.
 XX 25-MAY-1995; 95US-0450562.
 XX 04-APR-1988; 88US-0176899.
 PR 02-FEB-1990; 90US-0482384.
 PR 08-NOV-1990; 90US-0603751.
 PR 30-NOV-1990; 90US-0620250.
 PR 15-AUG-1991; 91US-0745206.
 PR 10-APR-1992; 92US-0868354.
 PR 13-JUL-1992; 92US-0914231.
 PR 11-AUG-1993; 93US-0105536.
 PR 05-NOV-1993; 93US-0149097.
 PR 07-FEB-1994; 94US-0193078.
 PR 04-APR-1994; 94US-0223305.
 PR 11-AUG-1994; 94US-0290012.
 PR 23-SEP-1994; 94US-0311363.
 PR 28-SEP-1994; 94US-0314083.
 PR 07-NOV-1994; 94US-0336257.
 PR 13-MAR-1995; 95US-0404950.
 XX (SIBI-) SIBIA NEUROSCIENCES INC.
 XX Ellis SB, Williams ME, McCue AF, Harpold MM;
 PI WPI; 2000-548230/50.
 DR N-PSDB; AAA71724.
 XX Human calcium channel beta subunit polynucleotides, useful for
 PT producing recombinant eukaryotic cells and for diagnosing Lambert Eaton
 PT Syndrome -
 XX Disclosure; Column 229-236; 153pp; English.
 XX This invention describes a novel isolated DNA molecule (1) comprising a
 CC sequence encoding a beta3-1 subunit of a human calcium channel.
 CC Nucleic acid probes comprising 14-30 contiguous nucleotides of
 CC beta_3 subunit encoding DNA are useful for isolation and cloning of
 CC calcium channel subunit-encoding DNA. Recombinant eukaryotic cells that
 CC express heterologous calcium channel activity and in assays for identifying
 CC that modulate calcium channel activity and in assays for identifying
 CC agonists and antagonists of calcium channel activity in humans. Human
 CC calcium channel subunit or eukaryotic cells expressing the channel are
 CC useful for diagnosing Lambert Eaton Syndrome (LES) in a human. This
 CC sequence represents the human calcium channel alpha-2a subunit which is
 CC described in the method of the invention.
 XX Sequence 1103 AA;
 SQ
 Query Match 98.6%; Score 5367; DB 21; Length 1103;
 Best Local Similarity 97.4%; Pred. No. 0;
 Matches 1028; Conservative 0; Mismatches 1; Indels 26; Gaps 2;
 QY 1 MAACLLALITLITLQSLIGSSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
 DB 1 maagcllaltlilqslilgsssepppsavtikswdkmqedlvtlaktasgvnqlvdi 60
 QY 61 YEKYQDLYTVEPNNAQQLVEIAARDIEKLLNSRKALVSLAEKVAQAAHQWREDFASN 120
 DB 61 yekyqdlytvepnnarqlveiaardiekllnsrkalslaleakvqaahqwrdfasn 120

QY 121 EVVYNAKDDLDPEKNDSEPGSQRKIPVIEDANFGRROISYOHAAVHIPTDIYEGSTIVL 180
 DB 121 evvynakddldpekndsepgsqrikpviedanfgrqisyaavhahptdiyegstivl 180
 QY 181 NELNWTSAIDVFKKNREEDPSLLAQVTSATGLARYYPASVPWDSNRTPNKIDYDVR 240
 DB 181 nelnwtalsaidvfkknreedpsllqvwfsgatglaryypasvpwdsnrtpnkidydvrr 240
 QY 241 RPWYIQAASPKDMLILVDVSGSVSLTILKLRISVSEMLETSSDDDFVNVASFNSNAOD 300
 DB 241 rpwyiqgaaspkdmlilvdvsgsvsltklirtssemletssdddfvnnvasfnasnaod 300
 QY 301 VSCFOHLVQANVRNKKVLDKAVNNITAKITDYKKGFSFAFOLLNYSRANCNKIIML 360
 DB 301 vscfqlhvcqanvrnkkvldkavnnitakitdykkkfsfafellnynsrancnkiml 360
 QY 361 FTDGGEERAQEIFNKYNKDKKVRFRFSVGOHNYERGPQWMACENKGYIYEPSIGAIR 420
 DB 361 ftdggeeraqeifnknkdkkvrfrfsvgoqhnyergpqlqwmacenkgyyieipsigair 420
 QY 421 INTQEVLDVLGRPMVLAKAKOVQWNTNVLDALEGLVITGHLVPVNTGQFENKTNLK 480
 DB 421 intqeyldvlgrpmvlakakovqwtvnyldalelglvitgltplvntgqfenktnlk 480
 QY 481 NQILGVMGVDSLEDTIKRLTPRTLCPNGYIFAIDPNGYVLLHPNLQPK 530
 DB 481 nqilgvmgvdsledtikrltprtlcpngyifaidpnyvllhpnlpkpgvgiptin 540
 QY 531 -----NPKSQEPTVLDLAELENDIKVEIRNMIDGESKEKFTLVKQSDERYI 581
 DB 531 lrkxrpnlqnpksqepvtldflaelelendikveirnmidgeskektftlvksqderiy 600
 QY 582 DKGRTYTWTPVNGTDYSLALVLPYSFYIYKAKLEETITQARSKKGMKSEILKPNDF 641
 DB 582 dkgtrtytwtpvngtdyslalvlpysfyyikakleetitqary-----setikpndf 653
 QY 601 EESGYTFIAPDYCNLDKISDNTEFLNFEFIDRKTPNPNPCNADLINRVLLDAGFTN 701
 DB 601 eesgytfiapdycndlkisdnteflnfnefidrktppnpscnadlinrvlldagftn 713
 QY 642 ELVQYWSKQNIKGKARFVVDGIGTRVYKPEAGENWQENPETEYEDSFYKRSLDNDY 761
 DB 642 elvqywsqknikgkarfvvtdgigtrvykpeagenwqenpeteyedsfyrslndndy 773
 QY 702 VTTAPYFNKSGPGAYESGIMVSKAVEIYIQGLKLPVAVVGIKIDVNSWIENFTKTSIRDP 821
 DB 702 vttapyfnkspgayesgimvskaveiyiqgklkpavvgikidvnswieftktsirdp 833
 QY 822 CAGPVCDCRNSDVMDCVITLDDGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNSVYA 881
 DB 822 cagpvcdcrrnsdvmcvtlddgflmlanhddytngqgrffgeidpslmrhlvnsvya 893
 QY 882 FNKSYDQSVCEPGAAPKQAGHRSAYSVADILQIGWATAAASILQOQLLSLTFPR 941
 DB 882 fnksydyqsvcepgaapkgaghrrsayvsvadilqlgwwataaasilqqlfllstfpr 953
 QY 894 FNKSYDQSVCEPGAAPKQAGHRSAYSVADILQIGWATAAASILQOQLLSLTFPR 953
 DB 894 fnksydyqsvcepgaapkgaghrrsayvsvadilqlgwwataaasilqqlfllstfpr 1001
 QY 942 LLEAVEMEDDDFTASLSKQSCITEQTYQYFPDNDKSFSGVLDGNCNSRIFPHGKLMNTNL 1001
 DB 942 lleavemedddftaslskqsciteqtyqyfpdndksfsgvldcncnsrifphgklmntnl 1013
 QY 1002 IFIMVESKGTCPDCTRLILQAEQTSFGPNPCDMVK 1036
 DB 1014 ifimveskgtcpdctrilliqaeqtsfgpncdmvk 1048

Search completed: July 23, 2001, 07:36:44
 Job time: 485 sec

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OM protein - protein search, using sw model

Run on: July 23, 2001, 07:38:46 ; Search time 37.55 Seconds
(without alignments)
555.788 Million cell updates/sec

Title: US-09-397-548-16
Perfect score: 5443
Sequence: 1 MAAGCLLALTFLFQSLIG.....RLLIQAQTSNGPNCMDWK 1036

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgnl_7/ptodata/1/iaa/5A-COMB.pap.*
2: /cgnl_7/ptodata/1/iaa/5B-COMB.pap.*
3: /cgnl_7/ptodata/1/iaa/6A-COMB.pap.*
4: /cgnl_7/ptodata/1/iaa/6B-COMB.pap.*
5: /cgnl_7/ptodata/1/iaa/PCTUS-COMB.pap.*
6: /cgnl_7/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5443	100.0	1091	1	US-07-745-206A-25
2	5443	100.0	1091	1	US-08-455-543A-52
3	5443	100.0	1091	2	US-08-223-305C-52
4	5443	100.0	1091	2	US-08-311-363-25
5	5439	99.9	1091	3	US-08-713-118-4
6	5439	99.9	1091	4	US-09-452-007-4
7	5403.5	99.3	1086	1	US-08-455-543A-54
8	5403.5	99.3	1086	2	US-08-223-305C-54
9	5386.5	99.0	1084	1	US-08-455-543A-56
10	5386.5	99.0	1084	2	US-08-223-305C-56
11	5367	98.6	1103	1	US-08-455-543A-53
12	5367	98.6	1103	2	US-08-223-305C-53
13	5347	98.2	1079	1	US-08-455-543A-55
14	5347	98.2	1079	2	US-08-223-305C-55
15	5229.5	96.1	1106	1	US-08-435-675B-5
16	5211.5	95.7	1106	1	US-08-336-257A-8
17	4978.5	91.5	1086	6	5386025-8
18	2581.5	47.4	508	1	US-08-435-675B-6
19	182	3.3	885	3	US-09-074-579-5
20	182	3.3	885	4	US-09-388-774-5
21	159.5	2.9	946	3	US-09-074-579-3
22	159.5	2.9	946	4	US-09-388-774-3
23	154	2.8	903	1	US-08-021-601-12
24	154	2.8	903	1	US-08-082-849B-12
25	154	2.8	903	5	PCT-US94-01624-12
26	152.5	2.8	789	1	US-08-471-033-32
27	152.5	2.8	789	2	US-08-471-044-32

28	152.5	2.8	789	2	US-08-463-483A-32	Sequence 32, Appl
29	152.5	2.8	789	2	US-08-471-046A-32	Sequence 32, Appl
30	152.5	2.8	789	2	US-08-470-566B-32	Sequence 32, Appl
31	152.5	2.8	789	2	US-08-838-219B-4	Sequence 4, Appl
32	152.5	2.8	789	3	US-08-469-334-32	Sequence 32, Appl
33	152.5	2.8	789	3	US-09-300-529-32	Sequence 32, Appl
34	152.5	2.8	789	3	US-09-233-336A-4	Sequence 4, Appl
35	152.5	2.8	789	4	US-09-233-732A-4	Sequence 4, Appl
36	150.5	2.8	789	4	US-08-960-780-6	Sequence 6, Appl
37	150.5	2.8	789	4	US-09-073-898-6	Sequence 6, Appl
38	148.5	2.7	790	4	US-08-960-780-4	Sequence 4, Appl
39	148.5	2.7	790	4	US-09-073-898-4	Sequence 4, Appl
40	147.5	2.7	746	2	US-08-838-219B-6	Sequence 6, Appl
41	147.5	2.7	746	3	US-09-233-336A-6	Sequence 6, Appl
42	147.5	2.7	746	4	US-09-233-732A-6	Sequence 6, Appl
43	145.5	2.7	790	4	US-08-960-780-8	Sequence 8, Appl
44	145.5	2.7	790	4	US-09-073-898-8	Sequence 8, Appl
45	141.5	2.6	789	1	US-08-471-033-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-07-745-206A-25
; Sequence 25, Application US/07745206A
; Patent No. 5429921
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: McCue, Ann
; APPLICANT: Feldman, Daniel
; TITLE OF INVENTION: Human Calcium Channel Compositions and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fitch, Even, Tabin & Flannery
; STREET: 135 S. LaSalle
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 19910815
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Feder, Scott B
; REFERENCE/DOCKET NUMBER: 51504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-372-7842
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1091 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-745-206A-25

Query Match 100.0%; Score 5443; DB 1; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAGCLLALTFLFQSLIGPSSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
DB 1 MAAGCLLALTFLFQSLIGPSSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

QY 61 YEKYODLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDEPASN 120
DB 61 YEKYODLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDEPASN 120
QY 121 EVVYNAKDDLDPEKNDSEPGSORIKPVFTEDANFRQISQYQAAVHIPTDIIYEGSTIVL 180
DB 121 EVVYNAKDDLDPEKNDSEPGSORIKPVFTEDANFRQISQYQAAVHIPTDIIYEGSTIVL 180
QY 181 NELNWTSALEDEKFKKNEEDPSLLWQVFSATGLARYYPASPWVNSRTPNPKIDLYDVR 240
DB 181 NELNWTSALEDEKFKKNEEDPSLLWQVFSATGLARYYPASPWVNSRTPNPKIDLYDVR 240
QY 241 RPWYIOGAASPKDMLILDVSGVSLTLKLTISVSEMLETLSDDDFYNVAFSNAQD 300
DB 241 RPWYIOGAASPKDMLILDVSGVSLTLKLTISVSEMLETLSDDDFYNVAFSNAQD 300
QY 301 VSCFOHLVQANVRNKKVLKDVANNITAKGIDYKKGFSEFAFQQLNLYNVRANCKNIIML 360
DB 301 VSCFOHLVQANVRNKKVLKDVANNITAKGIDYKKGFSEFAFQQLNLYNVRANCKNIIML 360
QY 361 FTDGGEERAQELFNKYNKDKVVRFSVGOHNYERGPIQWACENKGYIYIPISGAIR 420
DB 361 FTDGGEERAQELFNKYNKDKVVRFSVGOHNYERGPIQWACENKGYIYIPISGAIR 420
QY 421 INTQYLDVLGRPMVLGDKAKQVQWNTVYLDALBLGLVITGLTFVFNITGOFENKTNLK 480
DB 421 INTQYLDVLGRPMVLGDKAKQVQWNTVYLDALBLGLVITGLTFVFNITGOFENKTNLK 480
QY 481 NOLLILGVMGVDVSLIEDIKRLTPRTCLPNGYFFAIDPNGYVLLHPNLPKPKSOEPTVL 540
DB 481 NOLLILGVMGVDVSLIEDIKRLTPRTCLPNGYFFAIDPNGYVLLHPNLPKPKSOEPTVL 540
QY 541 DFLDAELNDIKVEIRNKMIDGSEKTFRLVKSQDERYIDKGNRYTWTVPVNGTDYSL 600
DB 541 DFLDAELNDIKVEIRNKMIDGSEKTFRLVKSQDERYIDKGNRYTWTVPVNGTDYSL 600
QY 601 ALVLPYTSFYIYIAKLEETITQARSKKGMKDSKSETLAPDNFEESGYTFIAPRDYCNDLKI 660
DB 601 ALVLPYTSFYIYIAKLEETITQARSKKGMKDSKSETLAPDNFEESGYTFIAPRDYCNDLKI 660
QY 661 SDNTEFLNFEIDRKTNNPSCNADLNVRLLDAGFTNELYVNSKQKNIKGVYKAR 720
DB 661 SDNTEFLNFEIDRKTNNPSCNADLNVRLLDAGFTNELYVNSKQKNIKGVYKAR 720
QY 721 FVYTDGGITRYPKEAGENQWENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
DB 721 FVYTDGGITRYPKEAGENQWENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
QY 781 MVSKEVEIYIOGKLLPAPVVGIKIDVNSWIENFTKTSIRDPCAGPVCDCRNSDVMDCVI 840
DB 781 MVSKEVEIYIOGKLLPAPVVGIKIDVNSWIENFTKTSIRDPCAGPVCDCRNSDVMDCVI 840
QY 841 LDDGFLMANHDDYTNOIGRFGEDTDPMLRHLNYSVAFNKSVDYQSVCEPAGPAKQ 900
DB 841 LDDGFLMANHDDYTNOIGRFGEDTDPMLRHLNYSVAFNKSVDYQSVCEPAGPAKQ 900
QY 901 GAGHSAYVPSVADILQIGWATAAWSILQOFLSLTPRLLAEVEMEDDDFTASLSQ 960
DB 901 GAGHSAYVPSVADILQIGWATAAWSILQOFLSLTPRLLAEVEMEDDDFTASLSQ 960
QY 961 SCITEQYFFNDNKSFGSVLDCGNCSEIFHGEKLMNTNLIFIMVESKGTCTPCTRLLI 1020
DB 961 SCITEQYFFNDNKSFGSVLDCGNCSEIFHGEKLMNTNLIFIMVESKGTCTPCTRLLI 1020
QY 1021 QAEQTSQDGNPCDMVK 1036
DB 1021 QAEQTSQDGNPCDMVK 1036

RESULT 2

US-08-455-543A-52

; Sequence 52, Application US/08455543A

; Patent No. 5792846
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,543A
; FILING DATE: May 31, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/223,305
; FILING DATE: April 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,250
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-52517
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1091 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-455-543A-52

Query Match

Best Local Similarity 100.0%; Score 5443; DB 1; Length 1091;

Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 MAAGCLLALTITLTFQSLILGPSSEPFPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

Db 1 MAAGCLLALTTLFQSLIGSPSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNQLYDI 60
Qy 61 YEKYODLYTPNNARQULVEIAARDIEKLLNSRKALYSLEAEKVKQAAHQRDEDFASN 120
Db 61 YEKYODLYTPNNARQULVEIAARDIEKLLNSRKALYSLEAEKVKQAAHQRDEDFASN 120
Qy 121 EWWYNKADDDLPKNDSEPSQRKPFIEDANFGROISVQHAHVHPTDIYEGSTIVL 180
Db 121 EWWYNKADDDLPKNDSEPSQRKPFIEDANFGROISVQHAHVHPTDIYEGSTIVL 180
Qy 181 NELNWTALDEVFKNREDESLWQVGSATGLARYYPASPVWDSRTPNKIDLYDVR 240
Db 181 NELNWTALDEVFKNREDESLWQVGSATGLARYYPASPVWDSRTPNKIDLYDVR 240
Qy 241 RPWYIQAASPKMDLILVDVSGSVGLTKLIRTSVSEMLETSLDDDFVNVASFNSAQD 300
Db 241 RPWYIQAASPKMDLILVDVSGSVGLTKLIRTSVSEMLETSLDDDFVNVASFNSAQD 300
Qy 301 VSCFOHLVQANRNKVKLKDANNITAKGIDYKKGFSFAFEQLLNYSRANCNKIIML 360
Db 301 VSCFOHLVQANRNKVKLKDANNITAKGIDYKKGFSFAFEQLLNYSRANCNKIIML 360
Qy 361 FTDGGEERAQEIFKNYKDKKVRVFRFVSGOHNYERGPQIOWMACENKGYEYIPEISGAIR 420
Db 361 FTDGGEERAQEIFKNYKDKKVRVFRFVSGOHNYERGPQIOWMACENKGYEYIPEISGAIR 420
Qy 421 INTOBYDLVLRPMYLAGDAKQVQWTVNYLDALGLVITGTLPVFNITGOFENKTNLK 480
Db 421 INTOBYDLVLRPMYLAGDAKQVQWTVNYLDALGLVITGTLPVFNITGOFENKTNLK 480
Qy 481 NOLILGVNGVDSLEIDIKRLPRTLCNGYFFAIDPNGYVLLHPNLPKPKSOEPTVL 540
Db 481 NOLILGVNGVDSLEIDIKRLPRTLCNGYFFAIDPNGYVLLHPNLPKPKSOEPTVL 540
Qy 541 DFLDALELNDIKVEIRNKMIDGSEKFTLVKSQDERYIDKGNRTYTWTPVNGTDSL 600
Db 541 DFLDALELNDIKVEIRNKMIDGSEKFTLVKSQDERYIDKGNRTYTWTPVNGTDSL 600
Qy 601 ALVPTYFYIYKAKLETITQAKSKKMKDSETPKPDNFEESGYTFIAPRDYCNLDKI 660
Db 601 ALVPTYFYIYKAKLETITQAKSKKMKDSETPKPDNFEESGYTFIAPRDYCNLDKI 660
Qy 661 SDNTEFLLNNEFTDRKTPNPNPCNADLINRVLLDAGFTNELVQNYWSKQKNIKGVKAR 720
Db 661 SDNTEFLLNNEFTDRKTPNPNPCNADLINRVLLDAGFTNELVQNYWSKQKNIKGVKAR 720
Qy 721 FVVTDDGITRVYKPEAGENWQENPTYEDSYKRSLDNDNVYFTAPYFNKSGPGAYESGI 780
Db 721 FVVTDDGITRVYKPEAGENWQENPTYEDSYKRSLDNDNVYFTAPYFNKSGPGAYESGI 780
Qy 781 MYSKAVEIYIOGKLLKPAVGIKIDVNSWENFTKTSIRDPKAGVCDCKRNSDVMDCVI 840
Db 781 MYSKAVEIYIOGKLLKPAVGIKIDVNSWENFTKTSIRDPKAGVCDCKRNSDVMDCVI 840
Qy 841 LDDGGFLLMANHDDYTNIGIRFFGEIDPSLRHLNIVSVYAFNKSQYDQVCEPAAAPKQ 900
Db 841 LDDGGFLLMANHDDYTNIGIRFFGEIDPSLRHLNIVSVYAFNKSQYDQVCEPAAAPKQ 900
Qy 901 GAGHRSAYVPSVADLIQGWATAAWSILOQFLLSLFPRLLEAVEMEDDDFTASLSQK 960
Db 901 GAGHRSAYVPSVADLIQGWATAAWSILOQFLLSLFPRLLEAVEMEDDDFTASLSQK 960
Qy 961 SCITEQTOYFFDNDKSPSGVLDGNCNCSIFHGEKLMNTNLIIFIMVESKGCPCDTRLLI 1020
Db 961 SCITEQTOYFFDNDKSPSGVLDGNCNCSIFHGEKLMNTNLIIFIMVESKGCPCDTRLLI 1020
Qy 1021 QAEQTSQDGNPCDMVK 1036
Db 1021 QAEQTSQDGNPCDMVK 1036

RESULT 3

US-08-223-305C-52
; Sequence 52, Application US/08223305C
; Patent No. 5851824
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/223.305C
; FILING DATE: April 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,250
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 52516 (P519739)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1091 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-223-305C-52

Query Match 100.0%; Score 5443; DB 2; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAAGCLLALTTLFQSLIGSPSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNQLYDI 60
|||||

Db 1 MAAGCLLALTTLTFLFOSLLIGPSSSEPPFSAVTIKSWVDKMQEDLVTLAKTAGVNLVDI 60
QY 61 YEKYQDLYTVEPNNAQRLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120
Db 61 YEKYQDLYTVEPNNAQRLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120
QY 121 EVVYNNAKDLDPEKNDSEPPGSRKIPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180
Db 121 EVVYNNAKDLDPEKNDSEPPGSRKIPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180
QY 181 NELNWTSSALDEVFKKNEEDPSLLWQVFGSATGLARYYPASPDVNSRTPNKIDLYDVR 240
Db 181 NELNWTSSALDEVFKKNEEDPSLLWQVFGSATGLARYYPASPDVNSRTPNKIDLYDVR 240
QY 241 RPWYIOGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETLSDDDDFVNVASFNNAQD 300
Db 241 RPWYIOGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETLSDDDDFVNVASFNNAQD 300
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGTDYKKGFSFAFEQLLNINVSANCNKIIML 360
Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGTDYKKGFSFAFEQLLNINVSANCNKIIML 360
QY 361 FTDCGERAQBIFNKNKDKVRVRESVQGHNYERGIOWMACENKGYIYEIPSGAIR 420
Db 361 FTDCGERAQBIFNKNKDKVRVRESVQGHNYERGIOWMACENKGYIYEIPSGAIR 420
QY 421 INTQEXLDVLRPMVLAGDKAKQVQWNTVYLDALGLVITGTLPVFNITGQFENKTLK 480
Db 421 INTQEXLDVLRPMVLAGDKAKQVQWNTVYLDALGLVITGTLPVFNITGQFENKTLK 480
QY 481 NQILGVMGVDSLEDKRTPFTLCPNGYYPFAIDPBGVLLHPNLPKNPKSQBPVTL 540
Db 481 NQILGVMGVDSLEDKRTPFTLCPNGYYPFAIDPBGVLLHPNLPKNPKSQBPVTL 540
QY 541 DFLDAELNDIKVEIRNKMIDGSGEKTFTLVKSDQERYIDKGNRTYTWTPVNGTDYSL 600
Db 541 DFLDAELNDIKVEIRNKMIDGSGEKTFTLVKSDQERYIDKGNRTYTWTPVNGTDYSL 600
QY 601 ALVLPYTFYIIKAKLEETITQARSKGKMKDSETLKPDNFESGYTFIAPRDYCNLDKI 660
Db 601 ALVLPYTFYIIKAKLEETITQARSKGKMKDSETLKPDNFESGYTFIAPRDYCNLDKI 660
QY 661 SDNTEFLNFEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQWYKQKNIKGVKAR 720
Db 661 SDNTEFLNFEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQWYKQKNIKGVKAR 720
QY 721 FVYTDGGITRVTPKEAGENWQENPETEYDSFKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
Db 721 FVYTDGGITRVTPKEAGENWQENPETEYDSFKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTKTSIRDPKAGPVCDCKRNSDVMDCVI 840
Db 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTKTSIRDPKAGPVCDCKRNSDVMDCVI 840
QY 841 LDDGGFLLMANHDDVTNQGIFGFEIDPSLMRHLVNI SYAFNKSVDYQSCVCEPAAKQ 900
Db 841 LDDGGFLLMANHDDVTNQGIFGFEIDPSLMRHLVNI SYAFNKSVDYQSCVCEPAAKQ 900
QY 901 GAGHSAYVPSVADILQIGWATAAWSILQFLLSLTFPRLLLEAVEMEDDFTASLSKQ 960
Db 901 GAGHSAYVPSVADILQIGWATAAWSILQFLLSLTFPRLLLEAVEMEDDFTASLSKQ 960
QY 961 SCITEQTOYFFDNDKSGSVLDCGNCRIHFGEKLMNTNLI FIMVESKGTCPDTRLLI 1020
Db 961 SCITEQTOYFFDNDKSGSVLDCGNCRIHFGEKLMNTNLI FIMVESKGTCPDTRLLI 1020
QY 1021 QAEQTSQDGNPCDMVK 1036
Db 1021 QAEQTSQDGNPCDMVK 1036

RESULT 4

US-08-311-363-25

; Sequence 25, Application US/08311363
; Patent No. 5876558
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: Human Calcium Channel Compositions and
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,363
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-51506
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1091 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-311-363-25

Query Match 100.0%; Score 5443; DB 2; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAGCLLALTTLTFLFOSLLIGPSSSEPPFSAVTIKSWVDKMQEDLVTLAKTAGVNLVDI 60
Db 1 MAAGCLLALTTLTFLFOSLLIGPSSSEPPFSAVTIKSWVDKMQEDLVTLAKTAGVNLVDI 60
QY 61 YEKYQDLYTVEPNNAQRLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120
Db 61 YEKYQDLYTVEPNNAQRLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120
QY 121 EVVYNNAKDLDPEKNDSEPPGSRKIPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180
Db 121 EVVYNNAKDLDPEKNDSEPPGSRKIPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180
QY 181 NELNWTSSALDEVFKKNEEDPSLLWQVFGSATGLARYYPASPDVNSRTPNKIDLYDVR 240
Db 181 NELNWTSSALDEVFKKNEEDPSLLWQVFGSATGLARYYPASPDVNSRTPNKIDLYDVR 240
QY 241 RPWYIOGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETLSDDDDFVNVASFNNAQD 300
Db 241 RPWYIOGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETLSDDDDFVNVASFNNAQD 300
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGTDYKKGFSFAFEQLLNINVSANCNKIIML 360
Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGTDYKKGFSFAFEQLLNINVSANCNKIIML 360

361 FTGGEERAEIENKYNKDKKRVFRFVSGQHNYERGPQIOMACENKGYIYPSIGAIR 420
Db FTGGEERAEIENKYNKDKKRVFRFVSGQHNYERGPQIOMACENKGYIYPSIGAIR 420
QY 421 INTQEVLDVLRPMVLGADKAKOVQNTNYLDALGLGLVITGLPVFNITGQENKTNLK 480
Db INTQEVLDVLRPMVLGADKAKOVQNTNYLDALGLGLVITGLPVFNITGQENKTNLK 480
QY 481 NQILGVMGVDVSLIEDIKRLTPFTLCPNGYIFAIDPBGVYLLHPNLQPNKPSQEPVTL 540
Db NQILGVMGVDVSLIEDIKRLTPFTLCPNGYIFAIDPBGVYLLHPNLQPNKPSQEPVTL 540
QY 541 DFLDAELENDIKVEIRNKMIDGSGEKTFRTLKQSDERYIDKGNRTYTWTPVNGTDYSL 600
Db DFLDAELENDIKVEIRNKMIDGSGEKTFRTLKQSDERYIDKGNRTYTWTPVNGTDYSL 600
QY 601 ALVLPYTFYIIRAKLEETITQARSKKGMKDSSETLKPDNFESGYTFIAPRDYCNLDKI 660
Db ALVLPYTFYIIRAKLEETITQARSKKGMKDSSETLKPDNFESGYTFIAPRDYCNLDKI 660
QY 661 SDNTEFLNFEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQNWYWSKQNIKGVKAR 720
Db SDNTEFLNFEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQNWYWSKQNIKGVKAR 720
QY 721 FVYTDGGITRVYPKEAGENQENPETEYDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
Db FVYTDGGITRVYPKEAGENQENPETEYDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
QY 781 MYSKAVEIYIQGLLPAVVGIIKIDVNSWIENFTKTSIRDPACAGPVCDCRNSDVMDCVI 840
Db MYSKAVEIYIQGLLPAVVGIIKIDVNSWIENFTKTSIRDPACAGPVCDCRNSDVMDCVI 840
QY 841 LDGSGELLMAHDDYTNQIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCPGAPKQ 900
Db LDGSGELLMAHDDYTNQIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCPGAPKQ 900
QY 901 GAGHSAYVPSVADIIQIGWATAAASIIQOFLSLTFPRLLLEAVEMEDDDFTASLSKQ 960
Db GAGHSAYVPSVADIIQIGWATAAASIIQOFLSLTFPRLLLEAVEMEDDDFTASLSKQ 960
QY 961 SCITEQTYFFDNDKSFSGVLDGNCGRIFHGEKLMNTNLIIFIMVESKGTCTCDTRLII 1020
Db SCITEQTYFFDNDKSFSGVLDGNCGRIFHGEKLMNTNLIIFIMVESKGTCTCDTRLII 1020
QY 1021 QAEQTSDEGNPCDMVK 1036
Db QAEQTSDEGNPCDMVK 1036

RESULT 5

US-08-713-118-4
; Sequence 4, Application US/08713118
; Patent No. 6040436
; GENERAL INFORMATION:
; APPLICANT: Franco, Rodrigo
; APPLICANT: Sun Chen, Ai Ru
; APPLICANT: Suey, David J.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL
; TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,118
; FILING DATE: 16-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mata, Elizabeth W.
; REGISTRATION NUMBER: 38,236
; REFERENCE/DOCKET NUMBER: ACC96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1091 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-713-118-4

Query Match 99.9%; Score 5439; DB 3; Length 1091;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1035; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAGCLIALTLTLFQSLIGPSSSEPPPSAVTTKSWDKMQEDLVTAKTASGVNQLVDI 60
Db 1 MAAGCLIALTLTLFQSLIGPSSSEPPPSAVTTKSWDKMQEDLVTAKTASGVNQLVDI 60
QY 61 YEKYQDLYTVEPNARQOLVEIAARDIEKLLSNRSKALVSIALAEKVOAAHQRDFASN 120
Db 61 YEKYQDLYTVEPNARQOLVEIAARDIEKLLSNRSKALVSIALAEKVOAAHQRDFASN 120
QY 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRIQISYQAAVHIPDIYEGSTIVL 180
Db 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRIQISYQAAVHIPDIYEGSTIVL 180
QY 181 NELNWTALDEVEKKNREEDPSLLMQVFGSATGLARYYPASPVWDNSRTNPKIDLYDVR 240
Db 181 NELNWTALDEVEKKNREEDPSLLMQVFGSATGLARYYPASPVWDNSRTNPKIDLYDVR 240
QY 241 RPVYIOGAASPKDMLILVDYSGVSGVGLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300
Db 241 RPVYIOGAASPKDMLILVDYSGVSGVGLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300
QY 301 VSCFQHLVQANVRNKKVLDVANNITAKGITDYKKGFSFAFEQLLNYSRANCNKIIML 360
Db 301 VSCFQHLVQANVRNKKVLDVANNITAKGITDYKKGFSFAFEQLLNYSRANCNKIIML 360
QY 361 FTGGEERAEIENKYNKDKKRVFRFVSGQHNYERGPQIOMACENKGYIYPSIGAIR 420
Db 361 FTGGEERAEIENKYNKDKKRVFRFVSGQHNYERGPQIOMACENKGYIYPSIGAIR 420
QY 421 INTQEVLDVLRPMVLGADKAKOVQNTNYLDALGLGLVITGLPVFNITGQENKTNLK 480
Db 421 INTQEVLDVLRPMVLGADKAKOVQNTNYLDALGLGLVITGLPVFNITGQENKTNLK 480
QY 481 NQILGVMGVDVSLIEDIKRLTPFTLCPNGYIFAIDPBGVYLLHPNLQPNKPSQEPVTL 540
Db 481 NQILGVMGVDVSLIEDIKRLTPFTLCPNGYIFAIDPBGVYLLHPNLQPNKPSQEPVTL 540
QY 541 DFLDAELENDIKVEIRNKMIDGSGEKTFRTLKQSDERYIDKGNRTYTWTPVNGTDYSL 600
Db 541 DFLDAELENDIKVEIRNKMIDGSGEKTFRTLKQSDERYIDKGNRTYTWTPVNGTDYSL 600
QY 601 ALVLPYTFYIIRAKLEETITQARSKKGMKDSSETLKPDNFESGYTFIAPRDYCNLDKI 660
Db 601 ALVLPYTFYIIRAKLEETITQARSKKGMKDSSETLKPDNFESGYTFIAPRDYCNLDKI 660
QY 661 SDNTEFLNFEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQNWYWSKQNIKGVKAR 720
Db 661 SDNTEFLNFEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQNWYWSKQNIKGVKAR 720
QY 721 FVYTDGGITRVYPKEAGENQENPETEYDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780

Db 721 FVTDGGITRVYKPEAGENQWENPEYEDSFYKRSNDNNTYFTAPIFNKSGPGAYESGI 780
QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWENFTKTSIRDPKAGVCDCKRNSDVMDCVI 840
Db 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWENFTKTSIRDPKAGVCDCKRNSDVMDCVI 840
QY 841 LDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNSVYAFNKSVDYQSVCEPGAAPKQ 900
Db 841 LDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNSVYAFNKSVDYQSVCEPGAAPKQ 900
QY 901 GAGHRSAYVPSVADILQIGWATAAASWTLQOFLSLTFPRLLLEAVEMEDDDFTASLSKQ 960
Db 901 GAGHRSAYVPSVADILQIGWATAAASWTLQOFLSLTFPRLLLEAVEMEDDDFTASLSKQ 960
QY 961 SCITEOTQYFFDNDKSKFSGLVDCGNCGRIFHGEKLMNTNLFIMVESKGTCPDTRLLI 1020
Db 961 SCITEOTQYFFDNDKSKFSGLVDCGNCGRIFHGEKLMNTNLFIMVESKGTCPDTRLLI 1020
QY 1021 QAEQTS DGNPCDMVK 1036
Db 1021 QAEQTS DGNPCDMVK 1036

RESULT 6

US-09-452-007-4
; Sequence 4, Application US/09452007
; Patent No. 6140485
; GENERAL INFORMATION:
; APPLICANT: Franco, Rodrigo
; APPLICANT: Sun Chen, Al Ru
; APPLICANT: Suey, David J.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/452,007
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,118
; FILING DATE: 16-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mata, Elizabeth W.
; REGISTRATION NUMBER: 38,236
; REFERENCE/DOCKET NUMBER: ACC96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1091 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-452-007-4

Query Match 99.9%; Score 5439; DB 4; Length 1091;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1035; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAGCLLALTTLTFLQSLILGPSSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
Db 1 MAAGCLLALTTLTFLQSLILGPSSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
QY 61 YEKYODLYTVPEPNNAQLVETAAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120
Db 61 YEKYODLYTVPEPNNAQLVETAAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120
QY 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRQISYQHAHVHPTDIYEGSTIVL 180
Db 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRQISYQHAHVHPTDIYEGSTIVL 180
QY 181 NELNWT SALDEVFKKNREDDPSLLMQVFGSATGLARYYPASPDWNSRTPNKIDLYDVR 240
Db 181 NELNWT SALDEVFKKNREDDPSLLMQVFGSATGLARYYPASPDWNSRTPNKIDLYDVR 240
QY 241 RPWYIQGAASPKDMLILVDVSGVSGSLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300
Db 241 RPWYIQGAASPKDMLILVDVSGVSGSLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300
QY 301 VSCFQHLVQANVRNKKVYLKDAVNNTAKGITDYKKGFSFAFEQLLNNVSRANCKIIML 360
Db 301 VSCFQHLVQANVRNKKVYLKDAVNNTAKGITDYKKGFSFAFEQLLNNVSRANCKIIML 360
QY 361 FTDGGEERAQEIENKYNKDKKRVFRFVSGOHNYERGPIONMACENKGYEYIPIPSIGAIR 420
Db 361 FTDGGEERAQEIENKYNKDKKRVFRFVSGOHNYERGPIONMACENKGYEYIPIPSIGAIR 420
QY 421 INTQEYLDVLGRPMVLADGKAKQVQWNTNVYLDALDELGLVITGTLPVFNITQGFENKTNLK 480
Db 421 INTQEYLDVLGRPMVLADGKAKQVQWNTNVYLDALDELGLVITGTLPVFNITQGFENKTNLK 480
QY 481 NQLILGVMGVDVSLIEDIKRLTPRTTLPNGYFFAIDPNGYVLLHPNLPKNPKSQEPVTL 540
Db 481 NQLILGVMGVDVSLIEDIKRLTPRTTLPNGYFFAIDPNGYVLLHPNLPKNPKSQEPVTL 540
QY 541 DFLDAELENDIKVEIRNMKIDGESGEKTFRTLVKSODRYDKGNRTVTTVPNGTDYSL 600
Db 541 DFLDAELENDIKVEIRNMKIDGESGEKTFRTLVKSODRYDKGNRTVTTVPNGTDYSL 600
QY 601 ALVLTYSFYIYKAKLEETITQARSKKGKMDSETLKPDPNFEESSGYTFIAPRDCNDLKI 660
Db 601 ALVLTYSFYIYKAKLEETITQARSKKGKMDSETLKPDPNFEESSGYTFIAPRDCNDLKI 660
QY 661 SDNTEFLNPFNEIDRKTNNPCNADLINRVLLDAGFTNELVQNYWSKOKNIKGVKAR 720
Db 661 SDNTEFLNPFNEIDRKTNNPCNADLINRVLLDAGFTNELVQNYWSKOKNIKGVKAR 720
QY 721 FVTDGGITRVYKPEAGENQWENPEYEDSFYKRSNDNNTYFTAPIFNKSGPGAYESGI 780
Db 721 FVTDGGITRVYKPEAGENQWENPEYEDSFYKRSNDNNTYFTAPIFNKSGPGAYESGI 780
QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWENFTKTSIRDPKAGVCDCKRNSDVMDCVI 840
Db 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWENFTKTSIRDPKAGVCDCKRNSDVMDCVI 840
QY 841 LDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNSVYAFNKSVDYQSVCEPGAAPKQ 900
Db 841 LDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNSVYAFNKSVDYQSVCEPGAAPKQ 900
QY 901 GAGHRSAYVPSVADILQIGWATAAASWTLQOFLSLTFPRLLLEAVEMEDDDFTASLSKQ 960
Db 901 GAGHRSAYVPSVADILQIGWATAAASWTLQOFLSLTFPRLLLEAVEMEDDDFTASLSKQ 960
QY 961 SCITEOTQYFFDNDKSKFSGLVDCGNCGRIFHGEKLMNTNLFIMVESKGTCPDTRLLI 1020
Db 961 SCITEOTQYFFDNDKSKFSGLVDCGNCGRIFHGEKLMNTNLFIMVESKGTCPDTRLLI 1020
QY 1021 QAEQTS DGNPCDMVK 1036
Db 1021 QAEQTS DGNPCDMVK 1036

RESULT 7
 US-08-455-543A-54
 ; Sequence 54, Application US/0845543A
 ; Patent No. 5792846
 ; GENERAL INFORMATION:
 ; APPLICANT: Harpold, Michael
 ; APPLICANT: Ellis, Steven
 ; APPLICANT: Williams, Mark
 ; APPLICANT: Feldman, Daniel
 ; APPLICANT: McCue, Ann
 ; APPLICANT: Brenner, Robert
 ; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 ; TITLE OF INVENTION: METHODS
 ; NUMBER OF SEQUENCES: 57
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Brown, Martin, Haller & McClain
 ; STREET: 1660 Union Street
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 92101-2926
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/455,543A
 ; FILING DATE: May 31, 1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/223,305
 ; FILING DATE: April 4, 1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/868,354
 ; FILING DATE: April 10, 1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/745,206
 ; FILING DATE: 15-AUG-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/620,250
 ; FILING DATE: 30-NOV-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/603,751
 ; FILING DATE: 04-APR-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/US89/01408
 ; FILING DATE: 04-APR-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/176,899
 ; FILING DATE: 04-APR-1988
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seidman, Stephanie L.
 ; REGISTRATION NUMBER: 33,779
 ; REFERENCE/DOCKET NUMBER: 6362-52517
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619)238-0999
 ; TELEFAX: (619)238-0062
 ; INFORMATION FOR SEQ ID NO: 54:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1086 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FRAGMENT TYPE: internal
 ; US-08-455-543A-54

Query Match 99.3%; Score 5403.5; DB 1; Length 1086;

Best Local Similarity 99.5%; Pred No. 0;
 Matches 1031; Conservative 0; Mismatches 0; Indels 5; Gaps 1;
 QY 1 MAAGCLLALTLTFLQSLIGPSSSEPPPSAVTIKSWDKWQEDLVTLAKTASGVNQLVDI 60
 DB 1 MAAGCLLALTLTFLQSLIGPSSSEPPPSAVTIKSWDKWQEDLVTLAKTASGVNQLVDI 60
 QY 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVAQAAHOWREDFASN 120
 DB 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVAQAAHOWREDFASN 120
 QY 121 EVVYNAKDDLDEKNDSEPGSQRIKPVFIEDANFGQISYQHAHVHPTDIYEGSTIVL 180
 DB 121 EVVYNAKDDLDEKNDSEPGSQRIKPVFIEDANFGQISYQHAHVHPTDIYEGSTIVL 180
 QY 181 NELNWTSSALDEVEFKKNEEDPSLLQVFGSATGLARYYPASPWDVNSRTPNKIDLYDVR 240
 DB 181 NELNWTSSALDEVEFKKNEEDPSLLQVFGSATGLARYYPASPWDVNSRTPNKIDLYDVR 240
 QY 241 RPWYIQGAASPDKMLILVDVSGSVGLTLKLI RTSVSEMLETLSDDDFVNVASTNSNAQD 300
 DB 241 RPWYIQGAASPDKMLILVDVSGSVGLTLKLI RTSVSEMLETLSDDDFVNVASTNSNAQD 300
 QY 301 VSCFOHLVQANVRNKKVLDVANNITAGITDYKKGSEFAEQLLNYSRANCKIIML 360
 DB 301 VSCFOHLVQANVRNKKVLDVANNITAGITDYKKGSEFAEQLLNYSRANCKIIML 360
 QY 361 FTGGEERAQEIFNKYNKDKKRVFRFVSQGHNYERGIQMACENKGYIYFISGAIR 420
 DB 361 FTGGEERAQEIFNKYNKDKKRVFRFVSQGHNYERGIQMACENKGYIYFISGAIR 420
 QY 421 INTQEYLDVLGRPMVLADGAKQVQWNTNVLDALEGLVITGTLPVNITQGFENKKNL 480
 DB 421 INTQEYLDVLGRPMVLADGAKQVQWNTNVLDALEGLVITGTLPVNITQGFENKKNL 480
 QY 481 NQLILGVMGVDSLEDIKRLTPRETLCPNGYPAIDPNGVYLLHPNLPKPKSOEPTVL 540
 DB 481 NQLILGVMGVDSLEDIKRLTPRETLCPNGYPAIDPNGVYLLHPNLPKPKSOEPTVL 540
 QY 541 DFLDAELENDIKVEIRNMIDGESGKFTFTLVKSQDERYIDKGNRTYTPVNGTDYSL 600
 DB 536 DFLDAELENDIKVEIRNMIDGESGKFTFTLVKSQDERYIDKGNRTYTPVNGTDYSL 595
 QY 601 ALVLPYTSFYIIRAKLEETITQARSKKGMKDSITLKPDPNFEESGYTFIAPRDYCNLDKI 660
 DB 596 ALVLPYTSFYIIRAKLEETITQARSKKGMKDSITLKPDPNFEESGYTFIAPRDYCNLDKI 655
 QY 661 SDNTEFLANFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELYQNTWSKOKNKGVKAR 720
 DB 656 SDNTEFLANFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELYQNTWSKOKNKGVKAR 715
 QY 721 FVYTDGGITRVYPKEAGENQENPETEYDSFYKSLDNDNYVFTAPYFNKSGPGAYESGI 780
 DB 716 FVYTDGGITRVYPKEAGENQENPETEYDSFYKSLDNDNYVFTAPYFNKSGPGAYESGI 775
 QY 781 MVSKAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKTSIRDPACGPDCKRNSDVMDCVI 840
 DB 776 MVSKAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKTSIRDPACGPDCKRNSDVMDCVI 835
 QY 841 LDDGGFLMANHDDYTNOIGRFGEIDPISLMRHLVNTSVYAFNKSVDYQSVCEPGAAPKQ 900
 DB 836 LDDGGFLMANHDDYTNOIGRFGEIDPISLMRHLVNTSVYAFNKSVDYQSVCEPGAAPKQ 895
 QY 901 GAGHRSAYVPSVADILQIGWATAAANSILQOFLSLTFFPRLLEAVEMEDDDFTASLSKQ 960
 DB 896 GAGHRSAYVPSVADILQIGWATAAANSILQOFLSLTFFPRLLEAVEMEDDDFTASLSKQ 955
 QY 961 SCITEQTYFFDNDKSFSGVLDCGNCGRPHGKLMNTNLIIFIMVPSKGCPCDTRLLI 1020
 DB 956 SCITEQTYFFDNDKSFSGVLDCGNCGRPHGKLMNTNLIIFIMVPSKGCPCDTRLLI 1015
 QY 1021 QAEQTSQGNPCDMVK 1036
 |||||||||||||||

RESULT 9
US-08-455-543A-56
: Sequence 56, Application US/0845543A
: Patent No. 5792846
: GENERAL INFORMATION:
: APPLICANT: Harpold, Michael
: APPLICANT: Ellis, Steven
: APPLICANT: Williams, Mark
: APPLICANT: Feldman, Daniel
: APPLICANT: McCue, Ann
: APPLICANT: Brenner, Robert
: TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
: TITLE OF INVENTION: METHODS
: NUMBER OF SEQUENCES: 57
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Brown, Martin, Haller & McClain
: STREET: 1660 Union Street
: CITY: San Diego
: STATE: California
: COUNTRY: USA
: ZIP: 92101-2926
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq Version 1.5
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/455,543A
: FILING DATE: May 31, 1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/223,305
: FILING DATE: April 4, 1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/868,354
: FILING DATE: April 10, 1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/745,206
: FILING DATE: 15-AUG-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/620,250
: FILING DATE: 30-NOV-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/482,384
: FILING DATE: 20-FEB-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/603,751
: FILING DATE: 04-APR-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO PCT/US89/01408
: FILING DATE: 04-APR-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/176,899
: FILING DATE: 04-APR-1988
: ATTORNEY/AGENT INFORMATION:
: NAME: Seidman, Stephanie L.
: REGISTRATION NUMBER: 33,779
: REFERENCE/DOCKET NUMBER: 6362-52517
: TELEPHONE: (619)238-0999
: TELEFAX: (619)238-0062
: INFORMATION FOR SEQ ID NO: 56:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1084 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: FRAGMENT TYPE: internal
US-08-455-543A-56

Query Match		99.0%	Score 5386.5	DB 1	Length 1084
Best Local Similarity		99.2%	Pred. No. 0		
Matches 1028		Conservative	0	Mismatches	1
				Indels	Gaps
Qy	1	MAAGCLLALTLT	1	MAAGCLLALTLT	1
Db	1	MAAGCLLALTLT	1	MAAGCLLALTLT	1
Qy	61	YKQYQDLYTVP	1	YKQYQDLYTVP	1
Db	61	YKQYQDLYTVP	1	YKQYQDLYTVP	1
Qy	121	EVVYNKADDD	1	EVVYNKADDD	1
Db	121	EVVYNKADDD	1	EVVYNKADDD	1
Qy	181	NELNWTALDE	1	NELNWTALDE	1
Db	181	NELNWTALDE	1	NELNWTALDE	1
Qy	241	RPWYIQAAS	1	RPWYIQAAS	1
Db	241	RPWYIQAAS	1	RPWYIQAAS	1
Qy	301	VSCFQHLVQ	1	VSCFQHLVQ	1
Db	301	VSCFQHLVQ	1	VSCFQHLVQ	1
Qy	361	FTDGGEEA	1	FTDGGEEA	1
Db	361	FTDGGEEA	1	FTDGGEEA	1
Qy	421	INTQEVLDV	1	INTQEVLDV	1
Db	421	INTQEVLDV	1	INTQEVLDV	1
Qy	481	NQILGVMG	1	NQILGVMG	1
Db	481	NQILGVMG	1	NQILGVMG	1
Qy	541	DFLDAELE	1	DFLDAELE	1
Db	541	DFLDAELE	1	DFLDAELE	1
Qy	601	ALVLPYSF	1	ALVLPYSF	1
Db	601	ALVLPYSF	1	ALVLPYSF	1
Qy	661	SDNTEFL	1	SDNTEFL	1
Db	661	SDNTEFL	1	SDNTEFL	1
Qy	721	FVTDGGIT	1	FVTDGGIT	1
Db	721	FVTDGGIT	1	FVTDGGIT	1
Qy	781	MVSKAVEI	1	MVSKAVEI	1
Db	781	MVSKAVEI	1	MVSKAVEI	1
Qy	841	LDGGLFL	1	LDGGLFL	1
Db	841	LDGGLFL	1	LDGGLFL	1
Qy	901	GAGHRSAY	1	GAGHRSAY	1
Db	901	GAGHRSAY	1	GAGHRSAY	1
Qy	961	SCITEQTY	1	SCITEQTY	1
Db	961	SCITEQTY	1	SCITEQTY	1
Qy	1021	QAEQTS	1	QAEQTS	1
Db	1021	QAEQTS	1	QAEQTS	1

Db 1014 QAEQTS DGNPCDVK 1029
|||||
RESULT 10
US-08-223-305C-56
; Sequence 56, Application US/08223305C
; Patent No. 5851824
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/223,305C
; FILING DATE: April 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,250
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 52516 (P519739)
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1084 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-223-305C-56

Query Match 99.0%; Score 5386.5; DB 2; Length 1084;

Best Local Similarity 99.2%; Pred. No. 0;
Matches 1028; Conservative 0; Mismatches 1; Indels 7; Gaps 1;
QY 1 MAAGCILLALTTLFQSLIGPSSEEPFSAVTKSWDKMQEDLVTLAKTASGVNQLVDI 60
|||||
Db 1 MAAGCILLALTTLFQSLIGPSSEEPFSAVTKSWDKMQEDLVTLAKTASGVNQLVDI 60
|||||
QY 61 YEKYQDLYTVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRWREFASN 120
|||||
Db 61 YEKYQDLYTVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRWREFASN 120
|||||
QY 121 EYVYNAKDDLDPEKNDSPGSGORIKPVIEDANFGROISYQHAHVHPTDIEYEGSTIVL 180
|||||
Db 121 EYVYNAKDDLDPEKNDSPGSGORIKPVIEDANFGROISYQHAHVHPTDIEYEGSTIVL 180
|||||
QY 181 NELNWTSSALDEVFKKNREEDPSLLMQVFGSATGLARYYPASPMVDNSRTPNKIDLYDVR 240
|||||
Db 181 NELNWTSSALDEVFKKNREEDPSLLMQVFGSATGLARYYPASPMVDNSRTPNKIDLYDVR 240
|||||
QY 241 RPWYIQAASPKDMLLVDVSGVSGLTILKLTISVSEMLETISDDDFYNVASFNSNAQD 300
|||||
Db 241 RPWYIQAASPKDMLLVDVSGVSGLTILKLTISVSEMLETISDDDFYNVASFNSNAQD 300
|||||
QY 301 VSCFOHLVQANVRNKKVLKDAVNNTAKGITYKKGFSAFEOLLNYSRANCKNIIML 360
|||||
Db 301 VSCFOHLVQANVRNKKVLKDAVNNTAKGITYKKGFSAFEOLLNYSRANCKNIIML 360
|||||
QY 361 FTDGGEERAQEIFNKYKDKVFRFSYQHNRYERGIQWMACENKGYEYIPEISGAIR 420
|||||
Db 361 FTDGGEERAQEIFNKYKDKVFRFSYQHNRYERGIQWMACENKGYEYIPEISGAIR 420
|||||
QY 421 INTQEYLDVLGRPMVLGAKAQOVNTNYLDALGLVITGTLPVFNITGPFENKTNLK 480
|||||
Db 421 INTQEYLDVLGRPMVLGAKAQOVNTNYLDALGLVITGTLPVFNITGPFENKTNLK 480
|||||
QY 481 NQLILGVMGVDVSLIEDIKRLTFRFLCPNGYFAIDPNGYVLLHPNLQPKNSQBPVTL 540
|||||
Db 481 NQLILGVMGVDVSLIEDIKRLTFRFLCPNGYFAIDPNGYVLLHPNLQPKNSQBPVTL 540
|||||
QY 541 DFLDAELENDIKVEIRNKMIDGESGEKTRTLVKSDERYIDKGNRTYTWTVPNGTDYSL 600
|||||
Db 541 DFLDAELENDIKVEIRNKMIDGESGEKTRTLVKSDERYIDKGNRTYTWTVPNGTDYSL 600
|||||
QY 601 ALVLTYSFYIYKALEETITQARSKKGMKDSITLKPDPNFESGYFTIAPRDYCNLDKI 660
|||||
Db 601 ALVLTYSFYIYKALEETITQARSKKGMKDSITLKPDPNFESGYFTIAPRDYCNLDKI 660
|||||
QY 661 SDNTEFLNFEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVQYWSKQKNKGVKAR 720
|||||
Db 661 SDNTEFLNFEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVQYWSKQKNKGVKAR 720
|||||
QY 721 FVYTDGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPAYESGI 780
|||||
Db 721 FVYTDGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPAYESGI 780
|||||
QY 781 MYSKAVEIYIQGLLKPVVGVKIDVNSWNIENFTKTSIRDPGAGPVCDCKRSDVMDCVI 840
|||||
Db 781 MYSKAVEIYIQGLLKPVVGVKIDVNSWNIENFTKTSIRDPGAGPVCDCKRSDVMDCVI 840
|||||
QY 841 LDDGGFLMANHDDVTNIGRFFGEIDPSLMRHLNIVSYAFNKSVDYOSVCEPGAAPQ 900
|||||
Db 841 LDDGGFLMANHDDVTNIGRFFGEIDPSLMRHLNIVSYAFNKSVDYOSVCEPGAAPQ 900
|||||
QY 901 GAGHRSAYVPSVADILQIGWATAAASLIQOFLSLTPEPRLEAVEMEDDDFTASLSQ 960
|||||
Db 901 GAGHRSAYVPSVADILQIGWATAAASLIQOFLSLTPEPRLEAVEMEDDDFTASLSQ 960
|||||
QY 961 SCITEQTYFFDNDKSFSGVLDGCNCSRFHGEKMLNTNLIIFIMVESGTCPCDTRLI 1020
|||||
Db 961 SCITEQTYFFDNDKSFSGVLDGCNCSRFHGEKMLNTNLIIFIMVESGTCPCDTRLI 1020
|||||
QY 1021 QAEQTS DGNPCDVK 1036
|||||

Db 1014 QAEQTSBGPNCMDVK 1029

RESULT 11

US-08-455-543A-53

; Sequence 53, Application US/08455543A

; Patent No. 5792846

; GENERAL INFORMATION:

; APPLICANT: Harpold, Michael

; APPLICANT: Ellis, Steven

; APPLICANT: Williams, Mark

; APPLICANT: Feldman, Daniel

; APPLICANT: McCue, Ann

; APPLICANT: Brenner, Robert

; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

; METHODS

; NUMBER OF SEQUENCES: 57

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Brown, Martin, Haller & McClain

; STREET: 1660 Union Street

; CITY: San Diego

; STATE: California

; COUNTRY: USA

; ZIP: 92101-2926

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/455,543A

; FILING DATE: May 31, 1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/223,305

; FILING DATE: April 4, 1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/868,354

; FILING DATE: April 10, 1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/745,206

; FILING DATE: 15-AUG-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/620,250

; FILING DATE: 30-NOV-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/482,384

; FILING DATE: 20-FEB-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/603,751

; FILING DATE: 04-APR-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US89/01408

; FILING DATE: 04-APR-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/176,899

; FILING DATE: 04-APR-1988

; ATTORNEY/AGENT INFORMATION:

; NAME: Seidman, Stephanie L.

; REGISTRATION NUMBER: 33,779

; REFERENCE/DOCKET NUMBER: 6362-52517

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619)238-0999

; TELEFAX: (619)238-0062

; INFORMATION FOR SEQ ID NO: 53:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1103 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FRAGMENT TYPE: internal

; US-08-455-543A-53

Query Match	98.6%	Score 5367;	DB 1;	Length 1103;
Best Local Similarity	97.4%	Pred. No. 0;		
Matches 1028;	Conservative	0;	Mismatches	1; Indels 26; Gaps 2;
QY	1	MAAGCLLALTLTQSLIGPSSEPPSPSAVTIKSWDKMOEDLVTLAKTAGSVNQLVDI	60	
DB	1	MAAGCLLALTLTQSLIGPSSEPPSPSAVTIKSWDKMOEDLVTLAKTAGSVNQLVDI	60	
QY	61	YEKYODLYTVEPNNAQOLVEIAARDIEKLNSRKALYSALAEAEKVAHAHQWREDFASN	120	
DB	61	YEKYODLYTVEPNNAQOLVEIAARDIEKLNSRKALYSALAEAEKVAHAHQWREDFASN	120	
QY	121	EVVYVNAKDDLDPEKNDSEPGSQRIKPVIEDANFGRQISYQAAVHIPTDIYEGSTIVL	180	
DB	121	EVVYVNAKDDLDPEKNDSEPGSQRIKPVIEDANFGRQISYQAAVHIPTDIYEGSTIVL	180	
QY	181	NELNMTSALDEVFKKNREEDPSLLMQVFGSATGLARYYPASPWDNSRTPNKIDLYDVR	240	
DB	181	NELNMTSALDEVFKKNREEDPSLLMQVFGSATGLARYYPASPWDNSRTPNKIDLYDVR	240	
QY	241	RPWYIOGAASPKDMLILVDVSGVSGLTLLKLRISYSEMLETSLDDDFVNVASFNSNAOD	300	
DB	241	RPWYIOGAASPKDMLILVDVSGVSGLTLLKLRISYSEMLETSLDDDFVNVASFNSNAOD	300	
QY	301	VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEGOLLNYSRANCKIIML	360	
DB	301	VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEGOLLNYSRANCKIIML	360	
QY	361	FTDGEERAQEIFNKYKDKKVRFRFSGVQHNYERGIOWMACENKGYEIPSGAIR	420	
DB	361	FTDGEERAQEIFNKYKDKKVRFRFSGVQHNYERGIOWMACENKGYEIPSGAIR	420	
QY	421	INTQEYLDVLGRPMVLAKAKQVQNTNVYLDALGLVITGTLPVFNITGQENKTNLK	480	
DB	421	INTQEYLDVLGRPMVLAKAKQVQNTNVYLDALGLVITGTLPVFNITGQENKTNLK	480	
QY	481	NQILGVMGVDVSLDIKRLTPRTLCPNGYYFAIDPNGVYLHPNLOPK	530	
DB	481	NQILGVMGVDVSLDIKRLTPRTLCPNGYYFAIDPNGVYLHPNLOPK	530	
QY	531	-----NPKSQEPVTLDFDAELENDIKVEIRNKMIDGSEKTFRTLVKSQDRIY	581	
DB	531	-----NPKSQEPVTLDFDAELENDIKVEIRNKMIDGSEKTFRTLVKSQDRIY	581	
QY	541	LRKRRNPIONPKSQEPVTLDFDAELENDIKVEIRNKMIDGSEKTFRTLVKSQDRIY	600	
DB	541	LRKRRNPIONPKSQEPVTLDFDAELENDIKVEIRNKMIDGSEKTFRTLVKSQDRIY	600	
QY	582	DGNRTYTPVNGTDSLALVLTYSFYIKAKLEETITQARSKKGMKSEITLKPDNF	641	
DB	582	DGNRTYTPVNGTDSLALVLTYSFYIKAKLEETITQARSKKGMKSEITLKPDNF	641	
QY	601	DGNRTYTPVNGTDSLALVLTYSFYIKAKLEETITQARY	653	
DB	601	DGNRTYTPVNGTDSLALVLTYSFYIKAKLEETITQARY	653	
QY	642	EESGYTFIAPRDYCNLDKISDNTEFLNFEFIDRKTTPNPNPCNADLINRVLLDAGFTN	701	
DB	642	EESGYTFIAPRDYCNLDKISDNTEFLNFEFIDRKTTPNPNPCNADLINRVLLDAGFTN	701	
QY	654	EESGYTFIAPRDYCNLDKISDNTEFLNFEFIDRKTTPNPNPCNADLINRVLLDAGFTN	713	
DB	654	EESGYTFIAPRDYCNLDKISDNTEFLNFEFIDRKTTPNPNPCNADLINRVLLDAGFTN	713	
QY	702	ELVQYWSKQKNIKGVKARFVTDGGITRVYPKEAGENQENPEYEDSFYKRSLDNDNY	761	
DB	702	ELVQYWSKQKNIKGVKARFVTDGGITRVYPKEAGENQENPEYEDSFYKRSLDNDNY	761	
QY	714	ELVQYWSKQKNIKGVKARFVTDGGITRVYPKEAGENQENPEYEDSFYKRSLDNDNY	773	
DB	714	ELVQYWSKQKNIKGVKARFVTDGGITRVYPKEAGENQENPEYEDSFYKRSLDNDNY	773	
QY	762	VFTAPYFNKSGPGAYESGIMYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTKTSIRDP	821	
DB	762	VFTAPYFNKSGPGAYESGIMYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTKTSIRDP	821	
QY	774	VFTAPYFNKSGPGAYESGIMYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTKTSIRDP	833	
DB	774	VFTAPYFNKSGPGAYESGIMYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTKTSIRDP	833	
QY	822	CAGPVCDCKRNSDVMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNSVYA	881	
DB	822	CAGPVCDCKRNSDVMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNSVYA	881	
QY	834	CAGPVCDCKRNSDVMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNSVYA	893	
DB	834	CAGPVCDCKRNSDVMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNSVYA	893	
QY	882	FNKSYDYOSVCEPGAAPKQAGHRSAYVPSVADIIQIGWATAAAWSILQQFLLSITFPR	941	
DB	882	FNKSYDYOSVCEPGAAPKQAGHRSAYVPSVADIIQIGWATAAAWSILQQFLLSITFPR	941	
QY	894	FNKSYDYOSVCEPGAAPKQAGHRSAYVPSVADIIQIGWATAAAWSILQQFLLSITFPR	953	
DB	894	FNKSYDYOSVCEPGAAPKQAGHRSAYVPSVADIIQIGWATAAAWSILQQFLLSITFPR	953	
QY	942	LLEAVEMEDDDFTASLSKQSCITEQTFDNDKSFSGVLDCGNCGRIFHGEKLMNTNL	1001	
DB	942	LLEAVEMEDDDFTASLSKQSCITEQTFDNDKSFSGVLDCGNCGRIFHGEKLMNTNL	1001	
QY	954	LLEAVEMEDDDFTASLSKQSCITEQTFDNDKSFSGVLDCGNCGRIFHGEKLMNTNL	1013	
DB	954	LLEAVEMEDDDFTASLSKQSCITEQTFDNDKSFSGVLDCGNCGRIFHGEKLMNTNL	1013	

QY 1002 IFIMVSKGTCPCDTRLLIOAEQTS DSGPNPCDMVK 1036
Db 1014 IFIMVSKGTCPCDTRLLIOAEQTS DSGPNPCDMVK 1048

RESULT 12

US-08-223-305C-53
; Sequence 53, Application US/08223305C
; Patent No. 5851824
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/223,305C
; FILING DATE: April 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,250
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1103 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-223-305C-53

Query Match 98.6%; Score 5367; DB 2; Length 1103;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 1028; Conservative 0; Mismatches 1; Indels 26; Gaps 2;
QY 1 MAAGCLALTLTFLQSLIGPSSSEPPPSAVTIKSWDKMQEDLVTLAKTAGVGNQLVDI 60
Db 1 MAAGCLALTLTFLQSLIGPSSSEPPPSAVTIKSWDKMQEDLVTLAKTAGVGNQLVDI 60
QY 61 YEKYQDLYTVEPNARQVETAAARDIEKLLSNRSKALVSLALEAEKVQAAHWRDFAFN 120
Db 61 YEKYQDLYTVEPNARQVETAAARDIEKLLSNRSKALVSLALEAEKVQAAHWRDFAFN 120
QY 121 EYVYNKADDDLDPEKNDSEPGSQRKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180
Db 121 EYVYNKADDDLDPEKNDSEPGSQRKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180
QY 181 NELNWT SALDEVFKKNREEDPSLLMQVFGSATGLARYYPASPVVDNSRTPNKIDLYDVR 240
Db 181 NELNWT SALDEVFKKNREEDPSLLMQVFGSATGLARYYPASPVVDNSRTPNKIDLYDVR 240
QY 241 RPWYIQGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSLDDDFNVASFNSAQD 300
Db 241 RPWYIQGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSLDDDFNVASFNSAQD 300
QY 301 VSCFOHLYQANVRNKKVLDKAVNNITAGKITDYKKGFSFAFEQLLNVNVRANCKNIIML 360
Db 301 VSCFOHLYQANVRNKKVLDKAVNNITAGKITDYKKGFSFAFEQLLNVNVRANCKNIIML 360
QY 361 FTDGGEERAQEIFNKYKNDKKVRVFRFVSGQHNYPERGPIQMACENKGYEIPISGAIR 420
Db 361 FTDGGEERAQEIFNKYKNDKKVRVFRFVSGQHNYPERGPIQMACENKGYEIPISGAIR 420
QY 421 INTQEYLDVLGRPMVLADGKAKOVQNTVYLDALBELGVITGTLPVNTGTFENKTNLK 480
Db 421 INTQEYLDVLGRPMVLADGKAKOVQNTVYLDALBELGVITGTLPVNTGTFENKTNLK 480
QY 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHLPNLOPK----- 530
Db 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHLPNLOPKPGVGIPTIN 540
QY 531 -----NPKSQBPVTLDFDAELENIDKVEIRKMKIDGESGKTFRTLVKSODERYI 581
Db 541 LRKRPNIQNPKSQBPVTLDFDAELENIDKVEIRKMKIDGESGKTFRTLVKSODERYI 600
QY 582 DKGRTYTWTPVNGTDYSLALVLPYSEYIKAKLEETITQARSKKMKDSETLKPNF 641
Db 601 DKGRTYTWTPVNGTDYSLALVLPYSEYIKAKLEETITQARSKKMKDSETLKPNF 653
QY 642 EESGYTFIAPDYCNDLKI SDNTEFLNFEFIDRKT PNPSCNADLINRVLLDAGFTN 701
Db 654 EESGYTFIAPDYCNDLKI SDNTEFLNFEFIDRKT PNPSCNADLINRVLLDAGFTN 713
QY 702 ELVQNYWSKQNKIKGVKARFVVDGGITRVYPKEAGENQENPETEYDSFYKRSLDNRY 761
Db 714 ELVQNYWSKQNKIKGVKARFVVDGGITRVYPKEAGENQENPETEYDSFYKRSLDNRY 773
QY 762 VETAPYFNKSGPGAYESGIMVSKAVEIYIQGLKLPVAVGKIDVNSWENFTKTSIRDP 821
Db 774 VETAPYFNKSGPGAYESGIMVSKAVEIYIQGLKLPVAVGKIDVNSWENFTKTSIRDP 833
QY 822 CAGPVCDCKRNSDVMDCVILDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI SYA 881
Db 834 CAGPVCDCKRNSDVMDCVILDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI SYA 893
QY 882 FNKSYDYOSVCEPGAAPKQAGHRSAVYPSVADIIQIGWATAAASIIQQFLLSLTTPR 941
Db 894 FNKSYDYOSVCEPGAAPKQAGHRSAVYPSVADIIQIGWATAAASIIQQFLLSLTTPR 953
QY 942 LLEAVEMEDDDFTASLSKOSCTEQTEQYFFDNDKSFSGVLDGCGNCSRFHGEKLMNTNL 1001
Db 954 LLEAVEMEDDDFTASLSKOSCTEQTEQYFFDNDKSFSGVLDGCGNCSRFHGEKLMNTNL 1013
QY 1002 IFIMVSKGTCPCDTRLLIOAEQTS DSGPNPCDMVK 1036

Db 1014 IFIMVESKGTCPDTRLLIOAEQTSDBGNPCDMVK 1048
|||||
RESULT 13
US-08-455-543A-55
; Sequence 55, Application US/0845543A
; Patent No. 5792846
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08455,543A
; FILING DATE: May 31, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/223,305
; FILING DATE: April 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,250
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-52517
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1079 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-455-543A-55

Query Match		98.28;	Score 5347;	DB 1;	Length 1079;
Best Local Similarity		98.7%;	Pred. No. 0;		
Matches 1023;		Conservative	0;	Mismatches 1;	Indels 12;
		Gaps 2;			
Qy	1	MAAGCLLALTLTLFOSLLIGSPSEPPFP	SAVTIKSWDKMQEDLVTLAKTAGSVNQLVDI	60	
Db	1	MAAGCLLALTLTLFOSLLIGSPSEPPFP	SAVTIKSWDKMQEDLVTLAKTAGSVNQLVDI	60	
Qy	61	YEKYQDLYTVEPNNAQQLVEIAARDIEK	LLSNRSKALVSLEAEKVQAAHQRDEFSN	120	
Db	61	YEKYQDLYTVEPNNAQQLVEIAARDIEK	LLSNRSKALVSLEAEKVQAAHQRDEFSN	120	
Qy	121	EYVYNKADDDLDPEKNDSEPGSQRIKPV	IEDANFGRQISYOHAAVHIPTDIYEGSTIVL	180	
Db	121	EYVYNKADDDLDPEKNDSEPGSQRIKPV	IEDANFGRQISYOHAAVHIPTDIYEGSTIVL	180	
Qy	181	NELNWTSAALDEVEFKKREEDPSLLQVFG	SATGLARYYPASPWVDSNRTPNKIDLYDVR	240	
Db	181	NELNWTSAALDEVEFKKREEDPSLLQVFG	SATGLARYYPASPWVDSNRTPNKIDLYDVR	240	
Qy	241	RPWYIQGAASPMDLILVDVSGVSLTLKL	IRTSVSEMLETSSDDDFVNVASFNSNAOD	300	
Db	241	RPWYIQGAASPMDLILVDVSGVSLTLKL	IRTSVSEMLETSSDDDFVNVASFNSNAOD	300	
Qy	301	VSCFQHLVQANVRNKKVLDKAVNNITAK	ITDYKKGFSFAPFOLLNRYNSRANCNKIIML	360	
Db	301	VSCFQHLVQANVRNKKVLDKAVNNITAK	ITDYKKGFSFAPFOLLNRYNSRANCNKIIML	360	
Qy	361	FTDGGEEAQAEIFNKYNKDKYVRFESY	GHOHNYERGPIOWMACENKGYEYIETPSIGAIR	420	
Db	361	FTDGGEEAQAEIFNKYNKDKYVRFESY	GHOHNYERGPIOWMACENKGYEYIETPSIGAIR	420	
Qy	421	INTQEYLDVLGRPMVLGDKAKQVQWNT	NYLDLDALEGLVITGTPLVENITGQENKTNL	480	
Db	421	INTQEYLDVLGRPMVLGDKAKQVQWNT	NYLDLDALEGLVITGTPLVENITGQENKTNL	480	
Qy	481	NQILGVMGVDVSLEDIKRLTPRFTLCP	NGYYPADPNQVYVLLHPNLPKNSQEPVTL	540	
Db	481	NQILGVMGVDVSLEDIKRLTPRFTLCP	NGYYPADPNQVYVLLHPNLPKNSQEPVTL	540	
Qy	541	DFLDAELENDIKVEIRKMKIDGESGK	FTFLVKSODERYIDKGNRTYTTPVNGTDYSL	600	
Db	541	DFLDAELENDIKVEIRKMKIDGESGK	FTFLVKSODERYIDKGNRTYTTPVNGTDYSL	600	
Qy	595	DFLDAELENDIKVEIRKMKIDGESGK	FTFLVKSODERYIDKGNRTYTTPVNGTDYSL	595	
Db	595	DFLDAELENDIKVEIRKMKIDGESGK	FTFLVKSODERYIDKGNRTYTTPVNGTDYSL	595	
Qy	601	ALVLPYTFYIIKAKLEETITQARSKK	MDSETLKPDNFESGYTTFIAPROYCNDLKI	660	
Db	601	ALVLPYTFYIIKAKLEETITQARSKK	MDSETLKPDNFESGYTTFIAPROYCNDLKI	660	
Qy	648	ALVLPYTFYIIKAKLEETITQARSKK	MDSETLKPDNFESGYTTFIAPROYCNDLKI	648	
Db	648	ALVLPYTFYIIKAKLEETITQARSKK	MDSETLKPDNFESGYTTFIAPROYCNDLKI	648	
Qy	661	SDNTEFLNFEFIDRKTPNPNFSCNAD	LINRVLLDAGFTNELVQVYVWSKOKIKGVKAR	720	
Db	661	SDNTEFLNFEFIDRKTPNPNFSCNAD	LINRVLLDAGFTNELVQVYVWSKOKIKGVKAR	720	
Qy	708	SDNTEFLNFEFIDRKTPNPNFSCNAD	LINRVLLDAGFTNELVQVYVWSKOKIKGVKAR	708	
Db	708	SDNTEFLNFEFIDRKTPNPNFSCNAD	LINRVLLDAGFTNELVQVYVWSKOKIKGVKAR	708	
Qy	721	FVYTDGGITRVYPKEAGENQENPET	YEDSFYKRSLDNDNVFTAPYFNKSGPGAYESGI	780	
Db	721	FVYTDGGITRVYPKEAGENQENPET	YEDSFYKRSLDNDNVFTAPYFNKSGPGAYESGI	780	
Qy	768	FVYTDGGITRVYPKEAGENQENPET	YEDSFYKRSLDNDNVFTAPYFNKSGPGAYESGI	768	
Db	768	FVYTDGGITRVYPKEAGENQENPET	YEDSFYKRSLDNDNVFTAPYFNKSGPGAYESGI	768	
Qy	781	MVSKAVEIYIQGKLLKPAVVGVGKI	DVNSWIENFTKTSIRDPACGVCDCRNSDVMDCVI	840	
Db	781	MVSKAVEIYIQGKLLKPAVVGVGKI	DVNSWIENFTKTSIRDPACGVCDCRNSDVMDCVI	840	
Qy	828	MVSKAVEIYIQGKLLKPAVVGVGKI	DVNSWIENFTKTSIRDPACGVCDCRNSDVMDCVI	828	
Db	828	MVSKAVEIYIQGKLLKPAVVGVGKI	DVNSWIENFTKTSIRDPACGVCDCRNSDVMDCVI	828	
Qy	841	LDGGFLLMANHDDYTQIGRFFGEIDP	SLMRHLVNSVYAFNKSVDYQSVCEPGAAPKQ	900	
Db	841	LDGGFLLMANHDDYTQIGRFFGEIDP	SLMRHLVNSVYAFNKSVDYQSVCEPGAAPKQ	900	
Qy	888	LDGGFLLMANHDDYTQIGRFFGEIDP	SLMRHLVNSVYAFNKSVDYQSVCEPGAAPKQ	888	
Db	888	LDGGFLLMANHDDYTQIGRFFGEIDP	SLMRHLVNSVYAFNKSVDYQSVCEPGAAPKQ	888	
Qy	901	GAGHRSAYVPSVADILQIGWATAA	WSILQOFLLSLTFPRLLEAVEMEDDDFTASLSKQ	960	
Db	901	GAGHRSAYVPSVADILQIGWATAA	WSILQOFLLSLTFPRLLEAVEMEDDDFTASLSKQ	960	
Qy	948	GAGHRSAYVPSVADILQIGWATAA	WSILQOFLLSLTFPRLLEAVEMEDDDFTASLSKQ	948	
Db	948	GAGHRSAYVPSVADILQIGWATAA	WSILQOFLLSLTFPRLLEAVEMEDDDFTASLSKQ	948	
Qy	961	SCITEQTYQFFDNDKSFSGVLDG	CNCSRIIPHGBKLMNTNLIIFIMVSKGTCPCDTRLLI	1020	
Db	961	SCITEQTYQFFDNDKSFSGVLDG	CNCSRIIPHGBKLMNTNLIIFIMVSKGTCPCDTRLLI	1020	
Qy	1008	SCITEQTYQFFDNDKSFSGVLDG	CNCSRIIPHGBKLMNTNLIIFIMVSKGTCPCDTRLLI	1008	
Db	1008	SCITEQTYQFFDNDKSFSGVLDG	CNCSRIIPHGBKLMNTNLIIFIMVSKGTCPCDTRLLI	1008	

QY 1021 QAEOTSDGNPCDMVK 1036
Db 1009 QAEOTSDGNPCDMVK 1024

RESULT 14

US-08-223-305C-55
Sequence 55, Application US/08223305C
Patent No. 5851824

GENERAL INFORMATION:

APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert

TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

TITLE OF INVENTION: METHODS

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Martin, Haller & McClain

STREET: 1660 Union Street

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/223,305C

FILING DATE: April 4, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/868,354

FILING DATE: April 10, 1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/745,206

FILING DATE: 15-AUG-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/620,250

FILING DATE: 30-NOV-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/482,384

FILING DATE: 20-FEB-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/603,751

FILING DATE: 04-APR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US89/01408

FILING DATE: 04-APR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/176,899

FILING DATE: 04-APR-1988

ATTORNEY/AGENT INFORMATION:

NAME: Seigman, Stephanie L.

REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 52516 (P519739)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619)238-0999

TELEFAX: (619)238-0062

INFORMATION FOR SEQ ID NO: 55:

SEQUENCE CHARACTERISTICS:

LENGTH: 1079 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

US-08-223-305C-55

Query Match 98.2%; Score 5347; DB 2; Length 1079;
Best Local Similarity 98.7%; Pred No. 0;
Matches 1023; Conservative 0; Mismatches 1; Indels 12; Gaps 2;

QY	1	MAAGCLLALTTLTFLQSLIGPSSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI	60
Db	1	MAAGCLLALTTLTFLQSLIGPSSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI	60
QY	61	YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDFASN	120
Db	61	YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDFASN	120
QY	121	EVYYNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROIYSQYHAAVHIPTDIYEGSTIVL	180
Db	121	EVYYNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROIYSQYHAAVHIPTDIYEGSTIVL	180
QY	181	NELNWTSSALDEVFKKNREEDPSLLMQVFGSATGLARYYPASVPWVDSNRTPNKIDLYVRR	240
Db	181	NELNWTSSALDEVFKKNREEDPSLLMQVFGSATGLARYYPASVPWVDSNRTPNKIDLYVRR	240
QY	241	RPWYIQGAASPKDMLILVDVSGSVSGLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD	300
Db	241	RPWYIQGAASPKDMLILVDVSGSVSGLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD	300
QY	301	VSCFOHLYQANVRNKKVLKDAVNNTAKGITDYKKGFSFAPFQQLLNYNVSRANCKNIIML	360
Db	301	VSCFOHLYQANVRNKKVLKDAVNNTAKGITDYKKGFSFAPFQQLLNYNVSRANCKNIIML	360
QY	361	FTDGEERAQEIFNKYNKDKKVRVFRFSVGHNYERGPQIOMACENKGYIYIPISGAIR	420
Db	361	FTDGEERAQEIFNKYNKDKKVRVFRFSVGHNYERGPQIOMACENKGYIYIPISGAIR	420
QY	421	INTQYLDVLRPMVLADGKAKQVQWNTWYLDALGLVITGTLVPFNITGOFENKTNLK	480
Db	421	INTQYLDVLRPMVLADGKAKQVQWNTWYLDALGLVITGTLVPFNITGOFENKTNLK	480
QY	481	NOLILGVNGVDVSLIEDIKRLTPRETLCPNGYFAIDPNGYVLLHNPLOPKPKSEPTVL	540
Db	481	NOLILGVNGVDVSLIEDIKRLTPRETLCPNGYFAIDPNGYVLLHNPLOPKPKSEPTVL	540
QY	541	DFDLAELENDIKVEIRNKMIDGESGEKTFRTLVKSDQERYIDKGNRTYTWTVPNGTDYSL	600
Db	536	DFDLAELENDIKVEIRNKMIDGESGEKTFRTLVKSDQERYIDKGNRTYTWTVPNGTDYSL	595
QY	601	ALVLPYTFYIYIKAKLEETITQARY-----SETLKPDPNFEEGYTFIAPRDYCNLKI	660
Db	596	ALVLPYTFYIYIKAKLEETITQARY-----SETLKPDPNFEEGYTFIAPRDYCNLKI	648
QY	661	SDNTEFLLNNEFIDRKTNNPNSCNADLINRVLDAGFTNELVONYKSKOKNIKGVKAR	720
Db	649	SDNTEFLLNNEFIDRKTNNPNSCNADLINRVLDAGFTNELVONYKSKOKNIKGVKAR	708
QY	721	FVVTGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESI	780
Db	709	FVVTGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESI	768
QY	781	MYSKAVEIYIOGKLLKPAVVGKIDVNSWNIENFTTSIRDPKAGVPCDCKRNSDVCVI	840
Db	769	MYSKAVEIYIOGKLLKPAVVGKIDVNSWNIENFTTSIRDPKAGVPCDCKRNSDVCVI	828
QY	841	LDDGGFLMANHDDYTNOIGRFFGIDPDLMLRHLNINISVYAFNKSDYQSVCEPGAAPKQ	900
Db	829	LDDGGFLMANHDDYTNOIGRFFGIDPDLMLRHLNINISVYAFNKSDYQSVCEPGAAPKQ	888
QY	901	GAGHSAYVPSVADILQIGWATAAAWSILQQLFLLSLTFPRLEAVEMEDDDFTASLSKQ	960
Db	889	GAGHSAYVPSVADILQIGWATAAAWSILQQLFLLSLTFPRLEAVEMEDDDFTASLSKQ	948
QY	961	SCITEQTQYFFDNDKSKFSGVLDCCGNCRIHFHGEKMLNTNLIIFIMVESKGTCPDTRLLI	1020
Db	949	SCITEQTQYFFDNDKSKFSGVLDCCGNCRIHFHGEKMLNTNLIIFIMVESKGTCPDTRLLI	1008

Qy 1021 QAEQTSQGNPCDMVK 1036
Db 1009 QAEQTSQGNPCDMVK 1024

RESULT 15

US-08-435-675B-5
; Sequence 5, Application US/08435675B
; Patent No. 5710250
; GENERAL INFORMATION:
; APPLICANT: Ellis, Steven Bradley
; APPLICANT: Williams, Mark E.
; APPLICANT: Harpold, Michael Miller
; APPLICANT: Schwartz, Arnold
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,675B
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,083
; FILING DATE: 28-SEP-1994
; APPLICATION NUMBER: US 07/914,231
; FILING DATE: 13-JUL-1992
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 08-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-53193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1106 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-435-675B-5

Query Match 96.1%; Score 5229.5; DB 1; Length 1106;
Best Local Similarity 94.8%; Pred. No. 0;
Matches 1003; Conservative 14; Mismatches 12; Indels 29; Gaps 4;

Qy 1 MAAGCLLALTLFQS--LLIGSPSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLV 58
Db 1 MAAGRPLATLILQAWLILIGSPSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLV 60
Qy 59 DIYEKQDLYTVEPNARQLVEIARDEIKLLSNRSKALVSLALEAEKQVAAHQWREDA 118
Db 61 DIYEKQDLYTVEPNARQLVEIARDEIKLLSNRSKALVRLALEAEKQVAAHQWREDA 120
Qy 119 SNEVYYNAKDDLPKNDSEPGSQRIKPVFDDANFRQVSYQHAHVHIPTDIYEGSTI 178

Db 121 SNEVYYNAKDDLPKNDSEPGSQRIKPVFDDANFRQVSYQHAHVHIPTDIYEGSTI 180
Qy 179 VLNELNWTSALEDEVKKNREEDPSLLMQVFGSATGLARIYPASPPWVDSNRTNPKIDLYDV 238
Db 181 VLNELNWTSALEDEVKKNREEDPSLLMQVFGSATGLARIYPASPPWVDSNRTNPKIDLYDV 240
Qy 239 RRPWYIOGAASPDKMLILVDVSGVSGTLLKLRISVSEMLETSDDDDFVNVASFNSNA 298
Db 241 RRPWYIOGAASPDKMLILVDVSGVSGTLLKLRISVSEMLETSDDDDFVNVASFNSNA 300
Qy 299 QDVSCFQHLVQANVRNKKVLDVANNITAKGIDTKKGFSAFEQLLNINVRANCKII 358
Db 301 QDVSCFQHLVQANVRNKKVLDVANNITAKGIDTKKGFSAFEQLLNINVRANCKII 360
Qy 359 MLFTDGGERAQEIENKYNKDKVRVFRFVSGOHNVREPIQWMACENKGYIYEIPSIGA 418
Db 361 MLFTDGGERAQEIENKYNKDKVRVFRFVSGOHNVREPIQWMACENKGYIYEIPSIGA 420
Qy 419 IRINTQEYLDVLGRPMVLADGAKAKOVQWTVNYLDALGLVITGTLVPFNITGQFENKTN 478
Db 421 IRINTQEYLDVLGRPMVLADGAKAKOVQWTVNYLDALGLVITGTLVPFNITGQFENKTN 480
Qy 479 LKNQLILGVMGVDVSLIEDIKRLTPRTFLCPNGYIFAIDPNGYVLLHPNLQPK----- 530
Db 481 LKNQLILGVMGVDVSLIEDIKRLTPRTFLCPNGYIFAIDPNGYVLLHPNLQPKIGVGIPT 540
Qy 531 -----NPKSQEPVTLDFDAELENDIKVEIRNKMIDGESGEKFTRLVKSQDER 579
Db 541 INLRKRRPNVQPKSQEPVTLDFDAELENDIKVEIRNKMIDGESGEKFTRLVKSQDER 600
Qy 580 YIDKGNRTYTWTPVNGTDY-SIALVLPYTFYIYKAKLEETITQARSKGKKMKDSTLKP 638
Db 601 YIDKGNRTYTWTPVNGTDYSSIALVLPYTFYIYKAKIEETITQARY-----SETLKP 653
Qy 639 DNFEESGYTFIAPRDYCNLDKISDNTEFLNPNFNEIDRKTNNPNSCNADLINRVLLDAG 698
Db 654 DNFEESGYTFIAPRDYCNLDKISDNTEFLNPNFNEIDRKTNNPNSCNADLINRVLLDAG 713
Qy 699 FTNELVQNYWSKOKNITGVKARFVVDGGITRVYKPEAGENMOENPETEYDSYKKSLOD 758
Db 714 FTNELVQNYWSKOKNITGVKARFVVDGGITRVYKPEAGENMOENPETEYDSYKKSLOD 773
Qy 759 DNYVFTAPYFNKSGPGAYESGIMVSKAVEYIOGKLLKPAVVGKIDVNSWIENFTKTSI 818
Db 774 DNYVFTAPYFNKSGPGAYESGIMVSKAVEYIOGKLLKPAVVGKIDVNSWIENFTKTSI 833
Qy 819 RDPGAGPVCDCRNSDVMDCVILDDGGFLIMANHDDYTQIGRFFGEIDPFLMRHLVNIS 878
Db 834 RDPGAGPVCDCRNSDVMDCVILDDGGFLIMANHDDYTQIGRFFGEIDPFLMRHLVNIS 893
Qy 879 VYAFNKSVDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAANSILOQFLLSLT 938
Db 894 VYAFNKSVDYQSVCEPGAAPKQAGHRSAYVPSIADILQIGWATAAANSILOQFLLSLT 953
Qy 939 FPLLEAVEMEDDDFTASLSKQSCITEQTYFFDNDPSKSGVLDGCGNCSRIHFGEKLMN 998
Db 954 FPLLEAVEMEDDDFTASLSKQSCITEQTYFFDNDPSKSGVLDGCGNCSRIHFGEKLMN 1013
Qy 999 TNLIFTWVESKGTCPCDTRLLIOAEQTSQGNPCDMVK 1036
Db 1014 TNLIFTWVESKGTCPCDTRLLIOAEQTSQGNPCDMVK 1051

Search completed: July 23, 2001, 07:39:05
Job time: 532 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 23, 2001, 07:37:58 ; Search time 84.28 Seconds

(without alignments)
936.365 Million cell updates/sec

Title: US-09-397-548-16

Perfect score: 5443

Sequence: 1 MAACLLALTLTFLQSLIG.....RLLIQAQTSQGNPCDMVK 1036

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_68:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5443	100.0	1091	2 JH0565	calcium channel al
2	5234	96.2	1091	2 A44147	calcium channel pr
3	5224.5	96.0	1106	1 CHRBA2	calcium channel al
4	1085	19.9	1091	2 T30256	calcium channel al
5	607	11.2	734	2 S44617	C50C3.11 protein
6	572	10.5	1148	2 T18770	probable calcium c
7	198	3.6	1450	2 C86880	hypothetical prote
8	194.5	3.6	886	2 S54355	inter-alpha-trypsi
9	185	3.4	885	2 S30350	inter-alpha-trypsi
10	164.5	3.0	889	2 JC5576	inter-alpha-trypsi
11	161	3.0	2706	2 T28155	variant-specific s
12	159	2.9	1984	2 A44396	p-type cation tran
13	157.5	2.9	575	2 D64998	hypothetical prote
14	155	2.8	1516	2 E71619	RAD2 endonuclease
15	155	2.8	2364	2 I40884	cytotoxin L - clos
16	154.5	2.8	946	1 IYH02	inter-alpha-trypsi
17	154.5	2.8	1315	2 T28679	inter-alpha-trypsi
18	153	2.8	932	2 JC5953	inter-alpha-inhibi
19	152	2.8	1291	2 S46431	botulinum neurotox
20	152	2.8	1291	2 A49777	botulinum neurotox
21	151.5	2.8	420	2 S76691	hypothetical prote
22	150.5	2.8	921	2 JC4625	inter-alpha-trypsi
23	150	2.8	634	2 A69856	methyl-accepting c
24	149	2.7	459	2 F64688	proteinase (ec 3.4
25	149	2.7	930	2 JX0368	inter-alpha-trypsi
26	148.5	2.7	2401	2 T28676	inter-alpha-trypsi
27	148	2.7	964	2 S25855	DNA-directed DNA p
28	146.5	2.7	1285	2 E72420	hypothetical prote
29	146	2.7	4688	2 F82885	hypothetical prote

30	145.5	2.7	676	2 T47637	hypothetical prote
31	145.5	2.7	689	2 F84811	probable retroelom
32	145.5	2.7	5005	2 F82884	hypothetical prote
33	144	2.6	1087	1 S41797	cellulose 1,4-beta
34	144	2.6	1091	2 S33850	fibronectin-binding
35	143	2.6	946	2 JC5575	inter-alpha-trypsi
36	143	2.6	1864	2 T18485	hypothetical prote
37	142.5	2.6	382	2 S44618	C50C3.10 protein -
38	142	2.6	1169	2 A64505	p115 homolog - Met
39	142	2.6	1599	2 S22737	glucosyltransferas
40	141	2.6	1252	2 B42771	reticulocyte-bind
41	140.5	2.6	2369	2 T28677	rhodry protein -
42	140	2.6	2710	2 A37052	toxin A - Clostrid
43	140	2.6	3305	2 T18358	apolipoprotein prec
44	139.5	2.6	764	2 I39934	protective antigen
45	139	2.6	1180	2 A26858	parasporal crystal

ALIGNMENTS

RESULT 1

JH0565
calcium channel alpha-2b chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug-1999
C:Accession: JH0565
R:Williams, M.E.; Feldman, D.H.; McCue, A.F.; Brenner, R.; Velicelebi, G.; Ellis, S.B
Neuron 8, 71-84, 1992
A:Title: Structure and functional expression of alpha1, alpha2, and beta subunits of
A:Reference number: JH0564; MUID:92110010
A:Accession: JH0565
A:Molecule type: mRNA
A:Residues: 1-1091 <MWL>
A:Cross-references: GB:M76559; NID:g179761; PIDN:AAA51903.1; PID:g179762
A:Experimental source: basal ganglia
A:Note: several conflicts are found between GenBank submission, authors' translation
C:Comment: This protein is a subunit of the voltage dependent calcium channel.
C:Superfamily: calcium channel alpha-2 chain
C:Keywords: glycoprotein; phosphoprotein
F:1-24/Domain: signal sequence #status Predicted <SIG>
F:25-1067/Product: calcium channel alpha-2b chain #status predicted <CAL>
F:32,268,326,539,635,1087/Binding site: phosphate (Thr) (covalent) (by protein kinase
F:91,142,250,625,817/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #
F:92,136,184,324,348,468,475,585,594,663,682,769,812,876,883,973,986/Binding site: ca
F:501/Binding site: phosphate (Thr) (covalent) #status predicted
F:833/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status pre

Query Match 100.0%; Score 5443; DB 2; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MAACLLALTLTFLQSLIGSPSEPPPSAVTIKSWDKMOEDLVTLAKTAGVNLVDI	60
DB	1	MAACLLALTLTFLQSLIGSPSEPPPSAVTIKSWDKMOEDLVTLAKTAGVNLVDI	60
QY	61	YEKYQDLYTVEPNARQLVEITAARDIEKLSNRKALVSLALEAEKVAQAHHQWREDFASN	120
DB	61	YEKYQDLYTVEPNARQLVEITAARDIEKLSNRKALVSLALEAEKVAQAHHQWREDFASN	120
QY	121	EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROISYQHAHVHPTDIYEGSTIVL	180
DB	121	EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROISYQHAHVHPTDIYEGSTIVL	180
QY	181	NELNWTALDEVFVKKNREDEPSLLMQVFGSATGLARYYPASPWDNSRTPNKIDLYDVR	240
DB	181	NELNWTALDEVFVKKNREDEPSLLMQVFGSATGLARYYPASPWDNSRTPNKIDLYDVR	240
QY	241	RPWTIQGAASPKDMILILVDVSGVSGGLTKLIRTSVSEMLETSLDDDDFVNVASFNSAQD	300
DB	241	RPWTIQGAASPKDMILILVDVSGVSGGLTKLIRTSVSEMLETSLDDDDFVNVASFNSAQD	300

QY 301 VSCFQRLVQANVRNKKVLKDAVNNTAKGIDYKKGFSFAFEQLLNLYNVRANCKNIIML 360
DB 301 VSCFQRLVQANVRNKKVLKDAVNNTAKGIDYKKGFSFAFEQLLNLYNVRANCKNIIML 360
QY 361 FTDGGEERAQEIFNKNYKDKKVRVFRFVSGQHNRYERGPIQMACENKGYIYEIPISGAIR 420
DB 361 FTDGGEERAQEIFNKNYKDKKVRVFRFVSGQHNRYERGPIQMACENKGYIYEIPISGAIR 420
QY 421 INTQEVLDVLRPMVLGDKAKQVQWNTVYLDALGLVITGTLVFNITGOFENKTNLK 480
DB 421 INTQEVLDVLRPMVLGDKAKQVQWNTVYLDALGLVITGTLVFNITGOFENKTNLK 480
QY 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHLPNLPKPKSQEPVTL 540
DB 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHLPNLPKPKSQEPVTL 540
QY 541 DFLDAELENDAKVEIRNKMIDGESGEKFTRLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600
DB 541 DFLDAELENDAKVEIRNKMIDGESGEKFTRLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600
QY 601 ALVLPYTSFYIYKAKLEETITQARSKKGMKDSKSETLKPDPNFEESGYTFTAPRDYCNLKI 660
DB 601 ALVLPYTSFYIYKAKLEETITQARSKKGMKDSKSETLKPDPNFEESGYTFTAPRDYCNLKI 660
QY 661 SDNNTFLLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELYQVYWSKQKNIKGVKAR 720
DB 661 SDNNTFLLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELYQVYWSKQKNIKGVKAR 720
QY 721 FVVTGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNRYFTAPYKPKSGPGAYESGI 780
DB 721 FVVTGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNRYFTAPYKPKSGPGAYESGI 780
QY 781 MYSKAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGPVCCKRNSDVMDCVI 840
DB 781 MYSKAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGPVCCKRNSDVMDCVI 840
QY 841 LDGCGFLLMANHDDYTNOIGRFFGEIDPSLMRHLNYSVYAFNKSQYDQVCEPGAAPKQ 900
DB 841 LDGCGFLLMANHDDYTNOIGRFFGEIDPSLMRHLNYSVYAFNKSQYDQVCEPGAAPKQ 900
QY 901 GAGHSAYVPSVADILQIGWATAAASILQOFLSLTFFPRLLLEAVEMEDDDFTASLSKQ 960
DB 901 GAGHSAYVPSVADILQIGWATAAASILQOFLSLTFFPRLLLEAVEMEDDDFTASLSKQ 960
QY 961 SCITEQTYFFDNDKSGVLDGCGNCSRIHFHGEKLMNTNLIFIMVESKGTGCPDTRLLI 1020
DB 961 SCITEQTYFFDNDKSGVLDGCGNCSRIHFHGEKLMNTNLIFIMVESKGTGCPDTRLLI 1020
QY 1021 QAEQTSQDGNPCDMVK 1036
DB 1021 QAEQTSQDGNPCDMVK 1036
RESULT 2
A44147
calcium channel protein alpha-2 chain precursor - rat
N:Alternate names: dihydropyridine-sensitive L-type
C:Contains: calcium channel alpha-2 chain
C:Species: Rattus norvegicus (Norway rat)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 20-Aug-1999
C:Accession: A44147
R:Kim, H.L.; Kim, H.; Lee, P.; King, R.G.; Chin, H.
Proc. Natl. Acad. Sci. U.S.A. 89, 3251-3255, 1992
A:Title: Rat brain expresses an alternatively spliced form of the dihydropyridine-sensitive
A:Reference number: A44147; MUID:92228762
A:Accession: A44147
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1091 <KIM>
A:Cross-references: GB:M86621; NID:g203954; PIDN:AAA41088.1; PID:g203955
C:Superfamily: calcium channel alpha-2 chain
C:Keywords: calcium; glycoprotein; ion channel; transmembrane protein

Query Match 96.28; Score 5234; DB 2; Length 1091;
Best Local Similarity 95.78; Pred. No. 0;
Matches 992; Conservative 24; Mismatches 19; Indels 2; Gaps 2;

QY 1 MAAGCLLALTTLTFLQSLTLPSSSEPPFSAVTIKSWDKMQEDLVTLAKTAGSVNQLYDI 60
DB 1 MAAGCLLALTTLTFLQSLTLPSSSEPPFSAVTIKSWDKMQEDLVTLAKTAGSVTQLADI 60
QY 61 YEKYQDLTYVEPNARQOLVEAARDIEKLLSNRSKALYSALAEKVOAAHQRDEFSAN 120
DB 61 YEKYQDLTYVEPNARQOLVEAARDIEKLLSNRSKALYLAAMEKVOAAHQRDEFSAN 120
QY 121 EWWYNKADDDLPKENDSPGSQRIKPVFIEDANFGROIYSQHAHVHTDIYEESTIVL 180
DB 121 EWWYNKADDDLPKENDSPGSQRIKPVFIEDANFGROIYSQHAHVHTDIYEESTIVL 180
QY 181 NELNWTALDEYFVKKNREEDPSLLMQVFGSATGLARYYPASPDVNSRTPNKKIDLYDVR 240
DB 181 NELNWTALDEYFVKKNREEDPSLLMQVFGSATGLARYYPASPDVNSRTPNKKIDLYDVR 240
QY 241 RPWYTOGAASPKDMLILVDVSGVSGLTCLKLIRTSVSEMLETSLDDDFVNVASFNSAQD 300
DB 241 RPWYTOGAASPKDMLILVDVSGVSGLTCLKLIRTSVSEMLETSLDDDFVNVASFNSAQD 300
QY 301 VSCFOHLVQANVRNKKVLKDAVNNTAKGIDYKKGFSFAFEQLLNLYNVRANCKNIIML 360
DB 301 VSCFOHLVQANVRNKKVLKDAVNNTAKGIDYKKGFSFAFEQLLNLYNVRANCKNIIML 360
QY 361 FTDGGEERAQEIFNKNYKDKKVRVFRFVSGQHNRYERGPIQMACENKGYIYEIPISGAIR 420
DB 361 FTDGGEERAQEIFNKNYKDKKVRVFRFVSGQHNRYERGPIQMACENKGYIYEIPISGAIR 420
QY 421 INTQEVLDVLRPMVLGDKAKQVQWNTVYLDALGLVITGTLVFNITGOFENKTNLK 480
DB 421 INTQEVLDVLRPMVLGDKAKQVQWNTVYLDALGLVITGTLVFNITGOFENKTNLK 480
QY 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHLPNLPKPKSQEPVTL 540
DB 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHLPNLPKPKSQEPVTL 540
QY 541 DFLDAELENDAKVEIRNKMIDGESGEKFTRLVKSQDERYIDKGNRTYTWTPVNGTDYS - 599
DB 541 DFLDAELENDAKVEIRNKMIDGESGEKFTRLVKSQDERYIDKGNRTYTWTPVNGTDYS 599
QY 600 LALVLPYTSFYIYKAKLEETITQARSKKGMKDSKSETLKPDPNFEESGYTFTAPRDYCNL 659
DB 600 LALVLPYTSFYIYKAKLEETITQARSKKGMKDSKSETLKPDPNFEESGYTFTAPRDYCNL 659
QY 660 ISDNNTFLLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELYQVYWSKQKNIKGVK 719
DB 660 ISDNNTFLLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELYQVYWSKQKNIKGVK 719
QY 720 RFVVTGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNRYFTAPYKPKSGPGAYESG 779
DB 720 RFVVTGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNRYFTAPYKPKSGPGAYESG 779
QY 780 IMVSKAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGPVCCKRNSDVMDCV 839
DB 780 IMVSKAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGPVCCKRNSDVMDCV 839
QY 840 ILDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLNYSVYAFNKSQYDQVCEPGAAPK 899
DB 840 ILDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLNYSVYAFNKSQYDQVCEPGAAPK 899
QY 900 QGAGHSAYVPSVADILQIGWATAAASILQOFLSLTFFPRLLLEAVEMEDDDFTASLSK 959
DB 900 QGAGHSAYVPSVADILQIGWATAAASILQOFLSLTFFPRLLLEAVEMEDDDFTASLSK 959
QY 960 QSCITEQTYFFDNDKSGVLDGCGNCSRIHFHGEKLMNTNLIFIMVESKGTGCPDTRLL 1019
DB 960 QSCITEQTYFFDNDKSGVLDGCGNCSRIHFHGEKLMNTNLIFIMVESKGTGCPDTRLL 1019

QY 1020 IQAEOTSDGPNPCDMVK 1036
 Db 1020 MQAEQTSDDGPDPCDMVK 1036

RESULT 3
 CHRB2
 calcium channel protein alpha-2 chain precursor - rabbit
 N:Alternate names: dihydropyridine-binding protein, 140K
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 22-Jun-1999
 R:Ellis, S.B.; Williams, M.E.; Ways, N.R.; Brenner, R.; Sharp, A.H.; Leung, A.T.; Campbell
 Science 241, 1661-1664, 1988
 A:Title: Sequence and expression of mRNAs encoding the alpha(1) and alpha(2) subunits of
 A:Reference number: S10579; MUID:88336904
 A:Accession: S10579
 A:Molecule type: mRNA
 A:Residues: 1-1106 <ELL>
 A:Cross-references: EMBL:M21948; NID:g164762; PIDN:AAA81562.1; PID:g164763
 A:Note: 57-Asn, 106-Lys, and deletion of 620-Ser were also found
 R:Jay, S.D.; Sharp, A.H.; Kahl, S.D.; Vedvick, T.S.; Harpold, M.M.; Campbell, K.P.
 J. Biol. Chem. 266, 3287-3293, 1991
 A:Title: Structural characterization of the dihydropyridine-sensitive calcium channel al
 A:Reference number: A39518; MUID:91131638
 A:Accession: A39518
 A:Molecule type: protein
 A:Residues: 961-973 <JAY>
 A:Note: This sequence represents the amino end of a glycosylated peptide that appears at
 e at the amino end and identical molecular weights (17K) following deglycosylation
 R:Hamilton, S.L.; Hawkes, M.J.; Brush, K.; Cook, R.
 Biochemistry 28, 7820-7828, 1989
 A:Title: Subunit composition of the purified dihydropyridine binding protein from skelet
 A:Reference number: A33409; MUID:90122765
 A:Accession: A33409
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 27-44, 'S', 46-47 <HAM>
 C:Superfamily: calcium channel alpha-2 chain
 C:Keywords: calcium; disulfide bond; glycoprotein; ion channel; membrane protein; phosph
 F:1-26/Domain: signal sequence #status predicted <SIG>
 F:27-1106/Product: calcium channel alpha-2 chain #status predicted <MAT>
 F:94,138,186,326,350,470,477,606,615,678,697,784,827,891,898,1001,1081,1081,1081 Binding site:

Query Match 96.0%; Score 5224.5; DB 1; Length 1106;
 Best Local Similarity 94.7%; Pred. No. 0;
 Matches 1002; Conservative 15; Mismatches 12; Indels 29; Gaps 4;

QY 1 MAAGCLLTLFQSG--LLIGPSSEPPPSAVTIKSWYDKMOEDLVTLAKTAGVGNQLV 58
 Db 1 MAAGRPLATLQAWLLIGPSSEPPPSAVTIKSWYDKMOEDLVTLAKTAGVHQLV 60

QY 59 DIYEKYDLYTEPNARQVLEIARDIEKLSNRSKALVSLALEAEKQAAHQRDEFA 118
 Db 61 DIYEKYDLYTEPNARQVLEIARDIEKLSNRSKALVSLALEAEKQAAHQRDEFA 120

QY 119 SNEVYVYNAKDDLPKNDSEPGSQRIKPVFTEDANFRQISYQHAHVPTDIYEGSTI 178
 Db 121 SNEVYVYNAKDDLPKNDSEPGSQRIKPVFTEDANFRQISYQHAHVPTDIYEGSTI 180

QY 179 VLNELNWTLSALDVFVKKNREEDPSLLQVFGSATGLARYYPASPVVDNSTRPNKIDLYD 238
 Db 181 VLNELNWTLSALDVFVKKNREEDPSLLQVFGSATGLARYYPASPVVDNSTRPNKIDLYD 240

QY 239 RRPWTYQGAASPKDMLILVDVSGVSGLTCLKIRTSVSEMLETLSDDDDFVNVASFNSNA 298
 Db 241 RRPWTYQGAASPKDMLILVDVSGVSGLTCLKIRTSVSEMLETLSDDDDFVNVASFNSNA 300

QY 299 QDVSCFOHLYQVARNKVKLDAVNNTAKGIDYKGFSAFQELLYNVNVRANCNKII 358
 Db 301 QDVSCFOHLYQVARNKVKLDAVNNTAKGIDYKGFSAFQELLYNVNVRANCNKII 360

QY 359 MLFTDGEERAQEIFNKNKDKKRVRFVSQGHNYVERGPIQMACENKGYIYEIPSIGA 418
 Db 361 MLFTDGEERAQEIFAKYNNKKKRVVTFVSQGHNYDRGPIQMACENKGYIYEIPSIGA 420

QY 419 IRIWTOEYLDVLRPWLADGKAKQVWNTNYLDALGLVITGTLVPVFNITGOFENKTN 478
 Db 421 IRIWTOEYLDVLRPWLADGKAKQVWNTNYLDALGLVITGTLVPVFNITGOFENKTN 480

QY 479 LKNQLILGVNGVDVSLDIKRLPRFTLCPNGYFAIDPNGYVLLHPLNLPK----- 530
 Db 481 LKNQLILGVNGVDVSLDIKRLPRFTLCPNGYFAIDPNGYVLLHPLNLPKPGIVGIPT 540

QY 531 -----NPKSQBPVTLDFLDAELNDIKVEIRNKMIDGESGKTRTLVKSODER 579
 Db 541 INLRKRPNVQNPQKQEPVTLDFLDAELNDIKVEIRNKMIDGESGKTRTLVKSODER 600

QY 580 YIDKGNRTYTWTPVNGTDY-SLALVLTYSFYIKAKLEETITQARSKKGMKQSETLKP 638
 Db 601 YIDKGNRTYTWTPVNGTDY-SLALVLTYSFYIKAKLEETITQARSKKGMKQSETLKP 653

QY 639 DNFEESGYTFIAPRDYCNLDKISDNNTFELNFEFIDRKTNNPNSCNADLINRVLLDAG 698
 Db 654 DNFEESGYTFIAPRDYCNLDKISDNNTFELNFEFIDRKTNNPNSCNADLINRVLLDAG 713

QY 699 FTNELVQVNSKQNIKGVKARFVVTGGITRVYKPEAGENWQENPETEYDFYKRSLDN 758
 Db 714 FTNELVQVNSKQNIKGVKARFVVTGGITRVYKPEAGENWQENPETEYDFYKRSLDN 773

QY 759 DNYVFTAPYFNKSPGAYESGIMVSKAVEIYQGLKLPVAVGIKIDVNSWNTENFTKSI 818
 Db 774 DNYVFTAPYFNKSPGAYESGIMVSKAVEIYQGLKLPVAVGIKIDVNSWNTENFTKSI 833

QY 819 RDPGAGPVCDCKRNSDVMDCVTLDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNIS 878
 Db 834 RDPGAGPVCDCKRNSDVMDCVTLDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNIS 893

QY 879 VYAFNKSVDYQSVCEPAGAPKOGAGHRSAYVPSADIQIGWATAAAWSILQQFLLSLT 938
 Db 894 VYAFNKSVDYQSVCEPAGAPKOGAGHRSAYVPSADIQIGWATAAAWSILQQFLLSLT 953

QY 939 FPRLEAVEMEDDDTASLSKQSCITEQYFFDNDKSFSGVLDGCGNCSRIFFHGEKLMN 998
 Db 954 FPRLEAVEMEDDDTASLSKQSCITEQYFFDNDKSFSGVLDGCGNCSRIFFHGEKLMN 1013

QY 999 TNLIIIVESKCTCPDTRLLIQAEQTSQGNPCDMVK 1036
 Db 1014 TNLIIIVESKCTCPDTRLLIQAEQTSQGNPCDMVK 1051

RESULT 4
 T30256
 calcium channel alpha-2-delta-C chain - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 20-Jun-2000
 C:Accession: T30256
 R:Klugbauer, N.; Lacinova, L.; Marais, E.; Hobom, M.; Hofmann, F.
 J. Neurosci. 19, 648-651, 1999
 A:Title: Molecular diversity of the calcium channel alpha2delta subunit.
 A:Reference number: Z20794
 A:Accession: T30256
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1091 <KLJ>
 A:Cross-references: EMBL:AJ010949; PIDN:CAA09423.1
 A:Experimental source: brain
 C:Superfamily: calcium channel alpha-2 chain

Query Match 19.9%; Score 1085; DB 2; Length 1091;
 Best Local Similarity 28.7%; Pred. No. 1.9e-57;
 Matches 309; Conservative 222; Mismatches 416; Indels 128; Gaps 40;

QY 3 AGCILLATLTLFQSLIGPSSEPPPSAVTIKSWYDKMOEDLVTLAKTAGVGNQLV 62

14 ASALLA-TALLYAALGDVVRSEQOIPLSV-VKLWASAFGEQIKSIAAKYSGSOLLQKKYK 71
63 KYODLYTVEPNNARQLEIARDIEKLLSNRSKALVSLALEAEKQVAAHQWREDFASNEV 122
72 EYKQVAFEEIDGGLVKKAKIMEEMPHKSEAVRRLVEAAEAHLKHEFDADL---QY 128
123 VYNAK---DLDPEKNDSESGSRQIKPVFIEDANFGR-QISYQHAHVHIPTDIYEGSTIV 179
129 EYFNVLINERDKDGNLELGEKEFI---LAPNDHFNLVYNISLSDVQVPTNMYNKPDAI 185
180 LNELNWTLSALDEVKKNREDDPSLLQVFGSATGLARYYPASPMPVDNRTNPKIDLYDVR 239
186 VNGYIWSESLNKVVDNFRDPSLIWYFGSAKGFRRQYPCIKWEPDE---NGVIAFDCR 242
240 RRPVYIOGAASPKDMLILVDVSGVSGLTILKLRISYSEMLETILSDDDFNVNVSFNSAQ 299
243 NRKWTIOQAASPKDVLILVDVSGMKGRLTIATQVTSSILDTLGGDDDFNITINEELH 302
300 DVS-CFO-HLVQANVRNKVKLDAVNNTAKGITDYKKGFSFAFEQLLNTNVSAN--CN 355
303 YVEPCLNGTLVQADRTNKEHREHLDKLFAKIGMLDIALNEAFNILSDFNHTQGSICS 362
356 KIIMLFDTGGEERAQETFNKYN-KDKKVRVRFVSGHNYERGIQMAKCNKGYIYEIP 414
363 QAIMLITDGAVDYDTIFAKYNWPDNRKVRIFTYLGREAAFAADNLKMWCAKNGFFFTQIS 422
415 SIGAIRNTOEYLDVLRPMVLADGKAKQVQWNVILD-----ALEGLVI--TGT 463
423 TLADVQENWEYLHLVSRKVI---DQEHVVVTEAYIDSTLPOAKLADDOGLVMTVA 480
464 LPVFNITQFENKTNLKNQILVGMGVDSLEDIKRLTPRTFCPCNGYYFAIDPNGYVLL 523
481 MPVFS---KQNETRSG-ILLGVGVDVVPVKKELTIPKYKLGHIHYAATNNGVILT 535
524 HPNLOP---KNPSQEP-VTLDFDLAELNDIKVEIRNMKIDGESGEKTRFLVKSQDE 578
536 HPELRPLYEEGKRRKPNYSVDLSEVWEWDRODV-LRNAWVRKTKG--FSMEVK--- 588
579 RYIDKGNRT-----TWTPVNGTDSLAVLPT-YSFYIKAKLEETIQAKSKGKMK 631
589 KTVDKGRVLVMTNDYYTIDIKTPFSLGVALSRGHGKIFF-----RGNVT 634
632 DSEFLKPDNFEESGYTFIAPRDYCN-DLKISDNNTEFLNFEFIDRKTNPNSCNADLI 690
635 IEGL--HDLHPDVSADWSYCNLDLHPEHRHLSQLEAIKLYLKGKEP-LIQCKELI 691
691 NRVLIDAGFTNELVQNWYS-----KQKNKIGVKARFVTDGGITRYP----- 733
692 OEVLFDA-VVSAPIEAYTSLALNKSNSDKGVEAFVFLGTRTGLSRINLFPVGAELTNQD 750
734 -KEAGNENQENPETYEDSFYKRSIDN-DNYVETAPY---FNKSGPAGESIMVSKAV 786
751 FLKAGKENIFNDHPLVTRAEQIAGSFVSIPTSTGVNKS-----NVVTASTSI 804
787 EYIQGKLLKPAVVGKIDVNSWIENTFTKTSIRDPACGAPVCDCKRNSDVMDCVILDDGGF 846
805 QLLDERKSPVAAVGIOMKEFFORKEWFTASROCASLDGKCSICDDETVNCLIDNNGF 864
847 LLMANHDDYTNQIGRFGETDPSLMRLHVNISVYAFNKNYSYDVOSVCEPGAAPKQAGHRS 906
865 ILVS--EDYT-OTGDFEVEGAVMKNLLTMGSKFRITLYIQAMCR---ANKESSDSAH 918
907 AYPVSADILQIGWATAAWSILOQFLLSLTPRLLAEVEMEDDDFTASLSK-----QS 961
919 GLDDPYKAFI-----SAKWIIMTELVLFVEF-----NLCSWWHSMTAKAQLKQLEP 968
962 CITEOTQYFFDNDSKFSFGLDCGNSRIFPHGKLMNTNLIETWESKGTCPCDT 1016
969 CDTEYPAFVSERTIKETGTGNIACEDSKSFVIOQIPSSNLFVWVDS--SCICES 1021

RESULT 5

S44617
C50C3.11 protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C:Accession: S44617
R:Favelllo, A.D.
submitted to the EMBL Data Library, May 1993
A:Description: Sequence of the C. elegans cosmid C50C3.
A:Reference number: S44618
A:Accession: S44617
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-734 <FAV>
A:Cross-references: EMBL:L14433; NID:g289649; PID:g289650
C:Genetics: 24/2; 87/3; 175/1; 259/1; 290/3; 346/3; 460/3; 538/3
A:introns: 24/2; 87/3; 175/1; 259/1; 290/3; 346/3; 460/3; 538/3
Query Match 11.2%; Score 607; DB 2; Length 734;
Best Local Similarity 26.6%; Pred. No. 7.8e-29;
Matches 180; Conservative 127; Mismatches 258; Indels 112; Gaps 20;
QY 47 LAKTASGVNQLVDIYKYQDLYTVEPNNARQLVEIAARDIEKLSNRS----KALVSLAL 102
Db 36 MKETFSKISHETILKQYKLEVEEQDFPRAELKSKHRIEDYLKVSQFAYKAKIS--L 93
QY 103 EAKYQAAHQWREDFASNEVYVYNAKDDLDPEK-NDSEPGSORIKP-----VFIEDANP 155
Db 94 EARSVRNDSTVNDPQSKSFRFMSAKOGNDGTTIYESNHLGKRLKVNNETKSFNTONANF 153
QY 156 -GRQISYQHAHVHIPTDIYEGSTIVLNEALNTSALDVEFKKNEEDPSLLQVFGSATGL 214
Db 154 YTLPTSSVSAVHIPTLYDRNEDLLARKIDW-SDIDAVYTNREETKDLAFQLFCSAGY 212
QY 215 ARYPASPWV-DNSRTPNKIDLYDVRRRPPIYOGAASPKDMLILVDVSGVSGTLLKLR 273
Db 213 MRYTPAASWFWDNQ--DEHLDLDFCRNTEWYINSATNSKNVLIMLDMSGMLGQRYEVAK 270
QY 274 TSVSEMLETILSDDDFNVNVSFNSNA---QDVSCFOHLVQANVRNKVKLDAVNNTAKGI 330
Db 271 QTTEALLETLSHNDYFNIMTFSKNTFLDCGCTNGTLQATMRNKKALRRKMDTYQSEGG 330
QY 331 TDYKKGFSFAFEOLLNAN-----VSRANCNKIIMLFDTGGEERAQEIFNKYNKDKKVRVF 385
Db 331 AEYKALPLAFSVLLDINNGGDDNRRGACENVIMLITDGAPNAYKKIFDMYNADKKVRVF 390
QY 386 RFSVGQHNTERGPIQWMAKCNKGYIYEIPSIGAIRINTQEYL-----DVLGRPMVLAGDKA 441
Db 391 TFLVGDFAIDNEVREMACNNRGYVHVANNADVDDEKIHYYIRMSRVVGRHYKESGOLS 450
QY 442 KQVQWTVNVLDALELGL--VITGTLPVFNITGQFENKTN----- 478
Db 451 ---WMTGVTRERYLPRPEIFAEPVPTITNOSFVAMNKNMKSARKIRLQKSEARSMFTTV 507
QY 479 ----LKNQILVGMGVDSVLEDIKRLTPRTFCPCNGYYFAIDPNGYVLLHPNLPQKNP-- 532
Db 508 SYPVIVNETFMGVAANIPLTEVAQKSHPNIGSKSYFFMLDQNGFVWTHPQLRPIDPFT 567
QY 533 --KSQEPVTLDFLD-----AELENDIKVEIRNKMD 561
Db 568 KYHKQNYNNMDLLELVGQNONVRSSQKSAQVSDLVCEGANYAECDLDRKAVRKMID 627
QY 562 GESGEKTRFLVKSQDERY-----IDK---GNRTYTTVPNGTDYSLALVLPYTSFYIKA 614
Db 628 CDSND-----VOOLDVYATLDELDRVYPTNTYYACINHANFVLGLAVAKGDDYRVVK 681
QY 615 KLEETITQAKSKGKMK 631
Db 682 K-----QKKYDFGRVK 692

RESULT 6
T18770

probable calcium channel protein - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C:Accession: T18770; T25249
R: Sulston, J.
submitted to the EMBL Data Library, June 1995
A:Reference number: Z19019
A:Accession: T18770
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1148 <WIL>
A:Cross-references: EMBL:Z49907; PIDN:CAA90091.1; GSPDB:GN00020; CESP:T24F1.6
A:Experimental source: clone B0491
R: Chui, C.
submitted to the EMBL Data Library, June 1995
A:Reference number: Z20004
A:Accession: T25249
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1148 <W2>
A:Cross-references: EMBL:Z49912; PIDN:CAA90141.1; GSPDB:GN00020; CESP:T24F1.6
A:Experimental source: clone T24F1
C:Genetics:
A:Gene: CESP:T24F1.6
A:Map position: 2
A:Introns: 91/2; 131/3; 170/3; 283/1; 322/2; 410/3; 487/1; 563/1; 602/3; 654/3; 683/3; 7

Query Match 10.5%; Score 572; DB 2; Length 1148;
Best Local Similarity 21.2%; Pred. No. 2.1e-26;
Matches 238; Conservative 213; Mismatches 424; Indels 248; Gaps 41;
QY 37 VDKMQEDLVTLA-----KTASGVNOLVDIYERKYODLYTVEPNNAQRLVEIAARDI 86
DB 99 VDTIEAPASIAQFSANILKDFETQSFSLVQEEFKLPDIKSKEDAEKLRVATEHL 158
QY 87 EKLNSRSKALVSLALBAEQAQAHQWREDFASNEVYVYNAKDDLDPKNDSEPGSOR-- 144
DB 159 DRLVTNRVDALKKLASSAEASAVF-----DEYDQAVAVPOADKRCE 201
QY 145 --IKPFVIEDANFORISYQH---AAVHIPDIEGTVLNLNWTSA--LDEVFKNR 197
DB 202 AYMKMNESDMHFVSNM--VEHNSKSGIHITVESYQCDFVRMRDFDTGTRKLEKTSMDNK 260
QY 198 EEDSLMLQVGSATGLARYYPASFPWDNSPTPNKIDLYDVRPRPYTOGAASPKDMLIL 257
DB 261 EKAPEMGHQYIGTYSGLTRMYPRRHW--KVEPTPTIDLDPRFRFWFVNAESVPKDIYFL 319
QY 258 VDVSGSVGLTKLIRTSVSEMLETSLDDDFVNVASFNQAQ--VSCFQH--LVQANVRNK 315
DB 320 LDYSGSVKGPMTMLKITMWTILSTLSPNDYFFGVYFNHFNPIISCANRTFMPATTSNK 379
QY 316 KYLKDANNITAKGTYDKKGSFAFOL---LNVNS-----RANCKIIMLTDGEE 367
DB 380 KYFEEELGMBEKDQAHAFTPLKFLSLDLVRLGNLDSNQSLADYRSEGHKLIIITDGVDE 439
QY 368 RAQETFN---KYNKDKYRVFRFSVQOHYERGPQWACENKGYIYEPISGAIKRIHQ 424
DB 440 WPHQILDEEFQTRNSLIRIFGSMYGTSLPLQOQYACKSHGGYSEIDSIMDKVQPSR 499
QY 425 EYLDVLRPMVLADGAK-----QVQWNTVYLDALGLVITGLPVFNITGOFENK 477
DB 500 TQONVLSQ---VRGDELKGTNAEKREPSWTQLYMETQGTGPIVTLSPILT-----SEQR 551
QY 478 NLKNQILGVMGVDSLEDKRLTFRFLCPNGYFAIDPNGYVLLHPNLQ--PKNPK--- 533
DB 552 IWRDQKLAGVVAIDISIKETKHL--TSSEQMGIYVDNNGMLIYHPQLQIPKTEVHCV 609
QY 534 -----SQEPV-----TLDFLDAELENKIKVEIRN 557
DB 610 RRSACYDAQOVKQKAGSLRVHYGFSDERYVLVGLIDSIPITLDMDYLDGDSFAIDRLR 669
QY 558 KMDGESGEKTFRTLVKQSODERYIDKGNRTYTWTVPNGTDYSLALV--LPTYFYIYKAK 615

DB 670 -----RITTKCYBEAIAKNSKEYCHSHIKDSPFTLVIVNNIQLKTVYIDSV 717
QY 616 LEETITQ-----ARSKGKMKDSETLKPNFNBESGVTFTAPRDYC--NDLKISDNNT 665
DB 718 QELGLTDNKLVTFFYPRDVCQWKDEYAADRFRV--WSDISEKEICAQDDMLRPRAFT 775
QY 666 EELLNFEFIDRKTNNPNPSCNADLINRVLLDAGFTNQLVNTYWSKQKNIKGVKARFVVD 725
DB 776 KGLSWTQSNPKSDIEHTC-----LLAQYPENASVPHVNS-----FVHTR 817
QY 726 GGITRVYKREAGENQENPETVEDSFYKSLDNDNVFTAPYFNKSGPGAYESGIMVSKA 785
DB 818 SKLTAFYPTCSSHDMKAVNKFEDEI--KLTDNDNFV---QFSMR-----SESLIYFT 866
QY 786 VEIYIOGKLLKPAVGIKIDVN---SWIENFTKTSIRDPAGVPCVCKRNSD-----VMD 837
DB 867 IADYDNNRL---AVGTQWKNENFFDQIFDNFT-----RQNPDKWICKRQE 908
QY 838 CVTLDDGGFLMANHDDYTNQIGRFFGEIDPDSLMRHLNIVSYAFNKSVDYQVCEPGAA 897
DB 909 CSITIRNGHVIASSAHPAHLAKF---DPQLFESLVKVLNVTNSWTVEQSECK---- 960
QY 898 PKOGAGHRSAYVPSVADIQIGWATAA--AWSILOQFLLSLTFPRLLEAVEMEDDDFTA 955
DB 961 -----AKRVAPWSAAAGSSSILRYFTSI-----FKLAKTSFWR 995
QY 956 SLSKQSCITEQTQYFFDNDKSFSGVLDCGNC--SRIFHGEKMLNTLFIWVESKGTG-- 1012
DB 996 NLLESALTLLVDAQFSMTGTCTTQKIKPFRCFMKFFHYMTLNLIK--QLQLAGMSTCSR 1054
QY 1013 -----PCDTRLLIOAEQTSQGNP-----CDMV 1035
DB 1055 YAKLYPVHTTSLIADACRACQYRPRIFESEPRKLEKCDVV 1097
RESULT 7
C86880
hypothetical protein yvcC [imported] - Lactococcus lactis subsp. lactis (strain IL140
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
C:Accession: C86880
R: Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Eh
Genome Res. in press, 2001
A:Title: The complete genome sequence of the lactic acid bacterium.
A:Reference number: A86625
A:Accession: C86880
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1450 <STO>
A:Cross-references: GB:AE005176; NID:g12725093; PIDN:AAK06141.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: yvcC
Query Match 3.6%; Score 198; DB 2; Length 1450;
Best Local Similarity 21.0%; Pred. No. 0.0012;
Matches 242; Conservative 149; Mismatches 439; Indels 322; Gaps 56;
QY 37 VDKMQEDLVTLAKTASGVNQLVDIYERKYODLYTVEPNNAQRLVEIAARDIEK-----L 89
DB 69 INKTENDKELKLFEGNQPIEIEE--NESWTLKEKNT-----IISDFEKENEGK1VL 120
QY 90 LSNRSKALVSLAEAKVQAHAQWR---EDFA-----SNEVYVNA 127
DB 121 RANNSISLNLLEIQADAKLIENDQEVISEDILAKKESTIFSLYIPENNAKDSKEKNKNT 180
QY 128 KDDLDEKNDSEPGSORIKP---VFIEDANFGRIQISYQHAHVH----- 167
DB 181 EEVLNNSEQETVSQLKKDSQLAFSPYFGIKAGFNLDLAQNYENISPEYRQDETGISP 240
QY 168 ----IPTDIYEGSTIVLNLNWTLSALDEVFKKNREEDPSLLNQVFGSATGLARYYPASPW 223

Db 241 NHTSPT---GNTTVNHQWNSF-----SSQWGVNSWN--GEATNLENSYIEVAG 287
Qy 224 VDN-----SRTPNKIDLY-DVRRPWTIOGAASPOMLILVDVSGSGVGLTK 270
Db 288 VNNPVDFAIRKRYAKETETGGLDYLYLVNRGN---VQNPPIKPVDTVLVDMSGSGMQGAKET 344
Qy 271 LIRTSVSEMLTSLDD---DRVNV--ASFNSADQVSCFQHLQVQANRNKKVLKD---A 321
Db 345 AVROGVSDFLSTQNTAYADVIVNVGVISPGNVYVAGSYIIVPI--DKVSSSEHVKS 402
Qy 322 VNNITA---KGITDYKKGFSAFQOLLNYSRANCNKIIMLFTDGGEEAQAEIFNKYNK 378
Db 403 INQALAPQFSGGTFTQLGRKGTEML---EQDSSDNQKMILMTDG---VPTESYKVN 455
Qy 379 DKVYR--VFRSVQVHNERG---PIQ---WMACENKGYEIEI-----PSGAIRINTQOE 425
Db 456 ASKYVDNVIYQSFASRDEPGNTSKIOSPYVVKDINGSNIEIRDTWAATLGEAEISKQE 515
Qy 426 YLDVLRPMVLGAD-----KAKQVQWTVNYLDLDELGLVITGTLVPVFNITGQFE 474
Db 516 ISEHTLGIQLCNDGVSLSQBEVKSRSLSIATNTGLYQDANSAN-----DITDYLK 565
Qy 475 NKTN-----LKNQILGYVMGVDSLEDIKRLTPRFTLCPNGYIEFAIDPENGVLHPN 526
Db 566 NOANVLSRFTNTINGLILDLPLGAQFEYKDKF-----FEITSVG----- 604
Qy 527 LQPNKPSQEPVTLDFDAELENDIKVIRNKMIDGESGEKFTTLVKSQDERVIDKGNR 586
Db 605 -----EDSIDNLPKTGINKEGLEISLNTI--GRNQEVQIHYQVRLNTETDDFKTNY 653
Qy 587 TY-----TWTPVNGT--DYSALVLTPTSPYIYKAKLE-----ETITQASKK 627
Db 654 WYQNGETTLTP--NGSPNDKNVNGVSPKSSGSLNLEKQWLANSNIPENVELLGRR 712
Qy 628 GKMDSE-----TLKPNFEBSGYFTIAPRDYCNLDKISDNNTFELNFEIDIRKTPNN 682
Db 713 SAQISSDWTKVTLKEDDEWSQLENLPKYSILGEEFYIEYKDEIVLN--SEIYDWITIGE 771
Qy 683 PSCNADLINRVLD-----AGFTNELVQWNSKQKNIKGVKARFVTTDGGITRVYPKAGE 738
Db 772 DKTTIANIEKRLQILKITSNHDNEPLSEVEFVLKNSQGEEDKAVTN-----EKGE 822
Qy 739 -NWOENPETYEDSYKSLDNDNVFTAPYFNKSGPGAYESGIMVSK-----AVEIYIQ 791
Db 823 ILFKTRNLNVEEQLHEIKSPGSLSGPWIKT---EFFENGQPIIKVDGQIALDSEHN 879
Qy 792 GKLLKPAVVGKIDVNSWNIENFTKITSIRDCPAGVPCDKRNSVMDCVLD-----DG-- 844
Db 880 KFMIS---LNTINDIN--VEEF-----RNSVTIDKRAVDSEKLDGAV 917
Qy 845 -GFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVYAFNKSQYQSVCEPGAAPKQAG 903
Db 918 FNLQIESVDDDELTLQKPL--EITNNLLPGL-----YALQESVSPNGYRDEV 964
Qy 904 H--RSAYVPSVADIIQIGWATAAWSILOQL-----LSLTFE- 939
Db 965 HFRVKFNGSIVAIGSEG-----IDIFLDENSGKNGVLNBEENGDLHLTLIFY 1015
Qy 940 ----PRLLEAVEMEDDDFTASLSKQSC-ITEQTOYFNDNS-----KSPSGVLDCGNGSRI 990
Db 1016 NOAVPPLQLEVDKIDDDFTSLAGVSEFELTRLGKSTDSQSVKRINSFDRILKTFN--NE 1073
Qy 991 FHGEKL-MNTNL 1001
Db 1074 FTGETALKSNL 1085

RESULT 8

S54355

inter-alpha-trypsin inhibitor heavy chain 3 precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 04-Feb-2000

C:Accession: S54355
R:Chan, P.; Risler, J.L.; Raguenez, G.; Salier, J.P.
Biochem. J. 306, 505-512, 1995
A:Title: The three heavy-chain precursors for the inter-alpha-inhibitor family in mou
A:Reference number: S54353; MUID:95194326
A:Accession: S54355
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-886 <CHA>
A:Cross-references: EMBL:X70393; NID:G695635; PIDN:CAA49843.1; PID:G695636
C:Superfamily: Inter-alpha-trypsin inhibitor complex component II

Query Match 3.6%; Score 194.5; DB 2; Length 886;
Best Local Similarity 19.9%; Pred. No. 0.00089;
Matches 105; Conservative 138; Mismatches 347; Indels 261; Gaps 44;

Qy 27 FPSAVTIKSWVDKQEDLVTLAKTAGSNQVLVDIYKYQDLTYVPEPNNARQLVEIAARDI 86
Db 98 YPGNVKEVAQKQYKAVSQGTAG---LVKASGRKLEKFTVSVNVAAGSKVTFELTY 153
Qy 87 EKLNSRSKALVSLALEAEKVQAAHQWREDFASNEVYVYNAKDDLDPEKNDSEPGSORIK 146
Db 154 EELL-KRNKGYEMLYKVPKQLVRRHEID-----AHIFEP-----Q 189
Qy 147 PVFTEDANFCRQISYQAAVHIPTDIYEGSTIVLNLNWT-SALDEVFKKNREEDPSLLWQ 206
Db 190 GIGMLDAE-----ASFYTNDL-LGSALTQSF----- 214
Qy 207 VFGSATGLARIYPASPWVDNSRT--PNKID-----LYDVRRRP-----WYI-- 245
Db 215 -----SGKKGHVSFKPSLDQQRSCPTCTDSLLNGDEFIVYDVNRESPGNVQVNGYEVHF 269
Qy 246 ---QG--AASPKDMLILVDVSGVSGSLTKLIRTSVSEMLETSLDDDDFVNVASPSNQAQDV 301
Db 270 FAPQGLPVVPKNIYFIVDVSGSMGRKIQTREALLKILDVDEKDDYLNFLTFTST---DV 326
Qy 302 SCFO-HLVQAVNRNKKVYLDKAVNNITAKGTDYKKGFSFAFEQLNLYNVRAN-----C 354
Db 327 TTWKDHLVQATPANKLEAKFVKNHQSWNTINDGLLKGIEML---NKAREDTVPERS 383
Qy 355 NKIIMLTQD-----GEERAQEIFNKYNK---DKYVRFVSVGQHNHYERGPQWMACENKG 408
Db 384 TSIIMLTQDGTANTGESRPEKIQENVRNAIGGKPPLYNLGFG--NNLNYNLETLEAHNG 442
Qy 409 YYEIPISGAIRINTQYLDVLRPMVLGDKAKQVQWTVNYLDLDELGL--VTIGILPV 466
Db 443 LARRIYEDSDANLQLOGFYEEVANPLL-----TNVEYEPENAILDLTRNSYPH 491
Qy 467 FNITQFENKTNLKNQILGYVMGVDSLEDIKRLTPRFTLCPNGYIEFAIDPENGVLHPN 526
Db 492 F-----YDG-----SEIVVAGRLVDRNDN-----PKADYKGGHGLN-- 523
Qy 527 LQPNKPSQEPVTLDFDAELENDIKVIRNKMIDGESGEK--TFRTLVKSQDERYIDKG 584
Db 524 ---DLAFTTEVDMEEADAALK-----EGYIFGYIERLMAYLITEQLLEKRNKAG 572
Qy 585 NRTVTWTPVNGTDSL--LVLPYISFYIYKAKLEEFITQARSKKGMKMDSET-----LK 637
Db 573 DEKENIT-AEALDLSLKYHFVTPLTSMVTKPEDNEQDTSTADNAGEEFAFAETMTSFLT 631
Qy 638 PDNFEESGYFIAPRDYCNLDKISDNNTFELNFEIDRKTNNPNSCNADLINRVLLDA 697
Db 632 TQSSQSPYIYV-----DGDPHFTIQI-----PKNDISICFNIDEKP 668
Qy 698 GFTNELVQWNSKQKNIKGVKARFVTTDGGITRVYPKAGEWNOENPETYEDSYKRSLD 757
Db 669 GTVLRLLIQD-----PVT--GIT-VTGGIIGD-----KRS-- 694
Qy 758 NDNVFTAPIFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWNIENFTKTS 817
Db 695 NASSRTGKTGYFGKLGITNAWMDFRVEVTEKIIIG-----TGAELSTFSWLDVTVTQ 747

QY 818 IRDPCAGPVCDCKRNSDWDVCDG-GFLMAN-----HDDYTNQIGRFGEDIDP 868
 Db 748 -----TGLSVTNRKKNV--VSFGDGISFVILHQVKKHVPVHODEFLG-----FYVYDS 795
 QY 869 SLMRHLNLSVYAPKNSYDQSV-CEPGAAP 898
 Db 796 HRMSAQTHGLGQFFQPFDFKVGIRPGSDP 826

RESULT 9
 S30350
 Inter-alpha-trypsin inhibitor heavy chain 3 precursor - human
 A:Alternate names: HC3; inter-alpha-trypsin inhibitor chain H3; pre-alpha-inhibitor heavy chain H3
 C:Species: Homo sapiens (man)
 C:Date: 03-May-1994 #sequence_revision 20-Feb-1995 #text_change 04-Feb-2000
 C:Accession: S30350; S34123; D34245; A39079; S50133; B53642; A59167
 R:Bourguignon, J.; Diarra-Mehrpour, M.; Thiberville, L.; Bost, F.; Sesbouee, R.; Martin, Eur. J. Biochem. 212, 771-776, 1993
 A:Title: Human pre-alpha-trypsin inhibitor-precursor heavy chain cDNA and deduced amino-acid sequence
 A:Reference number: S30350; MUID:93215656
 A:Accession: S30350
 A:Molecule type: mRNA
 A:Residues: 1-885 <BOU1>
 A:Cross-references: ENBL:X67055; NID:g288562
 R:Bourguignon, J. Submitted to the EMBL Data Library, June 1992
 A:Reference number: S34123
 A:Accession: S34123
 A:Molecule type: mRNA
 A:Residues: 1-310, 'K', 312-343, 'R', 345-885 <BOU2>
 A:Cross-references: ENBL:X67055; NID:g288562; PIDN:CAA7439.1; PID:g288563
 R:Diarra-Mehrpour, M.; Bourguignon, J.; Sesbouee, R.; Mattei, M.G.; Passage, E.; Saller, Eur. J. Biochem. 179, 147-154, 1989
 A:Title: Human plasma inter-alpha-trypsin inhibitor is encoded by four genes on three chromosomes
 A:Reference number: S02141; MUID:89137072
 A:Accession: S02141
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 341-356, 'G', 358-845, 'H', 847-885 <DIA1>
 A:Cross-references: ENBL:X14690; NID:g35464; PIDN:CAA32821.1; PID:g35465
 R:Engild, J.J.; Thøgersen, I.B.; Pizzo, S.V.; Salvesen, G. J. Biol. Chem. 264, 15975-15981, 1989
 A:Title: Analysis of inter-alpha-trypsin inhibitor and a novel trypsin inhibitor, pre-alpha-trypsin inhibitor
 A:Reference number: A92736; MUID:89380192
 A:Accession: D34245
 A:Molecule type: protein
 A:Residues: 30-49 <ENGI>
 R:Engild, J.J.; Salvesen, G.; Hefta, S.A.; Thøgersen, I.B.; Rutherford, S.; Pizzo, S.V. J. Biol. Chem. 266, 747-751, 1991
 A:Title: Chondroitin 4-sulfate covalently cross-links the chains of the human blood proteoglycan
 A:Reference number: A39079; MUID:91093267
 A:Accession: A39079
 A:Molecule type: protein
 A:Residues: 631-647 <ENG2>
 R:Diarra-Mehrpour, M.; Bourguignon, J.; Sarafan, N.; Bost, F.; Sesbouee, R.; Muschio-Boncompagni, Biophys. Acta 1219, 551-554, 1994
 A:Title: Tandem orientation of the inter-alpha-trypsin inhibitor heavy chain H1 and H3 genes
 A:Reference number: S50133; MUID:95002176
 A:Accession: S50133
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-27 <DIA2>
 A:Cross-references: ENBL:X75318
 R:Wisniewski, H.G.; Burgess, W.H.; Oppenheim, J.D.; Vilcek, J. Biochemistry 33, 7423-7429, 1994
 A:Title: TSG-6, an arthritis-associated hyaluronan binding protein, forms a stable complex with hyaluronan
 A:Reference number: A35642; MUID:94271799
 A:Accession: B53642
 A:Molecule type: protein
 A:Residues: 30-34, 'X' <WIS>
 R:Jessen, T.E.; Faarvang, K.L.; Ploug, M. FEBS Lett. 230, 195-200, 1988
 A:Title: Carbohydrate as covalent crosslink in human inter-alpha-trypsin inhibitor: a nd

A:Reference number: S02431; MUID:88167187
 A:Accession: A59167
 A:Molecule type: protein
 A:Residues: 30-32, 'GEKEQAVDT' <JES>
 C:Comment: As pre-alpha-inhibitor, this protein is covalently cross-linked by chondroitin-6-sulfate
 C:Genetics: As
 A:Gene: GDB:ITIH3
 A:Cross-references: GDB:120109; OMIM:146650
 A:Map position: 3p13-3p12
 C:Superfamily: inter-alpha-trypsin inhibitor complex component II
 C:Keywords: chondroitin sulfate proteoglycan; glycoprotein; heterodimer; proteinase 1
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-29/Domain: propeptide #status predicted <PRO>
 F:30-647/Product: inter-alpha-trypsin inhibitor heavy chain 3 #status experimental <M>
 F:648-885/Domain: carboxyl-terminal propeptide #status predicted <CTP>
 F:87,576/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:647/Modified site: chondroitin sulfate ester carboxyl end (Asp) (in mature form) #s

Query Match 3.4%; Score 185; DB 2; Length 885;
 Best Local Similarity 20.9%; Pred. No. 0.0033;
 Matches 137; Conservative 101; Mismatches 239; Indels 180; Gaps 34;

QY 27 FPSAVTIKSWDKMOEDLVTLAKTAGVGNQVLDIYEKYQDLYTVEPNNAQVLETAARDI 86
 Db 97 YPGNVKEKAVAKQYKAVSQGTAG-----LVKASGRKL 131
 QY 87 EKLSNRSKAL---VSLALEAEKVQAQAHQWREDFASNEVVYVNAKDDLDPEKNDESPGQ 143
 Db 132 ERTFVSNNVAAAGSKVTFTYELLKRHKG-----YEMYLKQVQK-----Q 173
 QY 144 RKPVFIEDANFGRQISYQAAHVPDIDYEGSTIVLNELNWTSDALDEKKNREEDPSL 203
 Db 174 LVKHFEIE-----VDIFEQGI-----SMLD-----AEASFI 200
 QY 204 LMQVFGSA-----TGLARYYPASPVVDNRT-PNKID-----LYDVRRP----- 242
 Db 201 TNDLIGSALTQSKGKGVHSPKSLDQQRSCPTCTDLSLLNGDFTITYDVNRESPGVQI 260
 QY 243 ---WYI-----QG-AASPKDMILVDVSGVSGLTUKLIRTSVSEMLETSDDDDFVNVAS 293
 Db 261 VNGYFVHFPAQGLPVVKNVAFVIGSMAGRKLEQTKALLRILEDQEDYLNFI 320
 QY 294 FNSAQDVSCF-QHLVQANVRKKVLDVANNITAGITDYKKGFSFAFEQLLNYSVR- 351
 Db 321 FSG---DVSTWKEHLVQATPENLQEAQTFVSKMEDGNTINDGLLRGISM---NKARE 374
 QY 352 ----ANCKIIMLFTDG---GEERAQEIFNKYNK---DKVVRVFRFSVGOHNYERGPIQ 400
 Db 375 EHRIPERSTIVIMLTDGDNVSGESPEKIQENVRNAIGKFPYLNLFQF---NNLNYLE 433
 QY 401 WMACENKYYEIPSGATIRINQEVLDVGRPMVLGAKQVQVNTVYLDALD----- 455
 Db 434 NMALENHGFARVIEDSDADLQGFYEEVANPL-LTGVEMEYPE--NAILDLTQNTYQH 490
 QY 456 ----LGLVITGLPVENITQGENKTNL-----NOLILGVMDVDSLEDIKRLTPRFTL 506
 Db 491 FYDGSSEIVVAGRL-VDEDNNSF--KADVGHGATNDL---TTFEVDKMEK-----AL 539
 QY 507 CPNGYVFAIDPN-----GYVLIHPNLQPK---NPKSQEPVTLDFDLAELENDIKVEIRN 557
 Db 540 QERDYIFG---NVIERLWAYLTIEQLLEKKNAGHEKENLTARALDLSLYKHFTVPLTS 596
 QY 558 KMIDGESGEKTFRLVKQSDERY-DKGNRTYTPVNV-GTDSYSLALVLPFTSYFYI 612
 Db 597 MVYTKPE-----DNEDEIRAIDKPGDEAETVPSPAMSYLTSYQPPQNPYYV 644

RESULT 10
 JC5576
 Inter-alpha-trypsin inhibitor heavy chain 3 - golden hamster
 C:Species: Mesocricetus auratus (golden hamster)
 C:Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 17-Mar-1999

308	WFEWAEEFCIRKI-----KLENVKKCRD-----EPNNKYCSGDGHCKRTYLLKNDTIF	350
79	VEIAARDIEKLLNSRKALVSLALEAEKQAAHOWEREDFASNEVYVYNAKDDLDPEKND	138
359	IDLNCPCENACSNYK-----WIEIQRQKQKQK--YMEI---KIKTINSENNDK	408
139	E-----PGSORIKPVFIEDANFGRSIOYQHAHVHPTDIYEGSTIVLNELNWTSALDE	191
409	EFVENLDKGYSTIN-TFLESLNHGKQC-----	438
192	VFKNREDSLLWQVFGSATGLARYYPASP-----WVDSRTPNKI	233
439	IDKKNKTFNNKL-ETFGP-----SGYCEACPIYGVKCSNEKCTPTVENEMWNNRLPTDT	493
234	DLVDVRRRPWYIQGAASPKDMLTLDVDSGSVGLTLEKLRTSVSEMLETSLDDDFVNVAS	293
494	STRNLN-----ATNDMLVNDGIGNAI-----	515
294	FNSNAQDVSCFHLVQANVRNK-----VLKDVAVNNITARGIDYKKGFSFAFEQLL	345
516	--DNELEKNTKYGILKIGKQKWCQYLLNNDIOCKINNVMNSGYFDNKIAFNVLFQWML	573
346	NYVVSRAVNCNIIWLTDDGEEBQAELFNKYKDKVVRPFRSVGQHNVERGPIQWACE	405
574	RYFYRDHNRLK-----EKIDYCIKKNENINENICIKRCKTN-----CE	610
406	NKGYYEIPISGAIIRI-----NTQYELDVLGRPVLADGAKAOWNTVYDLDALEGLVIT	461
611	CVGKWLKKBAEWKDNQHNQVKNHMLFILPWITGFYEK-ITFPNDFFKALE-----DV	665
462	GTLPVFVITQOFENKTNLKNQILGVMDVSLIEDIKRLTPRFTLPCNGYIYFAIDPNGVY	521
666	DTINVLDLKECOD-THCKIEKIRSI-DVDLIKEIISWLQNKIEVCKS--HHEDKHEVC	721
522	LLHPNLOPKNPKSQEPVTLDFDLAELENDIKVEIRKMKIDGSGEKT-----FFT	571
722	C---DILPKSVDDDEED-EBVDEEKESSQTTKRN--ISQKGGTKSACVKGACAIKVG	775
572	LKVSODERYID---KGNRTYTW-----TPVNGTD-----YSLALVLPTYSF	609
776	VLQOKSNGSIDNCAKNRKKNWQCOKNTFVDGNEGVCMPPRKRSICIHNLTLBEGTRNK	835
610	Y-----YIKAKLEET-ITQARSKKGMKDSETLK----PDNFEE--SGYFFIAPROYC--N	656
836	YQLREAFIKAAETNLLWDKYKNDKNEAEELLKKGKIPEDFMRIMFYTFGDFROFCLN	895
657	DL-----KISDNTEFLNNEFIDRK-----TPNPFSC--NADLINRVLDAGFTNEL	703
896	DMGKDVDKVKKNINKVFNNSKKRFGKIDPENWNNWNGPQIWNGLCALIHADTKDSIKN	955
704	VQNY-----	723
956	KDNYKEKVILAKRDSNGMTLSEFAKPKFLRWVFEWDDYCKRQKYLEVASTCKS	1011
724	TDGITRV-----YPKEAGENQENPETYEDSPYKRSLDN-----DNYV-	762
1016	IDGQLKCDRGCKNKDEYKYYMRKKKEEWNLDQKYKQKRENGKIDKGPGLIIVKDYVL	1071
763	-----FTAPYFNKSPGAYESGIWVSKAVEIYIOGKLLKPAVGIKIDVNSWI---	810
1076	ANAKEYLKKFTASCVTSSGKAQNSATEEYKKNIELLSEQY-----YDADQYCGC	1122
811	-----ENETKTSIRDPGACPVCDCK-----RNSDVMDCVIL	841
1127	TKFIHDDKYKISGRNCCGLNSDAKKNKIKWRNSDEKDYAFL	1169
RESULT	12	
A44396		
P-type	cation translocating ATPase - malaria parasite (Plasmodium falciparum	
C:Species:	Plasmodium falciparum	
C:Date:	10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jun-2000	
C:Accession:	A44396	

R.; Krishna, S.; Cowan, G.; Meade, J.C.; Wells, R.A.; Stringer, J.R.; Robson, K.J.
J. Cell Biol. 120, 385-398, 1993
A; Title: A family of cation A-type-like molecules from Plasmodium falciparum.
A; Reference number: A44396; MUID: 93132070
A; Accession: A44396
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: nucleic acid
A; Residues: 1-1984 <RR>
A; Note: sequence extracted from NCBI backbone (NCBIP:122678)

Query Match		2.9%	Score 159;	DB 2;	Length 1984;
Best Local Similarity		17.1%	Pred. No. 0.44;	359;	Indels 366; Gaps 45;
Matches 179;		Conservative 144;	Mismatches 359;	Indels 366;	Gaps 45;
Qy	58	VDIYEKQDLYTVPNNARQVEIAARDIEKLSNR-----SKALVSLALEAEK	106		
Db	128	INVY-RYNTSVIISS-----ELVPGDIYEIKNMTPICDIIILSGSVTSEHMTGES	180		
Qy	107	VOAAHQWREDFASNEVYVYNAKDDLPKND-----SEPGSRIKPVFIEDANFGROIS	160		
Db	181	V-PIHKERLPEGNAINKNKNDSEKDDYLRINNHASINMKRNHLEETILGKKDR	239		
Qy	161	YQRAVHIPDIYEGSTIVLNLNW-TSALDEVKKNREEDPSLLWQVFGSATGLARYP	219		
Db	240	EYKSNTH-----DLCSMNKLCYINNTYDDVHKNKMD-----	272		
Qy	220	ASPVVDNRTPKIDLYVRRPWTYIOGA-ASPKDMLTLDVSGVSLTLKLRTSVSE	278		
Db	273	YNNNNNNKKKINLN-----FVKTYINSNDLLY-----	303		
Qy	279	MLETSDDDFVNVAFSNAODVSCFOHLVQANVRNKVKLDVANNITAKGIDTYKKGFS	338		
Db	304	DDKIGVNI-----DVNNMKH--KFNORNINYNKDTNNL-----EYNNKHR	345		
Qy	339	FAFEOLLNYSRANCNKIIMLFTDGGERAQEIFNKYKDKVFRFVSQHNVERGP	398		
Db	346	YIYDCLLKKVEAISOKKIY-----SNEIDNKY-----	374		
Qy	399	IQMACENKGYEYPSIGAIRINTQEYLDVLRPMVLG-----DKAKQV	444		
Db	375	MYGGTVLSYLNKIKYNNKEENRILGL-VIKGFTTKGKIVNNLYHKREL	429		
Qy	445	QWNTYLDALGLVITGLPVNTGTFENKTNLKNOLLG-----	487		
Db	430	NLINDSYFLII-LIYALFSVILLYITLSNNEYTHIILKLDIITDAIPPALPTLT	488		
Qy	488	MGVDVSLERIKLTPRTFLCPNGYFA-----TDPNGYVLLHPNLO-----PKNPKSO	535		
Db	489	VGISAIARLKKFSICLCPHKINAGIOWMVDKYG-TUTENNLOFIIITONKKNK	547		
Qy	536	EPVTLDFDALENDIKVEIRKNMIDGESGEKTFTLVKSDERYIDKGNRTYITWTPVG	595		
Db	548	NMLS-DFTHIK-----EMNTESIHSKDDNHNKN-----	577		
Qy	596	TDYSIALVPTVSYFYIRAKLEETIQARKGKMKD-----SETLPKDNFEESG	645		
Db	578	SISEYVYKDNMKNLHTSSK-KKSIKERSNFVLQITKSLLDHYIKERK	627		
Qy	646	YTFIAPROYCDNLKISDN-TEFLN-----FNEF-IDRTPNPNCSADLNRVLDD	696		
Db	628	KEYTNTYNDLHNTSCSYLLNSETKDAICYINIDH-----LCD-----INKNMD	678		
Qy	697	AGFTNELQVNSKKNIKGVKARFVTDGTRVYPKEAGENWQENPETEYDSFKRSL	756		
Db	679	INSKNELMGKYSKNELMGKTIKNELM-----GKYSKNEI	712		
Qy	757	DNDNYVFTAPYFNKSGPAYESGIMVSKAVEIYIOGKLKPAVVG-----TKIDVNSHI	810		
Db	713	MGKYSKNELMGKYSKNELMGKYSKNELMGKYSKNELMGKYSKNELMGKYSKNELM	765		
Qy	811	ENFTKTSIRD-FCAGPVCDCKNSDVMDCV-----ILDDGFFLLMANHDDYTNOIGRF	862		

Db	766	MNCNDYNDYPCD---YNCNNDTYHRLEYHNINKDNSFNIPPEKNKSNYNNTSEHIKI	822		
Qy	863	FGEDPSLMRHLNYSVYAF-----NKSYDYQ	889		
Db	823	NYPLLEALACHTLSKVNKNKMGVLEILFMFNTCDMLNNNSFIKEKKKNCSDFO	882		
Qy	890	SVCEPGAAPKQAGHRSAYVPSVADILQIGWWATAAAASILQOFLLSLTFPRLLLEAVE	949		
Db	883	KI---DGDKNIGANDERCHLNN-----NLVSYNILKRF-----	912		
Qy	950	DDFTASLSKOSCTEOTQYFFDNDKS	977		
Db	913	EFQSLORMSVIVKST-YGNNDNDNN	937		
RESULT 13					
D64998					
hypothetical protein b2770 - Escherichia coli (strain K-12)					
C:Species: Escherichia coli					
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999					
A:Accession: D64998					
R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;					
A.; Rose, D.J.; Mau, B.; Shao, Y.					
Science 277, 1453-1462, 1997					
A; Title: The complete genome sequence of Escherichia coli K-12.					
A; Reference number: A64720; MUID: 97426617					
A; Accession: D64998					
A; Status: preliminary; nucleic acid sequence not shown; translation not shown					
A; Molecule type: DNA					
A; Residues: 1-575 <BLAT>					
A; Cross-references: GB:AF000317; GB:U00096; NID:gl788605; PIDN:AAC75330.1; PID:gl7886					
A; Experimental source: strain K-12, substrain M61655					
Query Match					
Best Local Similarity					
Matches 111;					
Conservative 93;					
Mismatches 206;					
Indels 105;					
Gaps 25;					
Qy	71	EPNARQIVETARIEKLLSNRSKALVSLALEAEKVOAAHQWREDFASNEVYVYNAKDD	130		
Db	22	OPENKESQQQSTPTEQQVLAQAQAIAK---EASQSA---AKALAQEQVQYSDQA	75		
Qy	131	LDPEKND-----SEPGSRIKPVFIEDANFGQISYQHAA---VHIPTDI	172		
Db	76	LOGRLOEAPTFAAAKAKATHANFTARYQF---DDNPVQVAQNPLATSLDVTGDS	132		
Qy	173	YEGSTIVLNE-----LNWTSALDEVKKNREEDPSLLWQVFGSATGLARY	218		
Db	133	YANVRRELNGGLPPPDVAVRVEIVNPPSDWDI--KDKQSIKPSKPIPFAMRYELA	187		
Qy	219	PASPVVDNRTPKIDLYVRRPWTYIOGAASPKDMLTLDVSGS-VSGLTLKLRTSVS	277		
Db	188	PA-PW-NEQRTLLKVDILAKDRKSEELPAS---NLVFLDTSGSMISDERLPLQSSLUK	241		
Qy	278	EMLETSDDDFVNVASNSNAODVSCFOHLVQANVRNKVKLDVANNITAKGIDTYKKG	337		
Db	242	LLVKELREODNTAIVTYAGDSRIA-----LPSISGSHKAEINAAIDSLDAEGSTNGGAGL	296		
Qy	338	SFAFQLLNYSRANCNKIIMLFTDG-----GEERAQEIFNKYKDKVFRFVSQ	391		
Db	297	ELAYQOATK-GFIKGGIINR-ILLATDGFNVGDIDDPKSIKESVMVKQSGVTLSTFGVGN	354		
Qy	392	HNVERGPIONMACENKGYEYIPSGAIRINTQEYLDVLRPMVL--ACDKAKQVQ---	445		
Db	355	SYNEAMVYRIADVGNNGNSYIDTLS-----EAKVLNSENROMLITVAKDQRAIEFNA	410		
Qy	446	WTNVYLDALGLVITGLPVENITQGFENKTNLKNQLILGVMGVD-VSLEDI---KRLT	501		
Db	411	WTEY---RQIG-----YE-----KQLRVEHFNNDVDAGDIGACKHIT	447		
Qy	502	PRFTLCPNGYFYAIDPNGVYLLHPNLOPKNPKSQE	536		
Db	448	LLFELTLNGKASIDKLRYA--PDNKLAKSDKTK	480		

RESULT 14

E71619
RAD2 endonuclease PFB0265C - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C:Accession: E71619
R: Gardner, M.J.; Tetteglin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
Pierce, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
Science 282, 1128-1132, 1998
A:title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A:Reference number: A71600; MUID:99021743
A:Accession: E71619
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1516 <GAR>
A:Cross-references: GB:AE001383; GB:AE001362; NID:g3845135; PIDN:AAC71842.1; PID:g3845135
C:Experimental source: clone 3D7
C:Genetics:
A:Gene: PFB0265C

Query Match 2.8%; Score 155; DB 2; Length 1516;
Best Local Similarity 18.9%; Pred. No. 0.5;
Matches 178; Conservative 133; Mismatches 291; Indels 340; Gaps 52;

QY 119 SNEVYVNAKDDL--PEKNDSEPGSRIKPVFTEADANFGRIQSQAHAHVHPDIYEYS 176
DB 517 NDVIIHNKNMNIYNKYNECSSEKINDNGISKNIN-----ILELPNNL-DTS 567
QY 177 TIVLNELNWTSSALDE--VFKNREEDPSLLW-----QVFGSATGLARYYPASPWDNSRT 229
DB 568 NIPL-----EGKDEYKVYVYVKKEIRIPLFKEINKEIF-----EKL 603
QY 230 PNKID--LYDVRRPY----TGAASPDMLILVDYSGVSCLT-LKLIRT----- 274
DB 604 PLKIQQILOLDIKEE-WYTDNRKAIRAKSKDDM-----DVFSQVQLTYVRMIKTDFIEKL 658
QY 275 --SYSEMLETLSDDDFVN---VASFNNAQDVSCFOHLVQANVRNKVKLKDAVN--NIT 326
DB 659 KIRMAENIQSVGELLNKSMTDNINIKYINVLRQ-KRSKKKKKKFLMDIINTYNT 717
QY 327 A-----KGITYKKGFSAFEQLL--NYNVSRANCNKIIIMLFTDGGERAQEIF 373
DB 718 TESKYQDLYVKGESSEDIKNQIDFVTQECYRNNDIIRDTHDK-----SDIF 764
QY 374 N--KYNKDCKVVRFRFSVQH-----NYERGPQWACENKGYIYEIPSIGAIRINTQE 425
DB 765 KNIKIDNNKKYIYNLELEQBEINEKNKYNKNND--SNKTFE-----LKIE NEF 812
QY 426 YLDVLGRPWLAGDK---AKQVQT-----NVYLDALELGIVITGTLPVENIT 470
DB 813 KKDLLDDSQIFGSLLADIKEYNTADNLNNENKSLYEDGENF---ITRNEP---IT 866
QY 471 QOFENKTNL-----KNQILGVMGVDVSLEDIKRLTPTFLCPN---G 510
DB 867 NEYEKNNIYISDEQYNBEDIIFKQIKEREKNNDTSSDDFFENCSCVQEKIYYNEKIEE 926
QY 511 YYFAID---PNGYVLLHNPLOPKNPKSQEPVT-----LDPLD--AELEN-----DI 551
DB 927 YNNKNDKSSSSSIILEEIYKKEKDELVSPLCVLLDEFHSNDLENNYISVSSDDM 986
QY 552 KVEIRNMKIDGESKEFTRLVKSODERYIDKGRTTWTPVNGTDSLALVLTYSFY 611
DB 987 KTNVSKNNITG---WK-----VK---ENKVDKTVNEY----- 1010
QY 612 IKAKLEETITQARSKG-----KMKDSFTLKPDNFEESGYTF-----IAPROYCN 656
DB 1011 -----DKGGDGVIEISFDESHKLESKFDDNNIYDNDDELEKNLSKOIIS 1057
QY 657 DLKISDNNTEFLNF-----REFIDRKTPPNPS-----CHADL 689

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QY 421 INTQYLDVLGRPWLAGKAKO-----VQWTVNYLDALELGLVITGTL 465
Db 1518 IINK-----GDVKLLIGNYFDDMKVSLFTIEDNTIKLNGVILDE-----NGVAQ 1564
QY 466 VFNITQGFENKTLKQILGVNGVDVSLIEDIKRLPFTLCPNGYGYFAIDPNGYVLLHP 525
Db 1565 ILKFMHNAKSALNTSNLNFLESINIK-----NIFYNNLDPNIEFILD 1609
QY 526 NQPKNPKSOEPTVTLDFLDAELENDIKVEIRKMDGESGEKTFRLVKQSODERYIDKGN 585
Db 1610 NF-----IISGSNSIGQFE-LICDKKN-----1631
QY 586 RTVTWTPVNGTDSLALVLPITYFYIKAKLEETIQARSKKGMKMDSETLKPDNFEESG 645
Db 1632 -----IOP-----YFINKIKET-----SYTLYVGNRQN-- 1655
QY 646 YTFIAPRYCNDLKISDNTEFLNFNE-----FIDR---KTPNNPSCNADLIN----- 691
Db 1656 -LIVEPSYHLDD---SGNISSTVINFSQKLYGIDRVVKNVIAIAPNLYTDEINITPVYKP 1711
QY 692 -----RVLDAGTNE-----LVQNYW-----SKOKNKGVKARFVVT 724
Db 1712 NYICPEVILLDANYINEKINVINLDIRVYVNDNGSDLLILIANSEEDNQPVKIRFV-- 1769
QY 725 DGGITRVYKPEAGE-----NWQENPE-----TYEDSFYKR-----SLDNDNY 761
Db 1770 -----NVFKSDTAADKLFSNFSDKQDVSVSKIIISTFSLAAYSDFGFEYFGLVSLDND-- 1822
QY 762 VFTAPYFNKSGPGAYESGIMVSKAVEYIQOKL--LKPAAVVGIKIDVNSWNIENFTKTSIR 819
Db 1823 -----YFYNISFCNMVSGL-----IYINDSLYFKP-----PKNNLITGFTTI-- 1860
QY 820 DPCAGPVCDCKRNSDVNDVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNISV 879
Db 1861 -----DGN-----KYFDPPTKSGAASIGEI-----TIDGKD 1886
QY 880 YAFNKSVDYQSVCEPGNAPKQAGHRSAYVPSVADILQIGWATAAWSILQOFLLSLTF 939
Db 1887 YYFN-----KOG-----ILOQGVINTSDG---LKYFAPAGTL 1915
QY 940 PRLEAVEME-----DDFTASLSKQSCITEQTOYFFDNDNSKFSFGVLDG 985
Db 1916 DENLEGESVNFICKLNIDGKIYYFEDNYRAV-EWKLDDDETYFNEPKTGEALKGLHQIG 1974
QY 986 NCSRIHFHGEKLMNTNLIFI 1004
Db 1975 DNKYFDDNGIMOTGFTI 1993

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Search completed: July 23, 2001, 07:38:14
Job time: 511 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model.

Run on: July 23, 2001, 07:48:12 ; Search time 66.28 Seconds
(without alignments)

535.436 Million cell updates/sec

Title: US-09-397-548-16

Perfect score: 5443

Sequence: 1 MAAGCLLALTFLFQSLIG.....RLIQAQRTSDGNPCDMVK 1036

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5443	100.0	1091	1	CIC2_HUMAN
2	5234	96.2	1091	1	CIC2_RAT
3	5244.5	96.0	1106	1	CIC2_RABIT
4	607	11.2	734	1	UN36_CABEL
5	194.5	3.6	886	1	ITH3_MOUSE
6	182	3.3	885	1	ITH3_HUMAN
7	180.5	3.3	887	1	ITH3_RAT
8	184.5	3.0	886	1	ITH3_MESAU
9	161	3.0	1829	1	DPOL_THEST
10	159	2.9	1956	1	ATX1_PLAFA
11	157.5	2.9	575	1	YFBK_ECOLI
12	154.5	2.8	946	1	ITH2_HUMAN
13	152	2.8	1290	1	EXCL_CLOBO
14	151.5	2.8	420	1	YH03_SYNY3
15	150.5	2.8	921	1	ITH4_PIG
16	150	2.8	654	1	MCPC_BACSU
17	149	2.7	930	1	ITH4_HUMAN
18	148	2.7	964	1	DPOL_CBEPI
19	144	2.6	1087	1	YXN_CLOTM
20	143	2.6	946	1	ITH2_MESAU
21	142.5	2.6	382	1	YH03_CABEL
22	141	2.6	1251	1	RBP2_PLAEB
23	140.5	2.6	935	1	ITH2_PIG
24	140	2.6	2710	1	TOXA_CLODI
25	140	2.6	3305	1	APLP_MANSE
26	139.5	2.6	764	1	PAG_BACAN
27	139	2.6	1513	1	STUT1_YEAST
28	138	2.5	1180	1	C4AA_BACTI
29	137	2.5	984	1	HVSA_STRAG
30	136.5	2.5	3063	1	CALC_HUMAN
31	135.5	2.5	946	1	ITH2_MOUSE
32	134.5	2.5	2077	1	TEGO_HSV6U
33	133	2.4	862	1	MUTS_BORBU

34	133	2.4	1323	1	ADRL_YEAST	P07248 saccharomyc
35	132.5	2.4	547	1	SYM_BUCAI	P57210 buchnera ap
36	132.5	2.4	929	1	CA1C_NOTVI	Q91145 notophthalm
37	132.5	2.4	1679	1	Y109_YEAST	P04057 saccharomyc
38	132	2.4	697	1	YE9C_SCHPO	O13773 schizosacch
39	131	2.4	1634	1	DPOL_METJA	Q58295 methanococc
40	131	2.4	1658	1	YH67_YEAST	Q03661 saccharomyc
41	130.5	2.4	987	1	YD94_METJA	Q58789 methanococc
42	130.5	2.4	1018	1	YC14_METJA	Q58611 methanococc
43	129	2.4	1244	1	Y307_MYCPN	P75342 mycoplasma
44	128.5	2.4	1254	1	UEPC_YEAST	P39538 saccharomyc
45	128	2.4	1113	1	Y140_MYCPN	P75033 mycoplasma

ALIGNMENTS

RESULT 1

CIC2_HUMAN

ID AC P54289; STANDARD; PRT; 1091 AA.

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-2/DELTA SUBUNITS PRECURSOR.

DE SUBUNITS PRECURSOR.

GN CACNA2D1 OR CACNL2A OR CCHL2A.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

XP MEDLINE=92110010; PubMed=1309651;

RA Williams M.E., Feldman D.H., McCue A.F., Brenner R., Velicelebi G., Ellis S.B., Harpold M.M.;

RT "Structure and functional expression of alpha 1, alpha 2, and beta subunits of a novel human neuronal calcium channel subtype.";

RL Neuron 8:71-84(1992).

CC -!- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN EXCITATION-CONTRACTION COUPLING.

CC -!- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS: ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS HETERODIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -!- TISSUE SPECIFICITY: CENTRAL NERVOUS SYSTEM, SKELETAL MUSCLE AND AORTA TISSUES.

CC -!- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM A PRECURSOR FORM (BY SIMILARITY).

CC -!- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.

CC -----

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CC -----

CC EMBL; M76559; AAA51903.1; -

DR MIM; 114204; -

DR InterPro; IPR002035; -

DR Pfam; PF00092; vwa.1.

DR PROSITE; PS00234; VWFA_DOMAIN; 1.

KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel; Calcium channel; Glycoprotein; Phosphorylation; Signal.

FT SIGNAL 1 24 POTENTIAL.

FT CHAIN 25 944 L-TYPE CALCIUM CHANNEL ALPHA-2 SUBUNIT (BY SIMILARITY).

FT CHAIN 945 1091 L-TYPE CALCIUM CHANNEL DELTA SUBUNIT (BY SIMILARITY).

FT TRANSMEM 446 469 POTENTIAL.

FT TRANSMEM 906 930 POTENTIAL.

FT TRANSMEM 1067 1086 POTENTIAL.
FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 324 324 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 348 348 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 475 475 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 585 585 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 594 594 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 663 663 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 769 769 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 876 876 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 883 883 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 973 973 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 986 986 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 501 501 PHOSPHORYLATION (BY CAPK)
FT MOD_RES 501 501 (BY SIMILARITY).
FT MOD_RES 833 833 PHOSPHORYLATION (BY CAPK)
FT MOD_RES 833 833 (BY SIMILARITY).
SQ SEQUENCE 1091 AA; 123183 MW; 2E4E13EE29A47837 CRC64;

Query Match 100.0%; Score 5443; DB 1; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTTLFOSLLIGPSSEPPFSAVTKSWDKMQEDLVTLAKTAGSVNQLVDI 60
DB 1 MAAGCLLALTTLFOSLLIGPSSEPPFSAVTKSWDKMQEDLVTLAKTAGSVNQLVDI 60

QY 61 YEKYQDLTVFENNAQQLVEIARDEIKLLSNRSKALVSLAEAEKVQAAHWRREDFASN 120
DB 61 YEKYQDLTVFENNAQQLVEIARDEIKLLSNRSKALVSLAEAEKVQAAHWRREDFASN 120

QY 121 EYVYNAKDDLPKNDSEPGSQRIKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180
DB 121 EYVYNAKDDLPKNDSEPGSQRIKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180

QY 181 NELNWTSLALDEYFKKNREDEPSLLMQVFGSATGLARYYPASVWVNSRTPNKIDLYDVR 240
DB 181 NELNWTSLALDEYFKKNREDEPSLLMQVFGSATGLARYYPASVWVNSRTPNKIDLYDVR 240

QY 241 RPWYIQQASPKDMLILVDVSGVSLGTLKLTSTVSEMLETLSDDDFVNVASFNSAQD 300
DB 241 RPWYIQQASPKDMLILVDVSGVSLGTLKLTSTVSEMLETLSDDDFVNVASFNSAQD 300

QY 301 VSCFQHLVQANVRNKKVLKDAVNNITAKGIDYKKGFSFAFQLELLNYSVRANCKNIIML 360
DB 301 VSCFQHLVQANVRNKKVLKDAVNNITAKGIDYKKGFSFAFQLELLNYSVRANCKNIIML 360

QY 361 FTDGGEERAQEIFNKYKDKKVRVFRFVSGQHNYSRGPQMACENKGYEYIPISGAIR 420
DB 361 FTDGGEERAQEIFNKYKDKKVRVFRFVSGQHNYSRGPQMACENKGYEYIPISGAIR 420

QY 421 INTQEVLDVLRPMVLADKAKQVQWNTVYLDALGLVITGTLVFNITGCFENKTNLK 480
DB 421 INTQEVLDVLRPMVLADKAKQVQWNTVYLDALGLVITGTLVFNITGCFENKTNLK 480

QY 481 NOLLILGVMGVDSLEIDKRLTPRFTLCPNGYVFAIDPNGYVLLHPNLPKPKSQEPVTL 540
DB 481 NOLLILGVMGVDSLEIDKRLTPRFTLCPNGYVFAIDPNGYVLLHPNLPKPKSQEPVTL 540

QY 541 DFLDAELENDIKVEIRNKMIDSEKFTRTLKVSQDERYIDKGNRTYVTPVNGTDSL 600
DB 541 DFLDAELENDIKVEIRNKMIDSEKFTRTLKVSQDERYIDKGNRTYVTPVNGTDSL 600

QY 601 ALVLPYSPYIIKALEETITQARSKGKMDSETLKPDNFEESGYTFTAPRDYCNLKI 660
DB 601 ALVLPYSPYIIKALEETITQARSKGKMDSETLKPDNFEESGYTFTAPRDYCNLKI 660

QY 661 SDNTEFLNFEIDRKTNNPNSCNADLINRVLLDAGFTNELVQYWSKQKNIGVKAR 720

DB 661 SDNTEFLNFEIDRKTNNPNSCNADLINRVLLDAGFTNELVQYWSKQKNIGVKAR 720
QY 721 FVVDGGITRYPKREAGENQWENPETYEDSFYKRSLODNDNYVFTAPYENKSGPGAYESGI 780
DB 721 FVVDGGITRYPKREAGENQWENPETYEDSFYKRSLODNDNYVFTAPYENKSGPGAYESGI 780
QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTSIRDPCAGPVCDCRNSDVMDCVI 840
DB 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTSIRDPCAGPVCDCRNSDVMDCVI 840
QY 841 LDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLNYSVYAFNKSYQSVCEPGAAPKQ 900
DB 841 LDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLNYSVYAFNKSYQSVCEPGAAPKQ 900
QY 901 GAGHSAYVPSVADILQIGWATAAANSILOQFLSLFPPRLLEAVEMEDDDFTASLSKQ 960
DB 901 GAGHSAYVPSVADILQIGWATAAANSILOQFLSLFPPRLLEAVEMEDDDFTASLSKQ 960
QY 961 SCITEQTYFFDNDKSFSGVLDGCGNCSRFHGEKLMNTNLFIMVESKGTCCPCTRLLI 1020
DB 961 SCITEQTYFFDNDKSFSGVLDGCGNCSRFHGEKLMNTNLFIMVESKGTCCPCTRLLI 1020
QY 1021 QAEQTSQDGNPCDMVK 1036
DB 1021 QAEQTSQDGNPCDMVK 1036

RESULT 2
CIC2_RAT
ID CIC2_RAT STANDARD; PRT; 1091 AA.
AC P54290;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE DIHYDROXYDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-2/DELTA
DE SUBUNIT PRECURSOR.
GN CACNA2D1 OR CACNL2A OR CCHL2A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-9222762; PubMed-1314383;
RA Kim H.L., Kim H., Lee P., King R.G., Chin H.;
RT "Rat brain expresses an alternatively spliced form of the
RT dihydropyridine-sensitive L-type calcium channel alpha 2 subunit.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:3251-3255(1992).
CC -! FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN
CC EXCITATION-CONTRACTION COUPLING.
CC -! SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:
CC ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS
CC HETERODIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).
CC -! SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -! ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -! PM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM
CC A PRECURSOR FORM (BY SIMILARITY).
CC -! SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M86621; AAA41088.1; -;
DR InterPro; IPR002035; -;
DR Pfam; PF00092; vwa; 1.
DR PROSITE; PS50234; VWF_A_DOMAIN; 1.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;

```
KW Calcium channel; Glycoprotein; Phosphorylation; Signal;
KW Alternative splicing.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 944 L-TYPE CALCIUM CHANNEL ALPHA-2 SUBUNIT
FT FT (BY SIMILARITY).
FT CHAIN 945 1091 L-TYPE CALCIUM CHANNEL DELTA SUBUNIT (BY
FT FT SIMILARITY).
FT TRANSMEM 445 468 POTENTIAL.
FT TRANSMEM 906 930 POTENTIAL.
FT TRANSMEM 1067 1086 POTENTIAL.
FT CARBOHYD 92 92 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 184 184 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 323 323 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 347 347 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 474 474 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 584 584 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 593 593 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 663 663 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 769 769 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 812 812 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 876 876 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 883 883 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 973 973 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 986 986 N-LINKED (GLCNAC. .) (POTENTIAL).
FT MOD_RES 500 500 PHOSPHORYLATION (BY CAPK)
FT FT (BY SIMILARITY).
FT MOD_RES 833 833 PHOSPHORYLATION (BY CAPK)
FT FT (BY SIMILARITY).
FT SEQUENCE 1091 AA; 123822 MW; 7054907D9D343B34 CRC64;

Query Match 96.2%; Score 5234; DB 1; Length 1091;
Best Local Similarity 95.7%; Pred. No. 2.9e-293;
Matches 992; Conservative 24; Mismatches 19; Indels 2; Gaps 2;

QY 1 MAAGCLLATLTLFQSLLLGPSEEPFPAVNIKSWDKMQEDLVTLAKTASGVNQLVDI 60
DB 1 MAAGCLLATLTLFQSLWLLGPSEEPFPAVNIKSWDKMQEDLVTLAKTASGVTLADI 60
QY 61 YEKYQDLYTEPNNAQLVEIARDETEKLSNRKALVSLALAEKVAQAAHWRDFASN 120
DB 61 YEKYQDLYTEPNNAQLVEIARDETEKLSNRKALVSLALAEKVAQAAHWRDFASN 120
QY 121 EYVYNAKDDLPKNDSPGSGORIKPVFIEDANFGRQISYQAAVHIPTDIYEGSTIVL 180
DB 121 EYVYNAKDDLPKNDSPGSGORIKPVFIEDANFGRQISYQAAVHIPTDIYEGSTIVL 180
QY 181 NELNWTSSALDEYFKKNEEDPSLLHQVFGSATGLARYYPASPWVDSRTPNKLIDLYDVR 240
DB 181 NELNWTSSALDEYFKKNEEDPSLLHQVFGSATGLARYYPASPWVDSRTPNKLIDLYDVR 240
QY 241 RPWYIGGAAPKMDLTLVDVSGVSLTLKLTSTVSEMLETSSDDFVNVASFNSNAOD 300
DB 240 RPWYIGGAAPKMDLTLVDVSGVSLTLKLTSTVSEMLETSSDDFVNVASFNSNAOD 300
QY 301 VSCFQHLVQANVRNKKVLDAVNNTAKGIDYTKGFSFAFQLLNYSRANCKIIML 360
DB 300 VSCFQHLVQANVRNKKVLDAVNNTAKGIDYTKGFSFAFQLLNYSRANCKIIML 360
QY 361 FTDGGERAQEAFENKYNKKVYRFRFSVGHNYERGPIQWACENKGYIYETPSIGAIR 420
DB 360 FTDGGERAQEAFENKYNKKVYRFRFSVGHNYERGPIQWACENKGYIYETPSIGAIR 420
QY 421 INTQEYLDVLRPMVLGAKQKQVQNTNYLDALGLVITGLPVFNITGQPNKTNLK 480
DB 420 INTQEYLDVLRPMVLGAKQKQVQNTNYLDALGLVITGLPVFNITGQPNKTNLK 480
QY 481 NOLILGVMGVDVSLDEIKRLTPRTFLCPNGYYPFADPNQVYLLHPNLPKPKSQBPVTL 540
DB 480 NOLILGVMGVDVSLDEIKRLTPRTFLCPNGYYPFADPNQVYLLHPNLPKPKSQBPVTL 540
QY 541 DFLDALENDIKVEIRNKMIDGESGEKTFRTLVKSQDERIDKGNRTYTWTPVNGTDYR 599
```

J. Biol. Chem. 265:14738-14741(1990).

- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN EXCITATION-CONTRACTION COUPLING.

- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS: ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS HETERODIMERS THAT ARE DISULFIDE-LINKED.

- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

- ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE SPLICING.

- TISSUE SPECIFICITY: SKELETAL MUSCLE.

- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM A PRECURSOR FORM.

- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.

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EMBL; M21948; AAA81562.1; -

PIR; S10579; CHRA2.

InterPro; IPR002035; -

Pfam; PF00092; vwa; 1.

PROSITE; PS0234; VWFA_DOMAIN; 1.

Ion channel; Transmembrane; Ion transport; Voltage-gated channel; Calcium channel; Glycoprotein; Phosphorylation; Signal;

Alternative splicing.

SIGNAL	1	26	POTENTIAL.
CHAIN	27	960	L-TYPE CALCIUM CHANNEL ALPHA-2 SUBUNIT.
CHAIN	961	1106	L-TYPE CALCIUM CHANNEL DELTA SUBUNIT.
TRANSMEM	448	471	POTENTIAL.
TRANSMEM	921	945	POTENTIAL.
TRANSMEM	1082	1101	POTENTIAL.
CARBOHYD	94	94	N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD	138	138	N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD	186	186	N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD	326	326	N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD	350	350	N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD	477	477	N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD	606	606	N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD	615	615	N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD	678	678	N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD	784	784	N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD	827	827	N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD	891	891	N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD	898	898	N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD	988	988	N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD	1001	1001	N-LINKED (GLCNAC. . .) (POTENTIAL).
MOD_RES	503	503	PHOSPHORYLATION (BY CAPK) (POTENTIAL).
MOD_RES	848	848	PHOSPHORYLATION (BY CAPK) (POTENTIAL).

SEQUENCE 1106 AA; 125042 MW; B00DE7F3C877B618 CRC64;

Query Match 96.08; Score 5224.5; DB 1; Length 1106;

Best Local Similarity 94.7%; Pred. No. 1e-292;

Matches 1002; Conservative 15; Mismatches 12; Indels 29; Gaps 4;

QY 1 MAAGCLLATLTFLQS--LLIGPSEEPFSAVTIKSWDKMQEDLVTLAKTASGVNOLV 58

DB 1 MAAGPLAWTLTLQWUWLLIGPSEEPFSAVTIKSWDKMQEDLVTLAKTASGVHOLV 60

QY 59 DIYEKYQDLYVEPNNAQVLEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDA 118

DB 61 DIYEKYQDLYVEPNNAQVLEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDA 120

QY 119 SNEVYVYNAKDDLPDEKNDSEPGSORIKPVFIEDANFRQSYQHAHVHPTDIYEGSTI 178

DB 121 SNEVYVYNAKDDLPDEKNDSEPGSORIKPVFIEDANFRQSYQHAHVHPTDIYEGSTI 180

RESULT 4

ID	UN36_CAEEL	STANDARD;	PRT;	734 AA.
AC	P34374;			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DE	01-OCT-2000 (Rel. 40, Last annotation update)			
GN	UNC-36 PROTEIN.			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;			

QY 999 TNLPIFIMVESKGTCTPCDTRLLIQAEQTSDDGNPCDMVK 1036

DB 1014 TNLPIFIMVESKGTCTPCDTRLLIQAEQTSDDGNPCDMVK 1051

OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fraser A.,
 RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
 RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
 RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
 RA Sims M., Smalton N., Smith A., Smith M., Sonhammer E., Staden R.,
 RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
 RA Watson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
 RA Wohlman P.;
 RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.;
 RL Nature 368:32-38(1994).
 CC -1- SIMILARITY: TO CALCIUM CHANNEL ALPHA-2B SUBUNIT.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: LJ4433; AAA27969.1; -;
 DR PIR: S44617; S44617.
 DR WormPep: CS0C3.11; CE00117.
 DR InterPro: IPR002035; -;
 DR Pfam: PF00092; vwa: 1.
 DR PROSITE: PS0234; VWFA_DOMAIN; 1.
 DR Ionic channel; Ion transport; Voltage-gated channel; Calcium channel;
 KW Glycoprotein.
 FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 476 476 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 514 514 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 734 734 MW: CCFB78C8DEB4B71F CRC64;
 SQ SEQUENCE 734 AA; 85034 MW; 85034 MW;
 Query Match 11.2%; Score 607; DB 1; Length 734;
 Best Local Similarity 26.6%; Pred. No. 1.3e-27;
 Matches 180; Conservative 127; Mismatches 258; Indels 112; Gaps 20;
 QY 47 LAKTAGVQLVDYKQYQDLYTEPNARQLVIAARDTEKLLSNRS----KALVSLAL 102
 DB 36 MKETFSKISHETILKQYKXELVEEQDPPRAELKSKHRIEDYLVKRSQFAYRAKIS--L 93
 QY 103 EAKVQAHHQWRDEFASNVYVYNAKDDLPDK-NDSEGSQRIK-----VFIEDANF 155
 DB 94 EARSVRNDSTVNDPQSKSFIREMSAKOGNDGTIYESHLGLKRLKVNETKSNLTQANF 153
 QY 156 -GROISVQHAHVHPTDYGSTIVLNELNWTSAIDVFKKNEEDPSLLWQVFGSATGL 214
 DB 154 YTLPTSSVSSAVHIPTPLDYDRNEDLLKIDW-SDIDAVYRTNRETKDLAFQFCSEAGY 212
 QY 215 ARYPASPFW-DNSRTNKTDLIDVRRPWTYIQGAASPDKMLIIVDVSQSGTLKLIR 273
 DB 213 MRYTPAASWFDNQ--DEHLDFDCRNTWYINSATSKNVNLMDSGSMGLQRYEVAK 270
 QY 274 TSVSEMLETSDDDFVNVASNSNA---QDVSCFOHLVQANRKNKYLKDAVNNTAKGI 330
 DB 271 QTTEAILETISHNDYFNIMTFKNTFLDCNGTNGTLLQATMRNKKALKRMDYQSEKG 330
 QY 331 TDYKKGFSFAPEQLLYN-----VSRANCKNIIMLTDGGEERAQEIFKNYKNDKRVVF 385

DB 331 AEYEKALPIAFSVLLDINNGGDNRRGACENVIMLTDGAPNAYKKIFDMYNADKKRVVF 390
 QY 386 RFSVGQHNRYERGPIQWACENKGYEIPSGAIRINTQEYL----DVLGRPMVLAGDKA 441
 DB 391 TFLVGDDEAIDFNEVREMACNNGYMHVANNADVDEKIHYYIRMSRVVGRHYKESQLS 450
 QY 442 KQVQWNNVYLDLELGL--VITGTLPVFNITGQFENKTN----- 478
 DB 451 ---WMTGVYRERLYLPRPEIFAEPVPIITNQSFAVMNKMASRRKIRLOKSPARSRMFTTV 507
 QY 479 ---LKNOLLIGVMGVDSVLESDIKRLTPREFTLCPNGYVFAIDPNGYVLLHPNLQPKNP-- 532
 DB 508 SYPIVNEFTMGVAANNIPLETAQKSHPANIGSKSVFFMLDQNGFVMTHPQLRPIDPFT 567
 QY 533 --KSQEPVTLDFLD-----AELENDIKVEIRNMKID 561
 DB 568 KYHKQNNNNMDLLELVGQNNVRSQSQAVSDLVCEGANTYAECDLRLKAVRKMID 627
 QY 562 GESGEKTRFLVKSQDERY---IDK---GNRTYTWTPVNGTDYSLALVLPITYSYFYIKA 614
 DB 628 CDNSD-----VOOLDVLYATELLDRVYPOTNTYAEICINHANFVLGLAVAKGDDYRVK 681
 QY 615 KLEETITQARSKKGMK 631
 DB 682 K-----QKKYDFGRVK 692
 RESULT 5
 ITH3_MOUSE
 ID ITH3_MOUSE STANDARD; PRT; 886 AA.
 AC Q61704;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY
 DE CHAIN H3).
 GN ITIH3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6N; TISSUE=Liver;
 RX MEDLINE=95194326; PubMed=7534067;
 RA Chan P., Risler J.-L., Raguenez G., Salier J.-P.;
 RL "The three heavy-chain precursors for the inter-alpha-inhibitor
 RT family in mouse: new members of the multicopper oxidase protein group
 RT with differential transcription in liver and brain.";
 RL Biochem. J. 306:505-512(1995).
 CC -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
 CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
 CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
 CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
 CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
 CC SIMILARITY).
 CC -1- SUBUNIT: I-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
 CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,
 CC BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-1) IS COMPOSED OF H1, H2
 CC AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND
 CC BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN BOTH LIVER AND BRAIN.
 CC -1- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
 CC 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE ITIH FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
 CC -----
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CC or send an email to license@isb-sib.ch).
CC -----

DR	EMBL; X70393; CAA49843.1; -				
DR	MGD; MGI:96620; Itih3.				
DR	InterPro; IPR002035; -				
DR	Pfam; PF00092; vwa; 1.				
DR	PROSITE; PS50234; VWFA_DOMAIN; 1.				
KW	Serine protease inhibitor; Repeat; Signal; Multigene family;				
KW	Glycoprotein.				
FT	SIGNAL	1	18	POTENTIAL	
FT	PROPEP	19	30	BY SIMILARITY.	
FT	CHAIN	31	645	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN	
FT				H3.	
FT	PROPEP	647	885	BY SIMILARITY.	
FT	DOMAIN	279	439	VWFA.	
FT	CARBOHYD	88	88	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	577	577	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	BINDING	646	646	CHONDROITIN 4-SULFATE, CROSS-LINK SITE	
FT				(BY SIMILARITY).	
SQ	SEQUENCE	886 AA;	98977 MW;	15955308CF5030A CRC64;	

```

Query Match      3.6%; Score 194.5; DB 1; Length 886;
Best Local Similarity 19.9%; Pred. No. 0.00088;
Matches 185; Conservative 138; Mismatches 347; Indels 261; Gaps 44;

QY 27 FPSAVTIKSWDKMQEDLVTLAKTAGVNLQDIYKYQDLYTVPNNARQLVEITAARDI 86
Db 98 YPGNVAKEVAQOYKAYVSOQKTAG---LVKASGRKLEKFTVSVNAAGSKVTFELTY 153
QY 87 EKLLSNRSKALVSLAEAEKYOAAHQWRREDFASNEVYYNAKDDLDPEKNREDSEPGSQRIK 146
Db 154 EELL-KRNGKGVENLYKQPKOLVRHFEID-----AHIEP-----Q 189
QY 147 PVFIEDANFGROISYCHAAVHIPTDIYEGSTIVLNELNWTLSALDEVFKKRNREDPSLLWQ 206
Db 190 GISMLDAE-----ASFITNDL-LGSALTKEF----- 214
QY 207 VFGSATGLARYPASPWVDNRSPT-PNKID-----LYDVRRP-----WYI-- 245
Db 215 -----SGKKGHVSEKPSLDQORSCPTCDSLNGDFTIYDVNRSPGNQVINGYFVHF 269
QY 246 --QC-AASPDKMLILDVSGVSLGTLKLRTSVSEMLETSLDDDFVNAFNSNAQDV 301
Db 270 FAPQGLPVVPNIHFVIDVSGMSGRKIQQTRALKILDDVKEDDYLNFLFST---DV 326
QY 302 SCFQ-HLYQANVRNKVKLKDVAVNNITAKGIIDYKKGFSFAEQLLNLYNVRAN-----C 354
Db 327 TTKRDHLVQATPANLKEAKTFVKNIHQSMFNINDGLLKGIEML---NKAREDTVPERS 383
QY 355 NKIIMLTGDC---GEERAQEIFNKYNK--DKKVRVFRFSVGQHNRYERGPLOMACENKG 408
Db 384 TSIIMLTGDCANTGESRPEKIQENVRNAGIGKPEPLNLGFG-NLNYNLETALLENHG 442
QY 409 YVEIPEISGAIINTQBYLDVLRPPVLAGDKAKQOVMTNYLDALBGL--VITGTLVP 466
Db 443 LARIYEDSDANLOLOGFYEVANPLL-----TNVEVEYPENAILDLTRNSYPH 491
QY 467 FNITGOPENKTNLKNQILGVMGVVDVSLDDIKRLTPRTLCPNGYFPAIDPNGVYLLHPN 526
Db 492 F-----YDG-----SEIVVAGRLVDRNNDN-----FKADVKGHGALN-- 523
QY 527 LQPNKPKSQBPVTLDFDLDAELENDIKVEIRKNKIDGESGK--TERTLYKSQDERIDKG 584
Db 524 ----DLTFTTEVDWEEMDAALK-----EQGYFGDYIERLWAYITIBOLLEKKNAG 572
QY 585 NRYTYTPVNGTQYSLA--LVLPFYFYIKAKLEETITQARSKGKMKMDSET-----LK 637
Db 573 DEKENIT-ABALDLSLKHYFVTPLTSMWYTKPEDNEDQTSIADNAGEEAFETTTMSFLT 631
QY 638 PDNFESGYTFIAPROYCNDLKLKISDNTNTEFLNFNFEIDRKTTPNPNPCSNADLINRYLLDA 697

```

Db 632 TQSSQSPYVV-----DGDPHFIQI-----PGKNDSCFNIDEKP 668
 QY 698 GFTNELVQVWYWKQNIKGVARFVVTGGITRVVPKEAGENWQENPETYEDSYKRSLD 757
 Db 669 GTVLRLIQD-----PVT--GIT-VTQGIIGD-----KRS-- 694
 QY 758 NDNYVTATYFNKSGPGAYESGIMYKAVEIYIOCKLLKPAVVGKIDVNSWIENFTKTS 817
 Db 695 NASRRTGKTYFGKLGITNAMDMFREVETEKILG-----TGAELSTFSWLDVTVTQ 747
 QY 818 IRDPCAGPVCDCKRSDVMDCVILDDG--GFLIMAN-----HDDYTNQIGRFFGEIDP 868
 Db 748 -----TGLSVTINRKNKV--VSFGDGSFIVILHQVWKHPHQDFLG-----FYVWDS 795
 QY 869 SLMRHLVNISVYAFNKSVDYQSV--CEPGAAP 898
 Db 796 HRMSAQTHGLLGQFFQPFDFKVFGRGSDP 826

 RESULT 6
 ID ITH3_HUMAN
 AC Q06033; Q99085; STANDARD; PRT; 885 AA.
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY
 DE CHAIN H3) (SERUM-DERIVED HYALURONAN-ASSOCIATED PROTEIN) (SHAP).
 GN ITH3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=93215656; PubMed=7681778;
 RA Bourguignon J., Diarra-Mehrpour M., Thiberville L., Bost F.,
 RA Sesboue R., Martin J.P.;
 RT "Human pre-alpha-1-trypsin inhibitor-precursor heavy chain. cDNA and
 RT deduced amino-acid sequence.";
 RL Eur. J. Biochem. 212:771-776(1993).
 RN [2]
 RP SEQUENCE OF 341-885 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=89137072; PubMed=2465147;
 RA Diarra-Mehrpour M., Bourguignon J., Sesboue R., Mattel M.-G.,
 RA Passage E., Salier J.P., Martin J.P.;
 RT "Human plasma inter-alpha-1-trypsin inhibitor is encoded by four genes
 RT on three chromosomes.";
 RL Eur. J. Biochem. 179:147-154(1989).
 RN [3]
 RP SEQUENCE OF 30-49; 463-477 AND 497-515.
 RX MEDLINE=89380192; PubMed=2476436;
 RA Engbild J.J., Thøgersen I.B., Pizzo S.V., Salvesen G.;
 RT "Analysis of inter-alpha-1-trypsin inhibitor and a novel trypsin
 RT inhibitor, pre-alpha-1-trypsin inhibitor, from human plasma.";
 RL J. Biol. Chem. 264:15975-15981(1989).
 RN [4]
 RP SEQUENCE OF 631-647, AND CROSS-LINKAGE SITE TO BIKUNIN.
 RX MEDLINE=91093267; PubMed=1898736;
 RA Engbild J.J., Salvesen G., Hefta S.A., Thøgersen I.B.,
 RA Rutherford S., Pizzo S.V.;
 RT "Chondroitin 4-sulfate covalently cross-links the chains of the
 RT human blood protein pre-alpha-1-inhibitor.";
 RL J. Biol. Chem. 266:747-751(1991).
 CC -!- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
 CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
 CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
 CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
 CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES.
 CC -!- SUBUNIT: I-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
 CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN.

SQ SEQUENCE 1829 AA; 211875 MW; A113A8BC57EB9CB3 CRC64;

Query Match 3.0%; Score 161; DB 1; Length 1829;
Best Local Similarity 20.1%; Pred. No. 0.21;
Matches 172; Conservative 101; Mismatches 301; Indels 282; Gaps 39;

QY	16	SLLIGPSSEEPFPPS-----AVTIKSWV-----DKMOEDLVILA	48
DB	229	TLLOGRDEHEPEKTHRMGDSFAVEIKGRIHFDLPVVRRTINLPTYLEAVEYAVLGK	288
QY	49	KTASGVNOLVDIYKQDL-----YVTPNNARQLVETAARDIEKLLSNRSKALVSLALE	103
DB	289	RSKLGAEEIAAWEETESMKLAQYSME--DARATYEL-----GEFFPMEAR	334
QY	104	AEKVQAAHQWRDFAS--NEVVY-----NAKDDLDPEKNDSEPGSQRIKPVFI	150
DB	335	LAKLIGQSVMDVSSTGNLVEWYLLRVAYERNELAPKPDSEYRRRLRTYVLGGYVKE	394
QY	151	EDANFGROIISQHAAVHIPTD--IYEGSTIV-----LNELNWTSAIDVEFKKNREEDPSL	203
DB	395	PERGLWENIAYLDFRCH-PADTKVIVKGGIVNISDVKEGDYILGIDG-----	441
QY	204	LQOVFGSATGLARYYPASPVVNSR---TPN-KIDLYDVRRRPWYIQGAASPKDMLILVD	259
DB	442	-WQ---RVKKVWKHYEGKLININGLKCTPNHKVPVVTENDROTRI-----RDSLAKSF	491
QY	260	VSGSVSGLTKLIRTSVSEMLETSLDDDFVNVASFNSN-----NNITAKG	329
DB	492	LSGKVGK---KIITTKL-----PEKIAEFENKPESEEILKGLSGIILAEGLT	537
QY	298	-AODVSCF-----QHLVQANV-RNKKVYLKDAV-----NNITAKG	329
DB	538	LRKDIYFDSRRGKKRISHQYRVEITIGENEKELLERILYIFDKLFGIRFSVAKKGDNA	597
QY	330	--ITDYKKGFSFAFEOILLNWNVSRANCKIIMLFTDGGEEAEOEIFKNYKNDKVRVERF	387
DB	598	LKITAKKAVLYQIEELLK-NIESLYAPAVLRF-----FERDATVVKIRS	642
QY	388	SV---GOHNYERGPIQWACENKGY---YVEIPSIGAIRINTQYDVLVGRPMVLGDK	440
DB	643	TVIVTQGTNNKKKIDIVAKLLDSLGIPYSRYEYKYIENGKELKHILEITGRD	695
QY	441	AKOVMTNVYLDALGLVITGLPVFNITQGF-----NKNLKNOLLILGVMGVD	491
DB	696	-----GLILFQTLVGFISSEKNEALEKAIEVREMNRLKNNSFNLTSTFE	739
QY	492	VSLEDIKRLPRFTLCPNGYFAIDPNGYVLLHPNLOPKNPKSOEPTLDFLDALENDI	551
DB	740	VSSEYKGEVYDLTLEGNPYFA---NG-ILTHNSLYPSIIVTHN-VSPDTLERE	789
QY	552	KVEIRNKMIDGSEKFTRLVKSDERYIDKGNRTYVTPVNGTDSLALVLPYSFY	611
DB	790	-----GCKNDVAPIVG---YKFKDFFG---F	811
QY	612	IKAKLEETITQARSKKGMKMDSETLKPDPNFEEGY-----TFTAPRYCNDLKISD	662
DB	812	IPSLIGELITMRQEIKKMK--ATIDPIEKKMLDYRORAVKLLANSILPNW---LPIIE	866
QY	663	NTEFLNLFNEFDIRKTPNPNPNSCNADLINRVLLDAGFTNELVQVWWSKQKIKGVKARFV	722
DB	867	NGEVKFKIGEFIDRYMEEQDKVRTVDNTEVLEVDNTEVLEVDNTEVLEVDNTEVLEVDNTEV	924
QY	723	VTDGITRVYKPEAGE 738	
DB	925	-----IRHKYKGEAYE 935	

RESULT 10
ATX1_PLAFA
ID ATX1_PLAFA
AC Q04956;
DT 30-MAY-2000 (Rel. 39, Created)

QY	202	SLLMQVFGSATGLARYYPASPVVNSR--PNKID-----LYDVRR--PWYIOGA--	248
DB	208	SALTSPSGKGGHVSFKPS---LDQORSCPTCTDSSLNGDFTIYDVNRESFGNVYVNG	264
QY	249	-----ASPKMLILVDYSGVSGTLKLRISVSEMLETSLDDDFVNVASFNS	296
DB	265	YFVHFAPQGLPVVFKNTVFDIDISGSWAGRKIQOTRVALLKILDDMKQDDYLNFILEST	324
QY	297	NAQDVSCFQHLVQANVRNKKVYLKDAVNITAKGIDYKKGFSFAFEQLLN-----YVNSRA	352
DB	325	GV--TTWDSLVQVATPANLEARTVRSISDGMNTINDGLLRGIRMLTDAREQHTVPER	382
QY	353	NCNKIIMLFTDG-----GEARQEIFKNYKOKKVRVRSVG-QHNYERGPIQWACENK	407
DB	383	SFSIIIML--TDGANTGESRPEKIQENVRKATEGRFPLYNLGFGNNLNFLETMALENH	441
QY	408	GYIYEIPSGAIRINTQYDVLVGRPMVLGDKAKOVQVNTVYLD	452
DB	442	GVARRIEDSDANLQGFVEEVANPLL-----TNVEVE	475

RESULT 9
DPOL_THEST STANDARD; PRT; 1829 AA.
AC O33845;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE DNA POLYMERASE (EC 2.7.7.7).
GN POL.
OS Thermococcus sp. (strain TY).
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Thermococcus.
OX NCBI_TaxID=86030;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98094267; PubMed=94341178;
RX Niehaus F., Frey B., Antranikian G.;
RT "Cloning and characterization of a thermostable alpha-DNA polymerase
from the hyperthermophilic archaeon Thermococcus sp. TY";
RL Gene 204:153-158(1997).
CC -1- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE =
N PYROPHOSPHATE + DNA(N).
CC -1- PTM: THIS PROTEIN UNDERGOES A PROTEIN SELF SPLICING THAT INVOLVES
A POST-TRANSLATIONAL EXCISION OF THE THREE INTERVENING REGION
(INTEINS) FOLLOWED BY PEPTIDE LIGATION.
CC -1- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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entities requires a license agreement. (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC EMBL; Y13030; CAA73475.1;
CC InterPro; IPR002064;
CC InterPro; IPR002203;
CC Pfam; PF00136; DNA_pol_B; 4.
CC PRINTS; PR00379; INTEIN.
CC PROSITE; PS00116; DNA_POLYMERASE_B; FALSE_NEG.
CC PROSITE; PS00881; PROTEIN_SPLICING; 3.
KW transferase; DNA-directed DNA polymerase; DNA replication;
KW DNA-binding; Hydrolase; Endonuclease; Autocatalytic cleavage;
KW protein splicing.
FT CHAIN 1 409 DNA POLYMERASE, 1ST PART (POTENTIAL).
FT CHAIN 410 769 INTEIN I.
FT CHAIN 770 855 DNA POLYMERASE, 2ND PART (POTENTIAL).
FT CHAIN 856 1392 INTEIN II.
FT CHAIN 1393 1441 DNA POLYMERASE, 3RD PART (POTENTIAL).
FT CHAIN 1442 1598 INTEIN III.
FT CHAIN 1599 1829 DNA POLYMERASE, 4TH PART (POTENTIAL).

DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE PROBABLE CATION-TRANSPORTING ATPASE 1 (EC 3.6.1.-).
OS Plasmodium falciparum.
OX Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
RN NCBI_TaxID=5833;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=T9/96;
RX MEDLINE=93132070; PubMed=8421054;
RA Krishna S., Cowan G., Meade J.C., Wells R.A., Stringer J.R.,
RT "A family of cation ATPase-like molecules from Plasmodium
RT falciparum".
RL J. Cell Biol. 120:385-398(1993).
CC - CATALYTIC ACTIVITY: ATP + H₂O -> ADP + ORTHOPHOSPHATE.
CC - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC - SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2
CC ATPASES). SUBFAMILY V.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X65738; CAA46646.1; -
DR InterPro; IPR001757; -
DR Pfam; PF00122; E1-E2 ATPase; 4.
DR PROSITE; PS00154; ATPASE_E1_E2; 1.
KW Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding.
FT DOMAIN 1 35
FT TRANSMEM 36 58
FT DOMAIN 59 61
FT TRANSMEM 62 80
FT DOMAIN 81 407
FT TRANSMEM 408 427
FT DOMAIN 428 440
FT TRANSMEM 441 462
FT DOMAIN 463 1818
FT TRANSMEM 1819 1837
FT DOMAIN 1838 1845
FT TRANSMEM 1846 1863
FT DOMAIN 1864 1881
FT TRANSMEM 1882 1905
FT DOMAIN 1906 1928
FT TRANSMEM 1929 1952
FT DOMAIN 1953 1956
FT MOD_RES 496 496
FT METAL 1760 1760
FT METAL 1764 1764
FT DOMAIN 246 251
FT DOMAIN 252 256
FT DOMAIN 937 941
FT DOMAIN 1344 1347
FT DOMAIN 1363 1372
FT DOMAIN 1680 1684
FT POLY-ASN.
SQ SEQUENCE 1956 AA; AE708AAE99009335 CRC64;

Query Match 2.9%; Score 159; DB 1; Length 1956;
Best Local Similarity 17.1%; Pred. No. 0.3; Mismatches 359; Indels 366; Gaps 45;
Matches 179; Conservative 144;

QY 58 VDYEKQDLYTEPNNAQLVBIARIDIEKLNSR-----SKALVSLALEAEK 106
DB 100 INV-RNTSYIISSS-----ELVPGDIYEIKNNMTIPCDTIILSGSVTMSHMLTGES 152
QY 107 VQAHQHREDFASNEVYVNAKDDLPDKND-----SEPGSORIKPVFTEDANFGRIIS 160
DB 153 V-PHKRLPFEAGNAIKNNKYDSNDEKDDYLRINYNNHASINMKRNHLIEETLGKKDR 211

QY 161 YQAAVHIPTDIYEGSTIVLNLNW-TSALDEVFKKNREDEPSLLMQVEGSATGLARYYP 219
DB 212 EYKSNTH-----DLCSMNKLCYINNTYDDVMKNNKM----- 244
QY 220 ASPWVDNSTRPNKIDLYDVRRPWTIOGA-ASPDKMLILVDVSGSGVGLTLKILRTSVSE 278
DB 245 ---YNNNNNNKKKKINLN---FVKGTYINSNDLY----- 275
QY 279 MLETLSDDDFVNVASFNSNAQDVSCFOHLVQANVRNKKVLDKAVNNITAKGIDTYDKKGS 338
DB 276 -----DDKIGVNIPE---DDVNNMKH--KFNQRININYNDKTNL-----EYNNKHR 317
QY 339 FAFEQLLNVNVRANCKIIMLTGDEGEBAQEIFNKYNKDKKVRVFRFSVGOHNTERGP 398
DB 318 YIYDCLLKVEAISOKNKIY-----SNEDINKY----- 346
QY 399 IOWMACENKGYEYEPSIGAIRINQOEYLDVLRPMVLAG-----DKAKQV 444
DB 347 ----MLYGGTYVLSLYNINKIKYNKEENRIILG-VIKTGFTTKGIVNNILYHKKKEL 401
QY 445 QWNTNYLDALGLGLVITGTLPVFNITGQFENKTNLKNQILG-----V 487
DB 402 NLINDSYKELII-LIYALFSVILLIYILTSNNEYTNHIIKCLDIITDAIPALPTILT 460
QY 488 MGVDSVLEDIKRLTPRTTLCPCNGYFEA-----IDPNGYVLLHPNLQ-----PKNPKSQ 535
DB 461 VGISTAISRLKKKFSISCLCPHKINAGQINTMVPDKTG-TLTENNLFQIITQNKKNK 519
QY 536 EPVTDLFDLDAELNDIKVEIRNKMIDGESGEKTFRLVKSQDERYIDKGNRTYTWTPVNG 595
DB 520 NMLS-DFIHK-----EMNTESIYHSKDDNNHNNK----- 549
QY 596 TDYSLALVLTFSFYVYKAKLEETITQARSKGKMKD-----SETLKPDPNFEESG 645
DB 550 -----SIIEYIKONMMKMLHTSSK-KKSITKERSNLFVQTIKSCLLKDHYYKEKK 599
QY 646 YTFIAPRDYCNLDKISDNN-TEFLN-----FNEF--IDRKTNNPSCNADLINRVLLD 696
DB 600 KEYTNTNYCNDLHINDSTCSSYLLNSSETKDAYCEYVNIH-----LCD---INKNMD 650
QY 697 AGFTNELVQNSKQKNIGKARFVVVTDGGITRVYPKEAGENWQENPETEYDSFYKRS 756
DB 651 INSKNELMGKYSKNELMGKTIKELM-----GKYSKNEL 684
QY 757 DNDNYVFTAPYFNKSGGAYESGIMVSKAVEIYQGLKLPVVG-----IKIDVNSWI 810
DB 685 -----MGKYSKNELMGKYSKNELMGKYSKNELMGKTIKQVGVDTNIYH 737
QY 811 ENFTKTSIRD-PCAGPVCDCKRNSDVMDCV-----ILDDGGFLLMANHDDYTNOIGRF--- 862
DB 738 MNCNDNYNDYPCD---YNCNCCNDYHRLYHNINKDNSFNIPPEKNKSYNNISEHIKI 794
QY 863 -----FGEIDPSLMRHLNIVSYAF-----NKSYDYQ 889
DB 795 NYPLLFEALACCHTLKSVNNKIMGDVLEILMFNFTNCDMLNNSNFIKEKKKNCSDYFQ 854
QY 890 SVCEPAAAPQAGAGHSAYVPSYADILQIGWATAAWSILQOFLSLTTPRLLEAVEME 949
DB 855 KI---DGDKNIGNANDERCHLNN-----NLVSYNLIKRF----- 884
QY 950 DDDFTASLSKQSCITEQTQYFFDNDKS 977
DB 885 --EFQRLQRMVIVKST-YGNNDNNDN 909

RESULT 11
YFBK_ECOLI
ID YFBK_ECOLI STANDARD; PRT; 575 AA.
AC P76481;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)

PROSITE; PS00142; ZINC_PROTEASE; 1.
 Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc.
 DR KW INIT_MET 0 0
 FT CHAIN 1 448 BOTULINUM NEUROTOXIN C1, LIGHT-CHAIN.
 FT CHAIN 449 1290 BOTULINUM NEUROTOXIN C1, HEAVY-CHAIN.
 FT METAL 228 228 ZINC (CATALYTIC) (BY SIMILARITY).
 FT ACT_SITE 229 229 BY SIMILARITY.
 FT METAL 232 232 ZINC (CATALYTIC) (BY SIMILARITY).
 FT DISULFID 436 452 INTERCHAIN (PROBABLE).
 FT CONFLICT 84 P -> T (IN REF. 2).
 SQ SEQUENCE 1290 AA; 148734 MW; 71FBE379F97129E8 CRC64;
 Query Match 2.8%; Score 152; DB 1; Length 1290;
 Best Local Similarity 20.3%; Pred. No. 0.42;
 Matches 205; Conservative 125; Mismatches 346; Indels 334; Gaps 54;
 QY 106 KVOAHQWREDFASNEVYVYNAKDDLDPEKNDSEPSQRIK---PVFIEDANFR----- 157
 Db 138 KTRQGNVYKVTGINSINPSVIITG-----PRENIIDPSTFKLTNTTFAAGGFGALSIIIS 192
 QY 158 -----QISQOHAHVHIPTDIYEGS-----TIVLNELNWTSAIDVFK---KNRE 198
 Db 193 ISPRFLMTYSNAT---NDVGEGRFSKSEPCMDPILILMHELN---HAMHNLGIATPNDQ 246
 QY 199 EDPSLLMQVFGSATGLARYYP-----ASPVVNSRTPNKIDLYDVRPPVYIOGAASPKD 253
 Db 247 TISVTSNIEFYQVNVKLEYAIEYAFGGPTID--LIPKSARKYFEKALDYYSIAKRLN 304
 QY 254 MLILVDVSG---SVSGLTLLIR-----TSVSEMLTSLDDDFVNVASFNNAQDVSCF 304
 Db 305 SITANPSPFNKYGKQKILIRYFVPSSEGEV---TVNRNKFVEL---YNELTQIFTEF 360
 QY 305 QHLVQANVRNKKV-LKDAVNNTAK-----GITYKKGFSAFEOI---LNVYSR----- 351
 Db 361 NYAKIYVQNRKYLNVYTPVTANILDDNVYDIQNGFNIPKSNLNVLFMGONLSRNPAL 420
 QY 352 --ANCKNIIMLFT-----DGGEARQAEIENK-----YNKD-----KKRVYR 386
 Db 421 RKVPENMLYLFTRFKHKAIDG-----RSLYNTKTLDCRELKVKVTDLFFIGDISDKTDI 475
 QY 387 FSVGOHNVGRPIQWACENKGYEIPSGAIRI--NTQEV--LDVL----- 430
 Db 476 FLRKDINTEVEI-----YYPDNVSDVOILSKNTSEHGDLDLVPSIDSEILP 526
 QY 431 GRPMVLADKKAKOVQWNT--VYDLALEGLVITGLTPVFNITGQFENK----- 478
 Db 527 GENQFYDNRTQNDYLNLSYVLESQKL-----SDNVEDFTFRSIEEALDSAKYVITYPP 582
 QY 479 -LKNOLLIGVMG-----VDVSLIEDIKRLTPRFLCPNGYFAIDPNGYVLLHPNLOPK 530
 Db 583 TLANKVNAVQVGGFLMWANDVVEFTTNILRKDTLKDSDVSAIIP-----YIGPALNIS 638
 QY 531 NPKSQEPVTLDF-----DLAELENDI-----KVEIRKNMIDGESGEKTFRTL 572
 Db 639 NSVRNGNTEAFVAVTGVITLLEAFPEFTTPALGAFVIYSKVQVNEII-----KTDNC 692
 QY 573 VRSQDREYTDKGNRTYTW-----TPVNGTDSLALVLPFTSYFYIKAKLETITQ 622
 Db 693 LEQRIKRWKD-----SYEWMGMGTWLSLIITQFNINISQMYDSL-NYQAGAKAKID----- 742
 QY 623 ARSKKMKMDSETLKP--DNFEESGYFTIAPRDYCNLDKISDNNTFELLNFNEFI----- 675
 Db 743 LEYKKGSGDKENIKSOVENLKN-----LDVKIS-----EAMNINKFIRECSV 787
 QY 676 -----DRKTPNNPSCNADLINRVLLDA----- 697
 Db 788 TYLFKNMPLKVIDELNEFDRT-----KAKLIN--LIDSHIILVGEVDKAKVNVNSF 839
 QY 698 -----GFTN-----ELVQVYW-----SKQNKIGVKARFVVTGGTTRVYPKPAGE 738
 Db 840 QNTIPFNISYTNNSLLKDIINEYFNININDSKILSLQNRKNTLVDTSQ-----YNAEVS 894

SEQUENCE FROM N.A.
 MEDLINE-90370487; PubMed-2204031;
 RA Hauser D., Erlund M.W., Kurazona H., Binz T., Niemann H., Gill D.M.,
 RA Boquet P., Popoff M.R.;
 RT "Nucleotide sequence of Clostridium botulinum C1 neurotoxin.";
 RL Nucleic Acids Res. 18:4924-4924(1990).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN-TYPE C STOCKHOLM / C-ST;
 RX MEDLINE-91024998; PubMed-2222445;
 RA Kimura K., Fujii N., Tsuzuki K., Murakami T., Indoh T.,
 RA Yokosawa N., Takeshi K., Syuto B., Oguma K.;
 RT "The complete nucleotide sequence of the gene coding for botulinum
 type C1 toxin in the C-ST phage genome.";
 RL Biochem. Biophys. Res. Commun. 171:1304-1311(1990).
 RN [3]
 RN SEQUENCE OF 2-25.
 RC STRAIN-TYPE C STOCKHOLM / C-ST;
 RX MEDLINE-88153072; PubMed-2450068;
 RA Tsuzuki K., Yokosawa N., Syuto B., Ohishi I., Fujii N., Kimura K.,
 RA Oguma K.;
 RT "Establishment of a monoclonal antibody recognizing an antigenic site
 common to Clostridium botulinum type B, C1, D, and E toxins and
 tetanus toxin.";
 RL Infect. Immun. 56:898-902(1988).
 RN [4]
 RN IDENTIFICATION OF SUBSTRATE.
 RP MEDLINE-94038966; PubMed-7901002;
 RA Blas J., Chapman E.R., Yamasaki S., Binz T., Niemann H., Jahn R.;
 RT "Botulinum neurotoxin C1 blocks neurotransmitter release by means of
 cleaving HPC-1/syntaxin.";
 RL EMBO J. 12:4821-4828(1993).
 CC -1- FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER
 RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED
 AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD
 WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT
 INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
 ENDOPEPTIDASE THAT CLEAVES SYNTAXIN.
 CC -1- SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAIN (L) AND A
 HEAVY CHAIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL ACTIVITY,
 WHILE THE N- AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE CHANNEL
 FORMATION AND TOXIN BINDING, RESPECTIVELY.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- MISCELLANEOUS: THERE ARE SEVEN ANTIGENICALLY DISTINCT FORMS OF
 BOTULINUM NEUROTOXIN: TYPES A, B, C1, D, E, F, AND G.
 CC -1- MISCELLANEOUS: BOTULINUM TYPE C1 NEUROTOXIN IS SYNTHESIZED BY C
 STRAIN OF CLOSTRIDIUM BOTULINUM WHICH CARRY THE APPROPRIATE
 BACTERIOPHAGE.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27 (ZINC
 METALLOPROTEASE); ALSO KNOWN AS THE TETANUS/BOTULINUM NEUROTOXIN
 SUBFAMILY.
 CC
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 CC
 CC EMBL; X66433; CAA47060.1;
 CC EMBL; X72793; CAA51313.1;
 CC EMBL; X53751; CAA37780.1;
 CC EMBL; D90210; BAA14235.1;
 CC EMBL; X62389; CAA44263.1;
 CC PIR; S11291; S11291.
 CC PIR; A35396; A35396.
 CC PIR; A43503; A43503.
 CC MEROPS; M27.002;
 CC InterPro; IPR000130;
 CC InterPro; IPR000395;
 CC Pfam; PF01742; Peptidase_M27; 1.
 CC PRINTS; PR00760; BONTOTOXILYSIN.

```
QY 739 --NWQENPETYEDSFYKRSLDNDNYVFTAPYENKSGPGAYESSIMVSKAVETIYIOGKLK 796
Db 895 EGDVQLNP-----IF--PFDFKLGSSGEDRGKVIIVTQENINIVNSMTE 935
QY 797 PAVVGKIDVNSWIENTFTKTSIRDCAGPVCCKRNSDVMDCVILDDGGFLMANHD--- 853
Db 936 SFSISPIRWINKVSNLPGYTIID-----SVKNNSGWSIGIISNLFVTLKQNEDESEQ 988
QY 854 -----DYNQIGR-----PFGEIDPSLMRLHWNISVYAFNKSVDYQSVCE 893
Db 989 SINFSYDISNAPGVNKFVFTVNNMG-----NMKIYINGKLIDTIKVKRE 1035

RESULT 14
YI03_SYNY3
ID YI03_SYNY3 STANDARD; PRT; 420 AA.
AC Q55874;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL 45.8 KDA PROTEIN SLL0103.
GN SLL0103.
OS Synecocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96127529; PubMed=8590279;
RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA Sugita M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synecocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT region from map positions 64 to 92% of the genome.";
RL DNA Res. 2:153-166(1995).
CC -1- SIMILARITY: TO E.COLI YFBC.
CC -----
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CC -----
DR EMBL; D64004; BAA10635.1; --
DR InterPro; IPR002035; --
DR Pfam; PF00092; vwa; 1.
DR PROSITE; PS50234; VWFA_DOMAIN; 1.
KW Hypothetical protein.
SQ SEQUENCE 420 AA; 45849 MW; E7111B51478E74F3 CRC64;

Query Match 2.8%; Score 151.5; DB 1; Length 420;
Best Local Similarity 20.8%; Pred. No. 0.089;
Matches 85; Conservative 85; Mismatches 183; Indels 55; Gaps 16;

QY 251 PKDMLIIVDVGSGVGLTKLITTSVEMLETSDDFVNVASFNSNAQDVSCFHLVQA 310
Db 41 PLNLCLVLDHSGSDGQPLETVKSAALGLDLRLDEEDRLSVIAFDHRAKIV-----IENQ 95
QY 311 NVRNKKVLKDAVNNITAKGTTDYKKGFSFAFEOILLNVNVRANCNITMLTDDGGERAQ 370
Db 96 QVRNGAAIAKAEIKLKEAGTATDEGLKLGIAQAAGKEDRVS---HIFLLTQGENEHD 152
QY 371 E----IPFNKYNDKKVRVFSVQGHNYERGPQWACENKG---YYEIPSGAIRINTQ 424
Db 153 NDRCLKLGTVASDYKLVHTLGFQGDH*WQNDVLEAIAAQAQSLSYIENPS-EALHTFRQ 210
QY 425 EYLDVLRPVLADGKAKQVQWNVYLDALBLG-----LVITGLIPVNTIGQENKTNLK 480
Db 211 LF-----QRMNSNVGLTNNAHL*LELAPQAHLA1--VKPVAQVSPETMDLT-VQ 254
QY 481 NQLILGVMGVDVSLEDIKRLTPRTFLCPNGYYPFAIDPNGVYLLHPNLPKNPKSQE---- 536
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Db 255 NQGAEEVRLGLDMLTDQERV-----LLNLNLYLDQLPGOHVIGQVQIRYDDPASCOTNLL 309
QY 537 ----PVTLDLDAELENKIVKRNKMDGSEKGT--FRTLKKSODERYIDKGRNRYTW 590
Db 310 SDPLPLTIQ-VQTOQPSDVOQVESILTLAKYRQTOIAETKLRAGDRQGAATMLQTAAK 368
QY 591 TPVNGTDSLALVLTPTSYFYIKAKLEETITQARSKGKMKDSETLKP 638
Db 369 TALQMGDKNGATILQTN---TRLOSGEDLSEGRKRTKRWSKTTLQ 413

RESULT 15
ITH4_PIG
ID ITH4_PIG STANDARD; PRT; 921 AA.
AC P79263;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H4 PRECURSOR (ITI HEAVY
DE CHAIN H4) (INTER-ALPHA-TRYPsin INHIBITOR FAMILY HEAVY CHAIN-RELATED
DE PROTEIN) (IHRP) (MAJOR ACUTE PHASE PROTEIN) (MAP).
GN ITH4 OR IHRP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.; AND SEQUENCE OF 28-36; 595-703 AND 710-722.
RX TISSUE=Liver;
RX MEDLINE=96271024; PubMed=8830057;
RA Hashimoto K., Tobe T., Sumiya J.-I., Sano Y., Choi-Miura N.-H.,
RA Ozawa A., Yasue H., Tomita M.;
RT "Primary structure of the pig homologue of human IHRP: inter-alpha-
RT trypsin inhibitor family heavy chain-related protein.";
RL J. Biochem. 119:577-584(1996).
RN [2]
RP PRELIMINARY SEQUENCE OF 267-556 FROM N.A.
RX TISSUE=Liver;
RX MEDLINE=90371455; PubMed=1697703;
RA Buchman T.G., Cabin D.E., Vickers S., Deutschman C.S., Delgado E.,
RA Sussman M.M., Bulkley G.B.;
RT "Molecular biology of circulatory shock. Part II. Expression of four
RT groups of hepatic genes is enhanced after resuscitation from
RT cardiogenic shock.";
RL Surgery 108:559-566(1990).
RN [3]
RP SEQUENCE OF 28-54 AND 223-240.
RX TISSUE=Serum;
RX MEDLINE=96013138; PubMed=7556597;
RA Gonzalez-Ramon N., Alava M.A., Sarsa J.A., Pineiro M., Escartin A.,
RA Garcia-Gil A., Lampreave F., Pineiro A.;
RT "The major acute phase serum protein in pigs is homologous to human
RT plasma kallikrein sensitive PK-120.";
RL FEBS Lett. 371:227-230(1995).
CC -1- FUNCTION: MAY BE INVOLVED IN ACUTE PHASE REACTIONS.
CC -1- TISSUE SPECIFICITY: LIVER-SPECIFIC.
CC -1- INDUCTION: LEVELS INCREASE SIGNIFICANTLY AFTER CARDIOGENIC
CC SHOCK.
CC -1- PTM: APPEARS TO BE BOTH N- AND O-GLYCOSYLATED (BY SIMILARITY).
CC -1- PTM: CLEAVED BY PLASMA KALLIKREIN TO YIELD 55- AND 25-KDA
CC FRAGMENTS.
CC -1- SIMILARITY: BELONGS TO THE ITIH FAMILY.
CC -1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
CC -1- CAUTION: REF.2 SEQUENCE IS INCORRECT DUE TO FRAMESHIFTS AND OTHER
CC SEQUENCING ERRORS.
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CC EMBL; U43164; AAD00024.1; -
DR EMBL; S62800; AAB46821.1; -
DR EMBL; M29507; -; NOT_ANNOTATED_CDS.
DR InterPro; IPR002035; -
DR Pfam; PF00092; vwa; 1.
DR PROSITE; PS0234; VWFA_DOMAIN; 1.
KW Serine protease inhibitor; Repeat; Signal; Multigene family;
KW Glycoprotein. 1 27
FT SIGNAL 28 921 INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN
FT CHAIN 28 921 H4.
FT DOMAIN 270 428 VWFA.
FT CARBOHYD 80 80 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 513 513 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 577 577 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 49 50 HT -> SK (IN REF. 3).
FT CONFLICT 703 703 D -> H (IN REF. 1; AA SEQUENCE).
SQ SEQUENCE 921 AA; 102146 MW; E2BF95925DE8D07C CRC64;

Search completed: July 23, 2001, 07:48:25
Job time: 586 sec

Query Match 2.8%; Score 150.5; DB 1; Length 921;
Best Local Similarity 19.9%; Pred. No. 0.31;
Matches 156; Conservative 100; Mismatches 264; Indels 265; Gaps 36;

QY 4 GCLLALTL-----FQSLIGPSSEPPPSATIKSWDK---MOED--- 43
DB 10 GLLVPLLLAVLQSTAAHKNDIINISLTVDSKSSREFAHTVTSRVVKGNSAVGEATFQ 69
QY 44 -----LVTLAKTASGVNLVDIYEK--YQDLYT-VEPNNAQLVEIAARDIEKL--- 89
DB 70 MELPKAFITNFMIIDGVTPGNKEKAAAEQYSAVARGESAGLVRAIGTKTEQFOVA 129
QY 90 LSNRSKALVLALEAEKVAQAHQWREDFASNEVYVYNAKDDLDPEKNDSEPGSQRIKPVF 149
DB 130 VSVAPAAKVTELYEELLARH-----LGVEYLLKIQPQ-----QLVKHLQ 171
QY 150 IEDANFGQ-ISY-OHAAVHIPTDIYEGSTIVLNE---LWTSALDEVEFKKNEEDPSL 203
DB 172 MDIHIFEPQISFLETESTFTNELAELTISQNTKAHIREKPTLSQ-QKSPQEQQEV 230
QY 204 L-----WQVFGSATG-----LARYYPASFWVDNSRTPNKIDLYDVRRPWYIQG 247
DB 231 LDGNFIVRYDVNRTVGGSIQIENGIFYVHYFAPEW----- 266
QY 248 AASPDKMLILVDVSGVSGTLTKLINTSVSEMLETLSDDDFVNVSFNNAQDVSCFQHL 307
DB 267 SAIPKNVIFVIDTSGMRGKIQOTREALIKILGLGSRDQFNLVFSGEAPR----- 322
QY 308 VQANVRNKKVLDAVNNIYAKGIDYKGFSAFEGOLLNYSRANCNKI-----IM 359
DB 323 VAASAENVEEAKSYAAEIIHAQGTNTNDAMLMAVQLL-----ERANRELLPARSVTFII 377
QY 360 LFTDG-----GEERAQEIFNKYKDKVRV-----FRFSVQGHNYERGPQIOWMA 403
DB 378 LFTDGDFTVGETNPSKI-----QKNVREAIQGHSLFCGLFGFDVPYAFLEK----- 426
QY 404 CENKG-----YY-----YEIPSIGAIRINTQYLDVL--GR 432
DB 427 LENGGLARRIYEDSDSALQEDFYQEVANPLRLVAPEYPS-NAVEEVTQDNFRLPEKGS 485
QY 433 PMVLG---DKAKOVQNTVYLDALGLVITGTLPVFNITGQFENKTNLKNQLIG--- 486
DB 486 ELVVAGKLRDQSPDV-----LSAKYRGOLHMENTVFMESRVAEQAEFLSPKY 534
QY 487 -----VMGVDVSLEDI--KRLTPFTLCPNGYGYFAIDPNGYVLLHPNL 527
DB 535 IFHSFMERLWAYLTIOQLLAQTVAESAEEKALEARALSLSLNYSFVYPLTSMVITKPEG 594
QY 528 QPKNPKSQEPVTLDFDAELENDIKVEIRNKMIDGESGEKTFRTLKVSQDERYIDKGNRT 587

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 23, 2001, 07:47:07 ; Search time 125.88 Seconds
(without alignments)
1088.878 Million cell updates/sec

Title: US-09-397-548-16
Perfect score: 5443
Sequence: 1 MAAGCLLALTTLFQSLIIG.....RLLIQAEQTSQGNPCDMVK 1036

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: sp.archaea.*
- 2: sp.bacteria.*
- 3: sp.fungi.*
- 4: sp.human.*
- 5: sp.invertebrate.*
- 6: sp.mammal.*
- 7: sp.mhc.*
- 8: sp.organelle.*
- 9: sp.phage.*
- 10: sp.plant.*
- 11: sp.rodent.*
- 12: sp.unclassified.*
- 13: sp.vertebrate.*
- 14: sp.virus.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5409.5	99.4	1110	4 Q9U1U0	Q9U1U0 homo sapien
2	5380	98.8	1091	6 Q77773	Q77773 sus scrofa
3	5291	97.2	1091	11 Q9ERS3	Q9ERS3 rattus norv
4	5223	96.0	1103	11 Q08532	Q08532 mus musculus
5	3667	67.4	745	4 Q9UDQ3	Q9UDQ3 homo sapien
6	2948	54.2	1150	4 Q9NY47	Q9NY47 homo sapien
7	2920.5	53.7	1143	4 Q9NY48	Q9NY48 mus musculus
8	2918.5	53.6	1156	11 Q9EQG2	Q9EQG2 mus musculus
9	2907.5	53.4	1145	4 Q9Y268	Q9Y268 homo sapien
10	2886.5	53.0	1076	4 Q9U8W0	Q9U8W0 homo sapien
11	2717	49.9	975	4 Q9NSA6	Q9NSA6 homo sapien
12	1085	19.9	1091	11 Q9Z1L5	Q9Z1L5 mus musculus
13	1015	18.6	997	4 Q9NY16	Q9NY16 homo sapien
14	929.5	17.1	2190	5 Q9NK64	Q9NK64 drosophila
15	912.5	16.8	2172	5 Q9VJN0	Q9VJN0 drosophila
16	891	16.4	1191	5 Q9VJN7	Q9VJN7 drosophila
17	886	16.3	1255	5 Q9NK83	Q9NK83 drosophila
18	875	16.1	170	4 Q9UDL7	Q9UDL7 homo sapien
19	839	15.4	1022	5 Q9V6T7	Q9V6T7 drosophila

Q9ny18 homo sapien
Q17517 caenorhabdi
Q9ud81 homo sapien
Q9glh1 bos taurus
Q9ud82 homo sapien
Q9ud85 homo sapien
Q9ud80 homo sapien
Q95026 homo sapien
Q9ri42 mus musculu
Q9hcj9 homo sapien
Q9v917 drosophila
Q9u7p4 eufolliculi
Q9hjo4 thermoplasm
Q15870 plasmodium
Q9gly5 oryctolagus
Q96154 plasmodium
Q46342 clostridium
Q86488 staphylococ
Q35802 rattus norv
Q45793 bacillus th
Q9em28 ansacta moo
Q9n2m3 plasmodium
Q26216 plasmodium
Q94ly6 oryctolagus
Q25905 helicobacte
Q9uq54 homo sapien

ALIGNMENTS

RESULT 1

Q9U1U0
ID Q9U1U0 PRELIMINARY; PRT: 1110 AA.
AC Q9U1U0;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)
DE DIHYDROPIRIDINE RECEPTOR ALPHA 2 SUBUNIT.
GN CACNA2D1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=20005942; PubMed=10534405;
RX Schleithoff L., Mehrke G., Reutlinger B., Lehmann-Horn F.;
RA "Genomic structure and functional expression of a human alpha(2)/delta
RT calcium channel subunit gene (CACNA2).";
RL Genomics 61:201-209(1999).
DR EMBL; AF083854; AAF03259.1; JOINED.
DR EMBL; AF083817; AAF03259.1; JOINED.
DR EMBL; AF083818; AAF03259.1; JOINED.
DR EMBL; AF083819; AAF03259.1; JOINED.
DR EMBL; AF083820; AAF03259.1; JOINED.
DR EMBL; AF083821; AAF03259.1; JOINED.
DR EMBL; AF083822; AAF03259.1; JOINED.
DR EMBL; AF083823; AAF03259.1; JOINED.
DR EMBL; AF083824; AAF03259.1; JOINED.
DR EMBL; AF083825; AAF03259.1; JOINED.
DR EMBL; AF083826; AAF03259.1; JOINED.
DR EMBL; AF083827; AAF03259.1; JOINED.
DR EMBL; AF083828; AAF03259.1; JOINED.
DR EMBL; AF083829; AAF03259.1; JOINED.
DR EMBL; AF083830; AAF03259.1; JOINED.
DR EMBL; AF083831; AAF03259.1; JOINED.
DR EMBL; AF083832; AAF03259.1; JOINED.
DR EMBL; AF083833; AAF03259.1; JOINED.
DR EMBL; AF083834; AAF03259.1; JOINED.
DR EMBL; AF083835; AAF03259.1; JOINED.
DR EMBL; AF083836; AAF03259.1; JOINED.
DR EMBL; AF083837; AAF03259.1; JOINED.


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DR EMBL; AF083838; AAF03259.1; JOINED.
DR EMBL; AF083839; AAF03259.1; JOINED.
DR EMBL; AF083840; AAF03259.1; JOINED.
DR EMBL; AF083841; AAF03259.1; JOINED.
DR EMBL; AF083842; AAF03259.1; JOINED.
DR EMBL; AF083843; AAF03259.1; JOINED.
DR EMBL; AF083844; AAF03259.1; JOINED.
DR EMBL; AF083845; AAF03259.1; JOINED.
DR EMBL; AF083846; AAF03259.1; JOINED.
DR EMBL; AF083847; AAF03259.1; JOINED.
DR EMBL; AF083848; AAF03259.1; JOINED.
DR EMBL; AF083849; AAF03259.1; JOINED.
DR EMBL; AF083850; AAF03259.1; JOINED.
DR EMBL; AF083851; AAF03259.1; JOINED.
DR EMBL; AF083852; AAF03259.1; JOINED.
DR EMBL; AF083853; AAF03259.1; JOINED.
DR InterPro; IPR000885; -.
DR InterPro; IPR002035; -.
DR Pfam; PF00092; vwa; 1.
DR ProDom; PD002078; -. 1.
KW Receptor.
SQ SEQUENCE 1110 AA; 125307 MW; 8358DC6AD489C074 CRC64;

Query Match 99.4%; Score 5409.5; DB 4; Length 1110;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 1033; Conservative 1; Mismatches 2; Indels 19; Gaps 1;

QY 1 MAAGCLLALTTLTFLQSLIGPSSPEPPFSAVTIKSWDKMQEDLVTLAKTAGSVNQLVDI 60
DB 1 MAAGCLLALTTLTFLQSLIGPSSPEPPFSAVTIKSWDKMQEDLVTLAKTAGSVNQLVDI 60
QY 61 YEKYODLVTEPNNAQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRWEDFASN 120
DB 61 YEKYODLVTEPNNAQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRWEDFASN 120
QY 121 EVVYNNAKDLDPEKNDSEPGSQRIKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180
DB 121 EVVYNNAKDLDPEKNDSEPGSQRIKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180
QY 181 NELNWTSSALDEVFKKRNEDPSLWQVFGSATGLARYYPASPWVDNSRTPNKIDLYDVR 240
DB 181 NELNWTSSALDEVFKKRNEDPSLWQVFGSATGLARYYPASPWVDNSRTPNKIDLYDVR 240
QY 241 RPWYTOGAASPKDMLILVDVSGVSGSLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300
DB 241 RPWYTOGAASPKDMLILVDVSGVSGSLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300
QY 301 VSCFOHLVQANVRNKKVLKDAVNNITAKGITDYKGFSAFEOQLLNNVSRANCNKIIML 360
DB 301 VSCFOHLVQANVRNKKVLKDAVNNITAKGITDYKGFSAFEOQLLNNVSRANCNKIIML 360
QY 361 FTDGGEERAQEIFNKYNDKKVRFVSQGHYNERGPIQWMACENKGYIYEIPISGAIR 420
DB 361 FTDGGEERAQEIFNKYNDKKVRFVSQGHYNERGPIQWMACENKGYIYEIPISGAIR 420
QY 421 INTQEYLDVLGRPMVLADKAKQVQWNTYLDALBGLVITGTLPVFNITGTFENKTNLK 480
DB 421 INTQEYLDVLGRPMVLADKAKQVQWNTYLDALBGLVITGTLPVFNITGTFENKTNLK 480
QY 481 NQLILGVMGVDVSLIEDIKRLTFRFLCPNGYFFADDPNGYVLLHNLQPK----- 530
DB 481 NQLILGVMGVDVSLIEDIKRLTFRFLCPNGYFFADDPNGYVLLHNLQPK----- 530
QY 531 -----NPKSQEPVTLDFDAELENDIKVEIRNKMIDGESGKTFPLVKSDERYI 581
DB 541 LKRRPNIQNSQEPVTLDFDAELENDIKVEIRNKMIDGESGKTFPLVKSDERYI 600
QY 582 DKGNRITYTTPVNGTDYSLALVLPYTFYIYIKAKLEETITQARSKKGMKDSITLKPONF 641
DB 601 DKGNRITYTTPVNGTDYSLALVLPYTFYIYIKAKLEETITQARSKKGMKDSITLKPONF 660
QY 642 EESGYTFIAPROYCNDLKISDNNTEFLNFEIDRKTPNPNPCNADLINRVLLDAGFTN 701
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DB 661 EESGYTFIAPROYCNDLKISDNNTEFLNFEIDRKTPNPNPCNADLINRVLLDAGFTN 720
QY 702 ELVQNTWSKOKNIKGKARVVTDDGTRIVYPREAGENWQENPETYEDSYKKSLDNDNY 761
DB 721 ELVQNTWSKOKNIKGKARVVTDDGTRIVYPREAGENWQENPETYEDSYKKSLDNDNY 780
QY 762 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDP 821
DB 781 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDP 840
QY 822 CAGPVCDCCKRNSVDMDCVILDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLNVSIVA 881
DB 841 CAGPVCDCCKRNSVDMDCVILDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLNVSIVA 900
QY 882 FNKSYDYSQVCEGPAAPKQAGHRSATVPSVADILQIGWATAAANWILQOFLSLTFPR 941
DB 901 FNKSYDYSQVCEGPAAPKQAGHRSATVPSVADILQIGWATAAANWILQOFLSLTFPR 960
QY 942 LLEAVENEDDDFTASLSKQSCITEQTOYFFDNDSDKSGVLDGNCNCRIFHGEKLMNTNL 1001
DB 961 LLEAVENEDDDFTASLSKQSCITEQTOYFFDNDSDKSGVLDGNCNCRIFHGEKLMNTNL 1020
QY 1002 IFIMVESKGTCPCDTRLIIQAEQTSQDGNPCDMYK 1036
DB 1021 IFIMVESKGTCPCDTRLIIQAEQTSQDGNPCDMYK 1055

RESULT 2
QY 077773 PRELIMINARY; PRT; 1091 AA.
AC 077773;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE VOLTAGE-DEPENDENT CALCIUM CHANNEL ALPHA-2 DELTA SUBUNIT PRECURSOR.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CEREBRAL CORTEX;
RX MEDLINE=98411353; PubMed=9738015;
RA Brown J.P., Gee N.S.;
RT "Cloning and deletion mutagenesis of the alpha2 delta calcium channel
RT subunit from porcine cerebral cortex. Expression of a soluble form of
RT the protein that retains [3H]gabapentin binding activity.";
RL J. Biol. Chem. 273:25458-25465(1998).
DR EMBL; AF077665; AAC36289.1; -.
DR InterPro; IPR002035; -.
DR Pfam; PF00092; vwa; 1.
KW Signal.
FT SIGNAL 1 24
FT CHAIN 25 1091
FT SEQUENCE 1091 AA; 123150 MW; 293DDC7EBE9E560E CRC64;

Query Match 98.8%; Score 5380; DB 6; Length 1091;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1023; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 MAAGCLLALTTLTFLQSLIGPSSPEPPFSAVTIKSWDKMQEDLVTLAKTAGSVNQLVDI 60
DB 1 MAAGCLLALTTLTFLQSLIGPSSPEPPFSAVTIKSWDKMQEDLVTLAKTAGSVNQLVDI 60
QY 61 YEKYODLVTEPNNAQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRWEDFASN 120
DB 61 YEKYODLVTEPNNAQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRWEDFASN 120
QY 121 EVVYNNAKDLDPEKNDSEPGSQRIKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180
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Db 121 EVYYNAKDDLDPEKNDSEPGSQRIKPVFIDANFGRQISYQHAHVHIPTDIYEGSTIVL 180
QY 181 NELNWTSALEDEYFKKRNREDPSLLMQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240
Db 181 NELNWTSALEDEYFKKRNREDPSLLMQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240
QY 241 RPWYIQAASPKDMLILVDVSGSVGLTKLRTSVSEMLETLSDDDFFVNASFNSNAQ 300
Db 241 RPWYIQAASPKDMLILVDVSGSVGLTKLRTSVSEMLETLSDDDFFVNASFNSNAQ 300
QY 301 VSCFOHLVQANVRNKKVLDKADANNITAKGIDYKKGFSFAFQOLLNYSRANCKNIIML 360
Db 301 VSCFOHLVQANVRNKKVLDKADANNITAKGIDYKKGFSFAFQOLLNYSRANCKNIIML 360
QY 361 FTDGGERAQEINFKNYKDKKVRFRFSVGOHNYERGPQIOWMACENKGYIYEIPSGAIR 420
Db 361 FTDGGERAQEINFKNYKDKKVRFRFSVGOHNYERGPQIOWMACENKGYIYEIPSGAIR 420
QY 421 INTQEYLDVLRPMVLGADKAKQVQWNTYLDLLEGLVITGTLPVFNITGQFENKTNLK 480
Db 421 INTQEYLDVLRPMVLGADKAKQVQWNTYLDLLEGLVITGTLPVFNITGQFENKTNLK 480
QY 481 NQILGVMGVDVSLSDIKRLTPRTLCPCNGYYFAIDPNGYVLLHPNLQPNKPSQEPVTL 540
Db 481 NQILGVMGVDVSLSDIKRLTPRTLCPCNGYYFAIDPNGYVLLHPNLQPNKPSQEPVTL 540
QY 541 DFLDAELNDIKVEIRNKMIDGESGKFTLVKSDQERYIDKGNRTYTWTPVNGTDYSL 600
Db 541 DFLDAELNDIKVEIRNKMIDGESGKFTLVKSDQERYIDKGNRTYTWTPVNGTDYSL 600
QY 601 ALVLPYISYIYKAKLEETITQARSKKGMKQSETLKPDPNFESGYTFTAPRDYCNLDKI 660
Db 601 ALVLPYISYIYKAKLEETITQARSKKGMKQSETLKPDPNFESGYTFTAPRDYCNLDKI 660
QY 661 SDNTEFLNNEFIDRKTNNPNSCNADLINRVLLDAGFTNVLQVNSKQKNIKGVKAR 720
Db 661 SDNTEFLNNEFIDRKTNNPNSCNADLINRVLLDAGFTNVLQVNSKQKNIKGVKAR 720
QY 721 FVYTDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
Db 721 FVYTDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
QY 781 MYSKAVEIYIQGLKLPVAVGKIDVNSWIENFTKSIIRDPCAGPVCDCCKRNSDVMDCVI 840
Db 781 MYSKAVEIYIQGLKLPVAVGKIDVNSWIENFTKSIIRDPCAGPVCDCCKRNSDVMDCVI 840
QY 841 LDDGGFLMANHDDYTNQIGRFGEIDPSLMRHLVNSIYAFNKSIDYOSVCEPQAPK 900
Db 841 LDDGGFLMANHDDYTNQIGRFGEIDPSLMRHLVNSIYAFNKSIDYOSVCEPQAPK 900
QY 901 GAGHSAYVPSADILQIGWATAAASIIQOFLLSITPRLLEAVEMEDDDFTASLSKQ 960
Db 901 GAGHSAYVPSADILHIGWATAAASIIQOFLLSITPRLLEAVEMEDDDFTASLSKQ 960
QY 961 SCITEQTQFFDNDKSFSGVLDGNCGRIFHGEKLMNTNLIFIMVESKGTCPDTRLLI 1020
Db 961 SCITEQTQFFDNDKSFSGVLDGNCGRIFHGEKLMNTNLIFIMVESKGTCPDTRLLI 1020
QY 1021 QAEQTSDDGPNPCDMVK 1036
Db 1021 QAEQTSDDGPNPCDMVK 1036
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RESULT 3
Q9ERS3 PRELIMINARY; PRT; 1091 AA.
AC Q9ERS3;
DT 01-MAR-2001 (treMBLrel. 16, Created)
DT 01-MAR-2001 (treMBLrel. 16, Last sequence update)
DE 01-MAR-2001 (treMBLrel. 16, Last annotation update)
DE VOLTAGE-GATED CALCIUM CHANNEL ALPHA2/Delta-1 SUBUNIT.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=SUPERIOR CERVICAL GANGLIA;
RA Lin Y., Lipscombe D.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF286488; AAG28164.1; - GSAT -> AADR.
FT VARIANT 209 212 S -> T.
FT VARIANT 338 338 S -> T.
FT VARIANT 599 600 SL -> RY.
FT VARIANT 869 869 S -> R.
SQ SEQUENCE 1091 AA; 123467 MW; CL55088971628E19 CRC64;
```

Query Match 97.2%; Score 5291; DB 11; Length 1091;
Best Local Similarity 96.4%; Pred. No. 0;
Matches 999; Conservative 22; Mismatches 15; Indels 0; Gaps 0;

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QY 1 MAAGCLLALTLTLFQSLILGPSEEPFSAVITKSWDKMQEDLVTLAKTASGVNLVDI 60
Db 1 MAAGCLLALTLTLFQSLILGPSEEPFSAVITKSWDKMQEDLVTLAKTASGVNLVDI 60
QY 61 YEKYQDLYTEPNARQLVEIAARDIEKLLSNRSKALVSLAEAEKVQAAHQWREDFASN 120
Db 61 YEKYQDLYTEPNARQLVEIAARDIEKLLSNRSKALVSLAEAEKVQAAHQWREDFASN 120
QY 121 EVYYNAKDDLDPEKNDSEPGSQRIKPVFIDANFGRQISYQHAHVHIPTDIYEGSTIVL 180
Db 121 EVYYNAKDDLDPEKNDSEPGSQRIKPVFIDANFGRQISYQHAHVHIPTDIYEGSTIVL 180
QY 181 NELNWTSALEDEYFKKRNREDPSLLMQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240
Db 181 NELNWTSALEDEYFKKRNREDPSLLMQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240
QY 241 RPWYIQAASPKDMLILVDVSGSVGLTKLRTSVSEMLETLSDDDFFVNASFNSNAQ 300
Db 241 RPWYIQAASPKDMLILVDVSGSVGLTKLRTSVSEMLETLSDDDFFVNASFNSNAQ 300
QY 301 VSCFOHLVQANVRNKKVLDKADANNITAKGIDYKKGFSFAFQOLLNYSRANCKNIIML 360
Db 301 VSCFOHLVQANVRNKKVLDKADANNITAKGIDYKKGFSFAFQOLLNYSRANCKNIIML 360
QY 361 FTDGGERAQEINFKNYKDKKVRFRFSVGOHNYERGPQIOWMACENKGYIYEIPSGAIR 420
Db 361 FTDGGERAQEINFKNYKDKKVRFRFSVGOHNYERGPQIOWMACENKGYIYEIPSGAIR 420
QY 421 INTQEYLDVLRPMVLGADKAKQVQWNTYLDLLEGLVITGTLPVFNITGQFENKTNLK 480
Db 421 INTQEYLDVLRPMVLGADKAKQVQWNTYLDLLEGLVITGTLPVFNITGQFENKTNLK 480
QY 481 NQILGVMGVDVSLSDIKRLTPRTLCPCNGYYFAIDPNGYVLLHPNLQPNKPSQEPVTL 540
Db 481 NQILGVMGVDVSLSDIKRLTPRTLCPCNGYYFAIDPNGYVLLHPNLQPNKPSQEPVTL 540
QY 541 DFLDAELNDIKVEIRNKMIDGESGKFTLVKSDQERYIDKGNRTYTWTPVNGTDYSL 600
Db 541 DFLDAELNDIKVEIRNKMIDGESGKFTLVKSDQERYIDKGNRTYTWTPVNGTDYSL 600
QY 601 ALVLPYISYIYKAKLEETITQARSKKGMKQSETLKPDPNFESGYTFTAPRDYCNLDKI 660
Db 601 ALVLPYISYIYKAKLEETITQARSKKGMKQSETLKPDPNFESGYTFTAPRDYCNLDKI 660
QY 661 SDNTEFLNNEFIDRKTNNPNSCNADLINRVLLDAGFTNVLQVNSKQKNIKGVKAR 720
Db 661 SDNTEFLNNEFIDRKTNNPNSCNADLINRVLLDAGFTNVLQVNSKQKNIKGVKAR 720
QY 721 FVYTDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
Db 721 FVYTDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
QY 781 MYSKAVEIYIQGLKLPVAVGKIDVNSWIENFTKSIIRDPCAGPVCDCCKRNSDVMDCVI 840
Db 781 MYSKAVEIYIQGLKLPVAVGKIDVNSWIENFTKSIIRDPCAGPVCDCCKRNSDVMDCVI 840
```

Db 781 MYSKAVELYIOGKLLKPAVVIGIKIDVNSWIENTKTSIRDPCAGVCDCKRNSDYMDCVI 840
QY 841 LDGGGLMANHDDYTNQIGRFEIDPSLMRHLNYSVAFNKSYDYQVCEPGAAPKQ 900
Db 841 LDGGGLMANHDDYTNQIGRFEIDPSLMRHLNYSVAFNKSYDYQVCEPGAAPKQ 900
QY 901 GAGHSAYVPSVADILQIGWATAAAMSTLQOFLSLTPRLLLEAVEMDDFTASLSKQ 960
Db 901 GAGHSAYVPSVADILQIGWATAAAMSTLQOFLSLTPRLLLEAVEMDDFTASLSKQ 960
QY 961 SCITEQTYFFNDSCFSGVLDGCGNCRIFHGEKLMNTNLFIMVESKGTCPDTRLLI 1020
Db 961 SCITEQTYFFNDSCFSGVLDGCGNCRIFHGEKLMNTNLFIMVESKGTCPDTRLLI 1020
QY 1021 QAEQTSDDGPNCDWVK 1036
Db 1021 QAEQTSDDGPNCDWVK 1036

RESULT 4
O08532 PRELIMINARY; PRT: 1103 AA.
ID O08532; O08533; O08534; O08535; O08536;
AC 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE DIHYDROXYRINDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-2/DELTA
DE SUBUNITS PRECURSOR.
GN CACNA2D1 OR CACNA2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=97113514; PubMed=8955374;
RA Angelotti T., Hofmann F.;
RL FEBS Lett. 397:331-337(1996).
CC -1- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN
EXCITATION-CONTRACTION COUPLING.
CC -1- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:
ALPHA-1, ALPHA-2, BETA AND GAMMA.
CC -1- SUBUNIT: ALPHA-2 AND DELTA FORM HETERODIMERS THAT ARE DISULFIDE-
LINKED.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: FIVE FORMS OF THE PROTEIN, ISOFORMS 2A-2E,
ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THE
SEQUENCE SHOWN HERE IS THAT OF ISOFORM 2A.
CC -1- TISSUE SPECIFICITY: ISOFORM 2A IS EXPRESSED IN SKELETAL MUSCLE AND
AORTA, 2B IS EXPRESSED IN BRAIN, 2C IS EXPRESSED IN HEART, 2D IS
EXPRESSED IN HEART AND SMOOTH MUSCLE, AND 2E IS EXPRESSED IN
SMOOTH MUSCLE. ALL FIVE ISOFORMS ARE EXPRESSED IN THE
CARDIOVASCULAR SYSTEM.
CC -1- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM
A PRECURSOR FORM
CC -1- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.
DR EMBL: U73484; AAB50139.1;
DR EMBL: U73485; AAB50140.1;
DR EMBL: U73483; AAB50138.1;
DR EMBL: U73486; AAB50141.1;
DR EMBL: U73487; AAB50142.1;
DR MGI: 88295; CACNA2D1.
DR InterPro: IPR002035; 1.
DR Pfam: PF00092; vwa; 1.
KW Ionic channel; Glycoprotein; Ion transport; Voltage-gated channel;
KW Calcium channel; Glycoprotein; Phosphorylation; Signal;
KW Alternative splicing.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 957 L-TYPE CALCIUM CHANNEL ALPHA-2 SUBUNIT.
FT CHAIN 958 1103 L-TYPE CALCIUM CHANNEL DELTA SUBUNIT.
FT TRANSMEM 446 469 POTENTIAL.
FT TRANSMEM 918 942 POTENTIAL.

FT TRANSMEM 1079 1098
FT MOD_RES 501
FT MOD_RES 845
FT CARBOHYD 92
FT CARBOHYD 136
FT CARBOHYD 184
FT CARBOHYD 324
FT CARBOHYD 348
FT CARBOHYD 475
FT CARBOHYD 604
FT CARBOHYD 613
FT CARBOHYD 675
FT CARBOHYD 781
FT CARBOHYD 824
FT CARBOHYD 888
FT CARBOHYD 895
FT CARBOHYD 985
FT CARBOHYD 998
FT VARSPLIC 531
FT VARSPLIC 554
FT VARSPLIC 644
SQ SEQUENCE 1103 AA; 124629 MW; 103773BA735120D4 CRC64;
Query Match 96.0%; Score 5223; DB 11; Length 1103;
Best Local Similarity 94.1%; Pred. No. 0;
Matches 993; Conservative 22; Mismatches 14; Indels 26; Gaps 2;
QY 1 MAAGCLLALTFLFOSLLIGPSSEPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
Db 1 MAAGCLLALTFLFOSLLIGPSSEPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
QY 61 YEKYQDLYTPENNAQVLEIAARDIEKLLSNRSKALVSLAEAEKVQAQAHQWREFASN 120
Db 61 YEKYQDLYTPENNAQVLEIAARDIEKLLSNRSKALVSLAEAEKVQAQAHQWREFASN 120
QY 121 EYVYVNAKDDLDPEKNDSPEGSORIKPFVIEDANFQRQISYQHAHVHPTDIYEGSTIVL 180
Db 121 EYVYVNAKDDLDPEKNDSPEGSORIKPFVIEDANFQRQISYQHAHVHPTDIYEGSTIVL 180
QY 181 NELNMTSALDEYFKKNREEDPSLLMQVFGSATGLARYYPASPWVDNSRTPNKIDLYDVR 240
Db 181 NELNMTSALDEYFKKNREEDPSLLMQVFGSATGLARYYPASPWVDNSRTPNKIDLYDVR 240
QY 241 RWYIOGAASPKDMLILVDYSGVSGLTILKLTISVSEMLETSLDSDDFVNVASFNSNAQD 300
Db 241 RWYIOGAASPKDMLILVDYSGVSGLTILKLTISVSEMLETSLDSDDFVNVASFNSNAQD 300
QY 301 VSCFQHLVQANVRNKKVLKADVNNITAKGITYDKKGFSAFQOLLNVSRANCKIIML 360
Db 301 VSCFQHLVQANVRNKKVLKADVNNITAKGITYDKKGFSAFQOLLNVSRANCKIIML 360
QY 361 FTDGGEERAQEIFNKYKDKKVRVFRFSYQHNRYERGIOWMACENKGYEYIETPSIGAIR 420
Db 361 FTDGGEERAQEIFNKYKDKKVRVFRFSYQHNRYERGIOWMACENKGYEYIETPSIGAIR 420
QY 421 INTQEYLDVLGRPMVLGAKAKOVQNTNVLDALELGLVITGLTPVNTIGQFENKTNLK 480
Db 421 INTQEYLDVLGRPMVLGAKAKOVQNTNVLDALELGLVITGLTPVNTIGQFENKTNLK 480
QY 481 NQLILGMVGVDVSLDIKRLTPRTLCPCNGYIFAIDPNGVLLHPNLQPK----- 530
Db 481 NQLILGMVGVDVSLDIKRLTPRTLCPCNGYIFAIDPNGVLLHPNLQPK----- 530
QY 531 -----NPKSQEPVTLDFDAELENDIKVEIRNKMIDGESSEKTFRTLVSQDERYI 581
Db 541 LKRRRNQVQKSPQEPVTLDFDAELENEIKVIRNKMIDGESSEKTFRTLVSQDERYI 600
QY 582 DKGNTTYTTPVNGTDYSLALVPTYSFYIKAKLETTITQARKSGKGMKDSSTLPKDNF 641
Db 601 DKGNTTYTTPVNGTDYSLALVPTYSFYIKAKLETTITQARY-----SETLPKDNF 653

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QY 642 EESGVTFTAPRDYCNLDKISDNTNTEFLNFEFIDRKTNNPNSCNADLINRVLLDAGFTN 701
DB 654 EESGVTFTAPREYCNLDKPSDNTNTEFLNFEFIDRKTNNPNSCNTDLINRILLDAGFTN 713
QY 702 ELVQYNSKORNIKGVKARFVVTGGITRVYPKAGENWQENPETEYDSFYKRSILDNDNY 761
DB 714 ELVQYNSKORNIKGVKARFVVTGGITRVYPKAGENWQENPETEYDSFYKRSILDNDNY 773
QY 762 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWNIENFTKTSIRDP 821
DB 774 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWNIENFTKTSIRDP 833
QY 822 CAGPVCDCRNSDVMDCVILDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNSIYA 881
DB 834 CAGPVCDCRNSDVMDCVILDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNSIYA 893
QY 882 FNKSYDYOSVCEPGAAPKQAGHRSAYVPSVADIIQIGWATAAAWSILQQFLLSLTTPR 941
DB 894 FNKSYDYOSVCEPGAAPKQAGHRSAYVPSIADIQIGWATAAAWSILQQFLLSLTTPR 953
QY 942 LLEAVEMEDDDFTASLSKQSCITEQTQYFFDNDKSFSGVLDCGNCRSIFHGEKLMNTNL 1001
DB 954 LLEAVEMEDDDFTASLSKQSCITEQTQYFFDNDKSFSGVLDCGNCRSIFHGEKLMNTNL 1013
QY 1002 IFIMVESKGTCPDTRLLIQAQTSIDGPNPCDMVK 1036
DB 1014 VFIMVESKGTCPDTRLLIQAQTSIDGPNPCDMVK 1048

RESULT 5
QY 09UDQ3 PRELIMINARY; PRT: 745 AA.
ID 09UDQ3
AC 09UDQ3
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE WUGSC:H.DJ0560014.1 PROTEIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE-99063792; PubMed-9847074;
RX Sulston J.E., Waterston R.;
RA "Toward a complete human genome sequence.";
RL Genome Res. 8:1097-1108(1998).
[2]
RN SEQUENCE FROM N.A.
RP Mead K., Bauer C.;
RA "The sequence of Homo sapiens PAC clone RP4-560014.";
RT Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RP Waterston R.H.;
RA Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
[4]
RN SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC006145; AAD20938.1;
DR InterPro: IPR02035;
FT NON_TER 1
SQ SEQUENCE 745 AA; 84396 MW; BC07B53484B71EA4 CRC64;

Query Match 67.4%; Score 3667; DB 4; Length 745;
Best Local Similarity 99.7%; Pred. No. 3.2e-226;
Matches 688; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 347 YNVSRRANCKIIMLFTDGGEEAQAIFNKYNKDKKRVFRFSVGHQNYERGIQWACEN 406
DB 1 YNVSRRANCKIIMLFTDGGEEAQAIFNKYNKDKKRVFRFSVGHQNYERGIQWACEN 60

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QY 407 KGYEYEPSIGAIRINTOEYLDVLGRPMVLAGDKAKQVOMTVNYLDALGLVITGILPV 466
DB 61 KGYEYEPSIGAIRINTOEYLDVLGRPMVLAGDKAKQVOMTVNYLDALGLVITGILPV 120
QY 467 FNITQGFENKTNLKNQILGVMDVDSLEDIKRLTPRTILCPNGYVFAIDPNGYVLLHPN 526
DB 121 FNITQGFENKTNLKNQILGVMDVDSLEDIKRLTPRTILCPNGYVFAIDPNGYVLLHPN 180
QY 527 LOPKNPKSQEPVTLDFDLAELENDIKVEIRNMIDGESGEKTFRTLVSQDERYIDKGNR 586
DB 181 LOPKNPKSQEPVTLDFDLAELENDIKVEIRNMIDGESGEKTFRTLVSQDERYIDKGNR 240
QY 587 TYTWPVNGTYSIALVLPYTSFYIKAKLETITQARSKKGMKDSSETLKPDNFEESGY 646
DB 241 TYTWPVNGTYSIALVLPYTSFYIKAKLETITQARSKKGMKDSSETLKPDNFEESGY 300
QY 647 TFIAPRDYCNLDKISDNTNTEFLNFEFIDRKTNNPNSCNADLINRVLLDAGFTN 706
DB 301 TFIAPRDYCNLDKISDNTNTEFLNFEFIDRKTNNPNSCNADLINRVLLDAGFTN 360
QY 707 YNSKORNIKGVKARFVVTGGITRVYPKAGENWQENPETEYDSFYKRSILDNDNYVFTAP 766
DB 361 YNSKORNIKGVKARFVVTGGITRVYPKAGENWQENPETEYDSFYKRSILDNDNYVFTAP 420
QY 767 YNKSQPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWNIENFTKTSIRDP 826
DB 421 YNKSQPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWNIENFTKTSIRDP 480
QY 827 CDCRNSDVMDCVILDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNSIYA 886
DB 481 CDCRNSDVMDCVILDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNSIYA 540
QY 887 DYOSVCEPGAAPKQAGHRSAYVPSVADIIQIGWATAAAWSILQQFLLSLTTPR 946
DB 541 DYOSVCEPGAAPKQAGHRSAYVPSVADIIQIGWATAAAWSILQQFLLSLTTPR 600
QY 947 EMEDDDDFTASLSKQSCITEQTQYFFDNDKSFSGVLDCGNCRSIFHGEKLMNTNL 1006
DB 601 EMEDDDDFTASLSKQSCITEQTQYFFDNDKSFSGVLDCGNCRSIFHGEKLMNTNL 660
QY 1007 ESKGTCPDTRLLIQAQTSIDGPNPCDMVK 1036
DB 661 ESKGTCPDTRLLIQAQTSIDGPNPCDMVK 690

RESULT 6
QY 09NY47 PRELIMINARY; PRT: 1150 AA.
ID 09NY47
AC 09NY47;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE CALCIUM CHANNEL, ALPHA 2/DELTA SUBUNIT 2.
GN CACNA2D2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE-THYROID;
RC Klugbauer N.;
RA Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RC TISSUE-THYROID;
RA Hobom M., Dai S., Marais E., Lacinova L.;
RT "Neuronal distribution and functional characterization of the calcium channel alpha2delta-2 subunit.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ251368; CAB86193.1;
DR InterPro: IPR002035;

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SQ SEQUENCE 1150 AA; 129875 MW; 37B75F687AF5E73C CRC64;

Query Match 54.2%; Score 2948; DB 4; Length 1150;
Best Local Similarity 54.5%; Pred. No. 6.3e-180;
Matches 573; Conservative 168; Mismatches 281; Indels 30; Gaps 13;

QY 7 LALTTLTQSLLLIGSSSEPPSAVTIKSWDKMCEDLVTLAKTASGVNQLVDIYKYOD 66
DB 44 LWLLPLPLLAAPGASAYSPQOHTMQHWRRLQEQVDGVMRIFGVQOQREIYKDNRN 103
QY 67 LYTVPPNARQVETAAARDIEKLLNSRKALVSLALEAEKQAAHOREDEASNEVYYIN 126
DB 104 LFEVQENEPQKLVKAGDIESLLDRKKVQALKRLADAENQKAHRWQDNKEEDIVYD 163
QY 127 AKDDL---DPEKNDSEPGSQ--RIKPVFIEDANFGRIQSIYQHAHVHIPTDIYEGSTIVLN 181
DB 164 AKADAEALDDPESEDVERGSKASTLRDLDFIEDPNFKKNVNSYAAVQIPTDIYKGVSTVLN 223
QY 182 ELNWTLSALDEYFKKNEEDPSLLMQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 241
DB 224 ELNWTLEALNFMENRRQDPTLLMQVFGSATGVTRYYPATPW---RAPKKIDLYDVR 279
QY 242 PWYIOGAASPKDMLTLDVYSGVSLTLKIRTSYSEMLETSDDDDFYNVASFNSNAQDV 301
DB 280 PWYIOGASSPRDMLTLDVYSGVSLTLKIRTSYSEMLETSDDDDFYNVASFNEKAQPV 339
QY 302 SCFOHLVQANRVKVKLVKDAVNNTAKGITDYKKGFSAFEQQLNLYNVRANCKIIMLF 361
DB 340 SCFTHLVQANRVKVKVKEAVQGMVAKGITGYKAGFAYAFDQLQNSNITRANCKIMMF 399
QY 362 TDGGERAQEIEFNKNY-KDKKRVFRFSVGOHNYERGPTOWMACENKGYIYETPSIGAIR 420
DB 400 TDGGERVQDVFEKYNPNRTVRVFTSVGOHNYDVTPLQWMACANKGYIFEIPSGAIR 459
QY 421 INTQEYLDVLGRPMVLGAKAKOVQNTNYLDALGLVITGTLPVFNITGFENKTNLK 480
DB 460 INTQEYLDVLGRPMVLGAKAKOVQNTNYLDALGLVITGTLPVFNITQ--DGPGEKK 517
QY 481 NQLILGVMDVSLIEDIKRLTPRTPLCPNGYFYAIDPNGYVLLHNPQLKPKNSOEPTVL 540
DB 518 NQLILGVMDVSLIEDIKRLTPRTPLCPNGYFYAIDPNGYVLLHNPQLKPKNSOEPTVL 577
QY 541 DFLDAELENDIKVEIRNKMIDGSEKFTRLVKSDERYIDKGNRTYTWTPVNGTDVSL 600
DB 578 DFLDAELENDIKVEIRNKMIDGSEKFTRLVKSDERYIDKGNRTYTWTPVNGTDVSL 637
QY 601 ALVLPYTFYIYKALEETITQARSKGKMDSETLKPNDPFEESGYTFIAPRDYCNLDKI 660
DB 638 GLVLPYTFYIYKALEETITQARSKGKMDSETLKPNDPFEESGYTFIAPRDYCNLDKI 697
QY 661 SDNTEFLNNEFIDRKTPNPNPCNADILNVLVDAGFTNELQVNYWSKQK-NIKGVKA 719
DB 698 SDNTEFLNNEFIDRKTPNPNPCNADILNVLVDAGFTNELQVNYWSKQK-NIKGVKA 757
QY 720 RFVVTGGTTRYTPKAGENQWENPETYEDSVKSLDNDNVFTVAPYENK-SGCGAYES 778
DB 758 RFVVTGGTTRYTPKAGENQWENPETYEDSVKSLDNDNVFTVAPYENK-SGCGAYES 817
QY 779 ---GIMVSKAVEIYIGKLLKPAVVGKIKDVANSWIENF-----TKTSIRDP--CAGP--- 825
DB 818 DTGVLVSTAVELSLGRRLRPAVGVKLDLEAWEKFKVLASNRTHQDPQKC-GPNSH 876
QY 826 -VCDKRNDSVMDVCLDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLNLSVYAFNK 884
DB 877 CEMDCVNNEDLLCVLDDGGFLVSNQNHQMDQVGRFFSEVDANLMLALYNNSFYTRKE 936
QY 885 SYDQSVCEPGAAPKAGHRSAYSVADILQIGWATAAANWSILQOFLSLTFFPRLLE 944
DB 937 SYDQSVCEPGAAPKAGHRSAYSVADILQIGWATAAANWSILQOFLSLTFFPRLLE 996
QY 945 AVEMEDDDFTASLSKOSCITEQYQYFFDNDKSKFSGLVDCGNCGRIFHGEKLMNTNLI 1004
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AC Q9Y268;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE KIAA0558 PROTEIN.
 GN KIAA0558
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRIN;
 RA Sekido Y., Duh F.-M., Latif F., Lin J., Mathis M.,
 RA Minna J.D.;
 RT "Gene 26, a new candidate human tumor suppressor gene located in the
 RT 3p21.3 small cell lung cancer homozygous deletion region homologous to
 RT a voltage gated calcium channel alpha 2/ delta subunit";
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RN SEQUENCE FROM N.A.
 RP Wei M.-H., Latif F., Duh F.-M., Adreazoli-Angeloni D., Kashuba V.,
 RA Zabarovsky E., Johnson B., Lerman M.I.;
 RA "A new alpha 2 delta subunit of the L-type voltage gated calcium
 RT channel resides in the lung cancer critical region on 3p21.3";
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN SEQUENCE FROM N.A.
 RP TISSUE=BRIN;
 RC MEDLINE=98290545; PubMed=9628581;
 RX Nagase T., Ishikawa K., Miyajima N., Tanaka A., Kotani H., Nomura N.,
 RA Ohara O.;
 RA "Prediction of the coding sequences of unidentified human genes. IX.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro";
 RL DNA Res. 5:31-39(1998).
 DR EMBL; AF040709; AAC70914.1; -
 DR EMBL; AF042792; AAB96913.1; -
 DR EMBL; AB011130; BAA25484.1; -
 DR InterPro; IPR02035; -
 DR SEQUENCE 1145 AA; 129268 MW; 9ADA4807FC70971B CRC64;
 SQ
 Query Match 53.4%; Score 2907.5; DB 4; Length 1145;
 Best Local Similarity 54.1%; Pred. No. 2.4e-177;
 Matches 570; Conservative 167; Mismatches 278; Indels 39; Gaps 15;
 QY 7 LAULTLFLQSLIGPSEPPPSNVITKSWDKMQEDLVTLAKTASGVNOLVIEKYQD 66
 DB 44 LWLLPLPLLAAPGASAYSPQOHTMOHARLEQVGVGMFRIFGVQOLREIYKDNRN 103
 QY 67 LYVEPNNAQOLVIAARDTEKLLSNKALVSLALEAKVQAQAAHQRDEFASNVVYN 126
 DB 104 LFEVQNEPKLVKQVAGDIESLLDRKQALKLADAAENFQAKRHQDNKEEDIVYD 163
 QY 127 AKDDL---DPEKNDSPGSO--RIKPVFIEDANFGROISYQHAHVHPTDIYEGSTIVLN 181
 DB 164 AKADAELODPESEDVERGSKASTRLDFIEDPNPKKNVYSYAAVQIPTDIYKGSIVLN 223
 QY 182 ELNWTSLALDEYFKNREEDPSLLNQVGSATGLARYYPASPFWVDNSRTPKNKIDLYDVR 241
 DB 224 ELNWTALENVFMNRQDPTLLNQVGSATGVTRYYPATPW----RAPKKIDLYDVR 279
 QY 242 PWYTOGAASPKDMLILVDVSGVSGGLTKLRTSVSEMLETSLDDEDFNVASFNQAQV 301
 DB 280 PWYTOGAASPKDMLILVDVSGVSGGLTKLRTSVSEMLETSLDDEDFNVASFNQAQV 339
 QY 302 SCFOHLVQANVRNKKVLDKAVNNITAKGTDYKKGFSFAPEQLLNYNVSRANCKIIMLF 361
 DB 340 SCFHLVQANVRNKKVLEKAVQGVKAGTTCYKAGFYAFDQLQNSNITRANCKNIMMF 399
 QY 362 TDGGERAQELFNKYN-KKKVVRFRSVGOHNYVERGPIQWACENKGYEIEISGAIR 420

DB 400 TDGGERVQDVFEKYNWPNRTYRVFTFSVGQHNVDVTPLOWMACANKGYEIEISGAIR 459
 QY 421 INTQYLDVLGRPMVLADKAKOVQWNTNYLDALGLGLVITGTLPVFNITGOFENKTNLK 480
 DB 460 INTQYLDVLGRPMVLADKAKOVQWNTNYLDALGLGLVITGTLPVFNITG--DGPGEKK 517
 QY 481 NGLILGVMGVDVSLIEDIKRLTREFLPCNPGYFAIDPNCYVLLHPNLPKPKSOEPVTL 540
 DB 518 NGLILGVMGIDVALNDIKRLTNYTLGANGYFAIDLNGYVLLHPNLPKPKQTNFREPVL 577
 QY 541 DFLDAELENDIKVEIRNKMIDGESKEFTLVKSDERYIDKGNRTYTWTPVNGDYSL 600
 DB 578 DFLDAELENDIKVEIRNKMIDGKHKQIRTLVKSUDERYIDVTRNYTWTPIRSTNYSL 637
 QY 601 ALVLPYSPYIYKALEETITQARSKKGMKSETLKPONFEESGYTFIAPRDYCNLDLKI 660
 DB 638 GLVLPYSPYIYKALEETITQARSKKGMKSETLKPONFEESGYTFIAPREYCKDLNA 690
 QY 661 SDNTEFLNENEFIDRKTNPNSCNADLINRVLLDAGFTNELVQNVWSKQK-NIKGVKA 719
 DB 691 SDNTEFLNENEFIDRKTNPNSCNADLINRVLLDAGFTNELVQNVWSKQK-NIKGVKA 750
 QY 720 RFVVTGGITRVYKPEAGENWOENPETYEDSFYKSLDNDNYVFTAPYFNK-SGPGAYES 778
 DB 751 VFAATDGGITRVYKPEAGENWOENPETYEDSFYKSLDNDNYVFTAPYFNK-SGPGAYES 810
 QY 779 ---GIMYSKAVEIYIOGKLLKPAVGIKIDVNSWIENF-----TKTSIRDP--CAGP--- 825
 DB 811 DTVGILVSTAVELSLGRTRLRPAVGVGKLDLEAWAEKFKVLASNRTHQDPQKQK-CPNSH 869
 QY 826 -VCDCKRNSDVMDCVILDGSGFLMANHDDYTNQIGRFFGEIDPSLMRLHVNISVYAFNK 884
 DB 870 CEMDCVNEEDLLCVLIDDGFLVLSNQHQWQVGRFFSEVDANLMLALYNNSTYTRKE 929
 QY 885 SYDYQVSCVPPGAAPKQAGHRSAYVPSVADILQIGWATAAAMSILQQLLSLSTFFRLLE 944
 DB 930 SYDYQVSCVPPGAAPKQAGHRSAYVPSVADILQIGWATAAAMSILQQLLSLSTFFRLLE 989
 QY 945 AVEMEDDDTASLUSKOSCITEQTYFFDNDKSKFSFVLDGCGNCSRIHGEKLNNTLIFI 1004
 DB 990 ADPAEAEQ-SPETRESSCVMKQTYFFGSVNASYNAIIDCGNCSRLFHAQRLTNTLLFV 1048
 QY 1005 MVESKCTCCDTRLLIQAEQ--TSDGPNPCDMVK 1036
 DB 1049 VAEKPLCSOAGERLLOKQTHCPADGPEQCELVQ 1082
 RESULT 10
 QYUEW0 PRELIMINARY; PRT; 1076 AA.
 AC QYUEW0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE ALPHA 2 DELTA CALCIUM CHANNEL SUBUNIT ISOFORM II.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wei M.-H., Latif F., Duh F.-M., Adreazoli-Angeloni D., Kashuba V.,
 RA Zabarovsky E., Johnson B., Lerman M.I.;
 RA "A new alpha 2 delta subunit of the L-type voltage gated calcium
 RT channel resides in the lung cancer critical region on 3p21.3";
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF042793; AAB96914.1; -
 DR InterPro; IPR02035; -
 DR SEQUENCE 1076 AA; 122116 MW; EEC474836B7EDA05 CRC64;
 SQ
 Query Match 53.0%; Score 2886.5; DB 4; Length 1076;
 Best Local Similarity 54.6%; Pred. No. 4.8e-176;

Matches 561; Conservative 166; Mismatches 262; Indels 39; Gaps 15;

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QY 33 IKSWVDKQEDLVTLAKTASGVNOLVDYIKYQDLYVTPNNARQLVEIAARDIEKLNS 92
Db 1 MQHWRLEQEVGVGMIFGVQQLREIYKDNRLNFVEQNEPKLVKVEKAGDIESLLDR 60
QY 93 RSKALVSIALEAEKQVAHQWREDFASNVVYNAKDL---DPEKNDSEPGSQ--RIKP 147
Db 61 KVQALKKLADAAEFQAHQWQDNKEEDIVYDADAKDAELDDPESDVERGSKASTLRL 120
QY 148 VFIEDANFGQISYQHOAAVHPTDIYEGSTIVLNELNWTSLDDEYFKKNEEDPSLLQV 207
Db 121 DFTEDPKNKKNVSYAAVQIPDIYKGSVILNENWALENFVFNRRQDDPTLLQV 180
QY 208 FGSATGLARYPASPWWDSNRPNKIDLYVRRRPWYIOGAASPDKMLILVDVSGSVGL 267
Db 181 FGSATGVTRYYPATPW---RAPKKIDLYVRRRPWYIOGASSPKMVIIVDVGSGVGL 236
QY 268 TLKLI RTSVSEMLETSLDDDFVNVASNSNAQDVSCFQHLVQANVRNKKVLKDAVNITA 327
Db 237 TLKLMKTSVCEMLDLSDDDYVNVASFNAQPVSCFTHLVQANVRNKKVFEKAVQGMVA 296
QY 328 KGITDYKKGFSFAFEOQLNVTNRANCKIIMLTGDEGEAEQIFNKYN-KDKKVRER 386
Db 297 KGTGKAGFEYAFDQLQNSNITRANCKIMMFTDGEDRVQDVFEKYNWPNRTVRFT 356
QY 387 FSVGQHNRYERGP IQMACENKGYEIPSGAINTQOEYLDVLRPMVLGAKAKOVQW 446
Db 357 FSVGQHNRYDVTPLQMACAKNGYFEIPSGAINTQOEYLDVLRPMVLGAKAKOVQW 416
QY 447 TNYVLDALGLVITGTPLVFNITGOFENKLNQILGVMGVDSLEDIKRLTPRFTL 506
Db 417 TNYVEDALGLVITGTPLVFNLTQ--DGPGEKKNLQILGVMGIDVALNDIKRLTPNLT 474
QY 507 CPNGYFAIDPNCYVLLHPNLQPNKPSQBPVTLDFDLAELENDIKVEIRNKMIDGESG 566
Db 475 GANGYFAIDNLGNYVLLHPNLKPTTNFRPVTDLDFDLAELENDIKVEIRNMIDGNKH 534
QY 567 KTFRTLVKSODERYIDKGNRTYTWTPVNGDYDSLALVLPYISFYIKAKLEETITQARSK 626
Db 535 KQIRTLVKSLDERYIDEVTNYTWVIRSNYSGLVLPYISFYIQANLSDQILQ---- 590
QY 627 KGKMKDSETLKPNFEESGTYFIAPRDYCNLDKISDNNTFLLNFEIDRKTNPNSCN 686
Db 591 ---VKYFEFLPSSFESEGHVFIAPREYCKDLNASDNNTFELKFIELMEKVTPDSKQCN 647
QY 687 ADLNRVLLDAGTNELVQYNSKQK-NIKGVKARFVVTGGITRYVPKAGENQWENPE 745
Db 648 NFLHLNILDGTITQQLVERWRDQDLNTYSLLAVFAATDGGITRVFPNKAEDWTENPE 707
QY 746 TYEDSFYKRSLDNDYVFTAPYFNK-SGPGAYES---GIMVSKAVYETIOGKLLKPAVVG 801
Db 708 PFNASYRSLDNHGYVFPHPHODALLRPLELENDVGLVSTAVELSIGRRITLRAVVG 767
QY 802 IKIDVNSWIENF-----TKTISIRDP--CAGP-----VCDCKRNSDVMDCVILDDGGFLLMA 850
Db 768 VKLDLEAWAEKFKVLASNRTHQDPQKQ-CPNSHCENDCVENEDLLCVILDDGGFVLVS 826
QY 851 NHDDYINQIGRPFGEIDPSLMRLHVNISYAFNKSVDYQSVCEPGAAPKQAGAHRSAYVP 910
Db 827 NQNHQDQVGRFSEFSDANLMLALYNSFYRKESYDQYAAACAPQPPGNLGAAPRGVFP 886
QY 911 SVADILQIGWATAAASWILQFLLSLTFPRLLAEVEMEDDDFTASLSKQTECITOXYF 970
Db 887 TVADFNLNLTWTSAAASWLFQQLLYGLIYHSWFQADPAEAG-SPETRESSCVNKQITQY 945
QY 971 FDNDSKSGVLDCGNCRIHFHGEKLMNTNLIIFIMVESKGTCTPCDTRLLTQABQ--TSDG 1028
Db 946 FGSVNASYNALIDCGNCSRLFHAQRLTNTNLLFVVAEKLPLCSQCEAGRLLQKETHCPADG 1005
QY 1029 PNPCDVVK 1036
Db 1006 PEQCELVQ 1013
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RESULT 11

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Q9NSA6 PRELIMINARY; PRT; 975 AA.
AC Q9NSA6;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (T-EMBLrel. 16, Last annotation update)
DE LUAC11.1 (CALCIUM CHANNEL, VOLTAGE-DEPENDENT, L TYPE, ALPHA 2D SUBUNIT
DE (KIAA0558)) (FRAGMENT).
GN LUAC11.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Barlow K.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z84492; CAB41767.2; -
DR InterPro; IPR002035; -
FT NON_TER 1
SQ SEQUENCE 975 AA; 110192 MW; C7874D46B88242BF CRC64;
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Query Match 49.9%; Score 2717; DB 4; Length 975;
Best Local Similarity 56.8%; Pred. No. 2.9e-165;
Matches 526; Conservative 139; Mismatches 225; Indels 36; Gaps 14;

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QY 132 DPEKNDSEPGSQ--RIKPVFIEDANFGQISYQHOAAVHPTDIYEGSTIVLNELNWTSL 189
Db 2 DPESEDVERGSKASTLRLDFIEDPNFKKNKYNYSVAAVQIPTDIYKGSVILNENWTEAL 61
QY 190 DEYFKKNEEDPSLLQVFGSATGLARYYPASPVWDSNRPNKIDLYVRRRPWYIOGAA 249
Db 62 ENYFMENRRQDPTLLMQVFGSATGVTRYYPATPW---RAPKKIDLYVRRRPWYIOGAS 117
QY 250 SPKDMILTVDSVSGSLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQDVSCFQHLVQ 309
Db 118 SPKDMILTVDSVSGSLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQDVSCFQHLVQ 177
QY 310 ANVRNKKVLKDAVNNTAKITDYKKGFSFAFQQLNLTNYSRANCKIIMLTGDEGEERA 369
Db 178 ANVRNKKVFEAYQGVAKCTGCKAGFEYAFDQLQNSNITRANCKIMMFTDGEDRV 237
QY 370 QEIFNKYN-KDKKVRFPFVSGQHNRYERGP IQMACENKGYEIPSGAINTQYSLD 428
Db 238 QDVFERYNWPNTVRVFTFSVGQHNRYDVTPLQMACAKNGYFEIPSGAINTQYSLD 297
QY 429 VLGRPMVLAGDKAKOVQWNTNYVLDALGLVITGTPLVFNITGOFENKLNKQILGVM 488
Db 298 VLGRPMVLAGDKAKOVQWNTNYVEDALGLGLVVTGTLDFVFNLTQ--DGPGEKKNLQILGVM 355
QY 489 GVDVSLIEDIKRLTPRETLCPNGYFFAIDPNGYVLLHPNLQPNKPSQBPVTLDFDLAELE 548
Db 356 GIDVALNDIKRLTPNYTLGANGYVFAIDNLGNYVLLHPNLKPTTNFRPVTDLDFDLAELE 415
QY 549 NDKIWEIRNKMIDGESGKTFRTLVKSQDERYIDKGNRTYTWTPVNGTYSLLALVLPYS 608
Db 416 DENKESTIRSMIDGNKHQIRTLVKSLDERYIDEVTNYTWVIRSNYSGLVLPYISFY 475
QY 609 FVYIKAKLEETITQARSKKMKDSETLKPDNEEESGTYFIAPRDYCNLDKISDNNTFEL 668
Db 476 TFYQLANLSDQILQ-----VKYFEFLPSSFESEGHVFIAPREYCKDLNASDNNTFEL 528
QY 669 LNFNEFIDRKTNPNSCNADLNRVLLDAGTNELVQYNSKQK-NIKGVKARFVVTGG 727
Db 529 KNFIELMEKVTPDSKQCNFLLNLTGITOQLVERWRDQDLNTYSLLAVFAATDGG 588
QY 728 ITRVYPKAGENQWENPEYEDSFYKRSLDNDYVFTAPYFNK-SGPGAYES---GIMVS 793
Db 589 ITRVFPNKAEDWTENPEPNASFYRRSLDNHGYVFPKPPHODALLRPLELENDVGLVS 648
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QY 784 KAVEIYIOGKLLPAPVGVKIDVNSWIEP-----TKTSIRDP--CAGP-----VDCCKRN 832
DB 649 TAVELSGRRTRLPAPVGVKIDLEAWAEKFKVLASNRTHQDQPKC--GPNSHCEMDECVN 707
QY 833 SDVMDCVILDDGGFLMANHDDYTNQIGREFGETDPSLMRHLVNIISVYAFNKSVDYQSV 892
DB 708 NEDLLCVILDDGGFLVLSNQHNDQVGRFSEVDANMLALNNSEFYTRKESVDYQAC 767
QY 893 EPGAAPKOGAGHSAYVPSVADILQIGWATAAAMSTILOFLSLFPRLEAVEMEDDD 952
DB 768 APQPPGNLGAAPRGVFPVTVADFLNLAAMTSAAMSLFOQLLYGLIYHSFQADPAEAG 827
QY 953 FTASLSKQSCITEOTQYFFDNDSKFSGLDGCNCSRFHGEKLMNTNLFIFVESKGT 1012
DB 828 -SPETRESSCMKOTQYFSGVSNASYNAIIDCGNCSRLFAQR/LTNTNLLFVVAERPLCS 886
QY 1013 PCDRLLIQAEQ--TSDGPNPCDMVK 1036
DB 887 QCEAGRLLQKETHCPADGPEQCELVQ 912

RESULT 12
Q921L5 PRELIMINARY; PRT; 1091 AA.
AC Q921L5
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE CALCIUM CHANNEL ALPHA-2-DELTA-C SUBUNIT.
GN CACNA2D3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE=9098955; PubMed=9880589;
RA Klugbauer N., Lacinova L., Marais E., Hobom M., Hofmann F.;
RT "Molecular diversity of the calcium channel alpha2delta subunit.";
RL J. Neurosci. 19:648-691(1999).
DR EMBL: AJ010949; CAA09423.1;
DR MGD; MGI:1338890; CACNA2D3.
DR InterPro; IPR002035; -.
SQ SEQUENCE 1091 AA; 122777 MW; 7ABEE2BDA10077A0A CRC64;

Query Match 19.98; Score 1085; DB 11; Length 1091;
Best Local Similarity 28.78; Pred. No. 8.3e-61;
Matches 309; Conservative 222; Mismatches 416; Indels 128; Gaps 40;

QY 3 AGCLLALTTLFOSLLIGPSSSEPPSAVTIKSVWDMQEDLVTLAKTAGVGNOLVDIYE 62
DB 14 ASALLA-TALLYAALGDVRESEQIPLSV-VKLWASAFGEIKSIAKYSGSOLLQKKYK 71
QY 63 KYQDLYTEPNNAQLVIAARDIEKILSNRSKALVSLALEAEKVAQAAHQRWEDFASNEV 122
DB 72 EYKDVAEEIDGLQVKKLAKIMEEMPHKSEAVRLVEAAEEAHLKHEFDADL--QY 128
QY 123 VYNAK--DDLDPEKNDSEPGSQIKPVFIEDANFR--QISYQHAAVHIPDIYEGSTIV 179
DB 129 EYFNAVLNERDKGNFLELGEFT--LAPNDHFNLPNLSISLSDVQVPTMYNKKDPAI 185
QY 180 LNELNWTSALEVEKKEEDPSLLWVFGSATGLARYPASPVWDSNRTNPKIDLDYDVR 239
DB 186 VNGVWSSSLNKFVNDPDRPSLWQYFGSAKGFYFPGIKWEPDE--NGVIAFPCR 242
QY 240 RPWYIOGAASPDKMLIILVDYSGVSGVTLKILRTSVSEMLETSDDDFVNVAFSNSNAQ 299
DB 243 NRKWIQAOTSPKDVILVDYSGSMKGLRLIAKTQVTSISLDTLGDGDFNLIYNEELH 302
QY 300 DVS-CFQ-HLVOANVRNKKVLKDAVNNTAKGIDTYKKGFSFAFEQLLNIVNSRAN--CN 355
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DB 303 YVEPCLNGTLVQADRTNKEHREHLKLFKAGIGMLDIALNEAFNILSDFNHTGQGSICS 362
QY 356 KIIMLTDDGGEERAQIFNKYN-KDKKRVRFRESVQGHNYERGPQIWMACENKGYIYEIP 414
DB 363 QAIMLTIDGAVDITDIFAKYNWPDKRVIFTYILIGREAAFDANLKWMACANGFFQIS 422
QY 415 SIGAIRINTOEYLDVLGRPMVLADKAKOVQWNTNVLVD-----ALEGLVI--TGT 463
DB 423 TLADVENWMEYLHLSRPKVI--DQEHVWVTEAYIDSTLPOAKLADDOGLVMTVA 480
QY 464 LPVFNITGPFENKTNLKNQLILGVMDVDSLEDIKRTPRTFTCPNGYIFAIDPNGVLL 523
DB 481 MPVES---KONETRSKG-ILLGVGTDVPVKELLTKIPYKLGIGHYAFAITNNGYILT 535
QY 524 HPNLQP---KNPKSQEP--VTDFDLAELENDIKVEIRNMIDGESCEKFTFRLVKQODE 578
DB 536 HPELRPLYEEGKKRRKPNYSVDLSEWEEDRDDV-LRNAMVNRKTKG--FSMEVK---- 588
QY 579 RYIDKGNRT-----YTWTPVNGTDSLALVLPY-YGYFIKAKLEETITQARSKKGMK 631
DB 589 KTYDKGRVLWNTNDYYITDIKTPFSLGVALSGHGKGYF-----RGNTV 634
QY 632 DSETLKPDNFEESGYTFIAPRDYCN-DLKISDNNTEFLNNEFIDRKTPNPNNSCNADLI 690
DB 635 IEESGL--HDLHPDVSLEADWSYCNLDLHPEHRHLSOLEAIKLYLKGEK-LLQCDKELI 691
QY 691 NRVLIDAGFTNELVQNTWS-----KOKNIKGVKARFVTDGGITRVYP----- 733
DB 692 QEVLFDA-VVSAPIEAYTSLALNKSNSDKGEVAFVLTGTRSLRNLNLFVGADELNQD 750
QY 734 -KAGENQWENPETEYDSFYKRSLDN--DNKYFTAPY---FNKSGPGAYESGLWMSKAV 786
DB 751 FLKAGDKENIFNADHFLNTRRAEQTAGSFVSIPTSTGVNKS-----NVYATSTSI 804
QY 787 EYIQGKLLKPAVVGKIDVNSWIEPNTKTSIRDPAGVPCDKRNSDMVDMCVILDGGF 846
DB 805 QLLDERKSPVVAAGVQIMKLEFFORKEFTWASOCASLDGKCSICDDDETVCYLIDNNGF 864
QY 847 LLMAHDDYTNQIGREFGETDPSLMRHLVNIISVYAFNKSVDYQSVCEPGAAPKOGAGHS 906
DB 865 ILVS--EDYT--QTGDFGEVEGAVNMKLLTMSGSKRITLDYQAMCR---ANKESSDSAH 918
QY 907 AYVPSVADILQIGWATAAAMSLQQLLSLTTPRLLEAVEMEDDDFTASLSK-----QS 961
DB 919 GLLDYPYKAFI-----SAAKWIMTELVLFLVEF---NLCSWHSDMTAKAKLKQLLEP 968
QY 962 CITQOTQYFFDNDSKFSGLDGCNCSRFHGEKLMNTNLFIMVESKGTCPDPT 1016
DB 969 CDTEYPAFVSERTIKETIGNIACEDCSKSFVIOIIPSSNLFMVVDS--SCLCES 1021

RESULT 13
Q9NY16 PRELIMINARY; PRT; 997 AA.
AC Q9NY16
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE CALCIUM CHANNEL ALPHA2-DELTA3 SUBUNIT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Bugert P., Hanke S., Chudek J., Kovacs G.;
RT "Analysis of a putative tumor suppressor gene region of 100 kb at chromosome 3p21.1 in conventional renal cell carcinoma.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ272268; CAB5962.1;
DR InterPro; IPR002035; -.
```

[illegible]

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Db 305 ENIEVFNOQIEQLDDPEGYANLTLAYETAFOLLRRKYDSSRHCVTNSTCNOQIMLVTDGVA 364
Qy 367 ERAOEIENKYN-----KDKKVRVFRFSVGOHNERGPIOMWACENKNGYIPIPSIGA 418
Db 365 GNTTEVOKYNGNGENGTSDMTQVRYTYLLGKEVTKVRELQWACLNRGYSHVQILDE 424
Qy 419 IRIHQEYLDVLGRPMVLGAKAKQVQWNTVYLDAL-----ELGLVTIGLPLVFN 469
Db 425 VHEEVLKYVDVIATPLVLQNEQHPPT-WTHAFTDKTYDPKTSNEKRPLMTISVGPFAFDR 483
Qy 470 TGOPEKTNLKNOLLGVMGVDSLEDKRLTPFTLPCNPGYFAIDPBGVYLLHPNLOP 529
Db 484 FYRANSTNPRARL-LGVAGDVPVEDIDKLTLPYKGVNGYSVFSVNGVYLLHPDURP 542
Qy 530 -----KNPKSQEPVTFDLDAE-LENDIK-----VEIRNKMDGESGE-KTFFTLV 573
Db 543 IGTGKNMNPYN---SIDFTEVHELFEDQSPREGESILHINRAWREANFEKSISVKE 599
Qy 574 KSQDERYIDKGNRTYWTVPVNGTYSIALVLPT-YSFYIKAKLEETITQARSKKGMKD 632
Db 600 HYDKMRRYSEKQDYFFAPLEPTFTLGIWMPSEYGTWIKVGEVD-----KNKHKMINI 655
Qy 633 SETLKPDMFEE-----SGYTFIAP---RDVC-----NDLKISDNNTEFLNEN 672
Db 656 SDFTEGEMKVPDWYCKYHYLEGHEKTEPEALRELEAKQNDKWSEYADESDWD 715
Qy 673 EFID-----RKTNPNS--CNADLINRVLDDAGFTNELQNTW-----SKQNKIGVKA-- 719
Db 716 DKDDLNCGRKTLGDDAYYCNKELNLLIFDAKVTNS-SYGVWRPESDEERQLIERFRADL 774
Qy 720 RPYVDGITRIVYKEAGENQ-----WQIFGEVEVDTRFEGYHTTAIDETWYKSAIQLHEDR 825
Db 775 RFVATMSGLTR-----WQIFGEVEVDTRFEGYHTTAIDETWYKSAIQLHEDR 825
Qy 758 NDNVYFTAPYENKSPGAYESGINYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTS 817
Db 826 AESFYVSKYID-----YDEIEDEYVAVGDGKSSA-----DPMEDSE 844
Qy 818 IRDPCAGPVCCKRNSVDMCVILDDGFLMANHDDVTNIGRFFGEIDPSLRHLVNI 877
Db 845 VKCNHCLPIC---TDDVDVCVINDNNAVIVIGN---INTTGRFEGFHGDVMTAMVER 897
Qy 878 SVYAFNKSYDQSVQ--EPGAPKOGAGHRSAVPSVAD-ILQIGWATAAANSILQOFL 934
Db 898 GIFLSIEYIDYQEOCKEPEKAVME-----YTDEIEDEYVAVGDGKSSA----- 941
Qy 935 LSLTPRLLEAVEMEDDDFTASLSK-----QSCITEQTQYFFDNDSKSPGVLDG--G 985
Db 942 -----SKPKODSDDENAMFEDEPEPDIYKACDKRSTLYAL--QPSALVGINDFVEA 990
Qy 986 NCSRIFHGEKLMNTNLIFIMV 1006
Db 991 PSTRPFLVKIPNSNLVLVV 1011

RESULT 15
QVJMO PRELIMINARY; PRT; 2172 AA.
AC QVJMO
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE CG12455 PROTEIN.
GN BG:DS07473.1 OR CG12455.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN NCBI_TaxID=7227;
RP SEQUENCE FROM N.A.
KC STRAIN=BERKELEY;
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RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananidis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Adair J.F., Agayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Slier E., Spadling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-F., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AE003650; AAF53505.1; -.
DR FlyBase; FBgn0028859; BG:DS07473.1.
DR InterPro; IPR002035; -.
SQ SEQUENCE 2172 AA; 247574 MW; 39AA7BCB470DIA39 CRC64;
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Query Match 16.8%; Score 912.5; DB 5; Length 2172;

Best Local Similarity 25.1%; Pred. No. 2.7e-49;

Matches 275; Conservative 207; Mismatches 383; Indels 229; Gaps 42;

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Db 13 SKATVGRWATQFGDELFALAKITKSQIEKYKEYN--ARVELKNGTELKSIKYNVR 70
Qy 89 LLNSRKALVSLALEAEKVAQAAHQWREDA--SNEVYVYNAKDDLDPEKNDSEPG----S 142
Db 71 ML-----ARKMDAVRCIQEHFTYFSSKYSIFNGNSEEPLEAEFAWMYRN 117
Qy 143 QRIRPVFTEDANF-GRQISYQAAHVHPTDIYEGSTIVNELNWTSDALDEFFKKNREDP 201
Db 118 MELNP-----DTHFYNTPVDTESHSVHPVPSNIWDRSERVLKTIIMSEHLDVFRQYQSDP 173
Qy 202 SLLQVFGSATGLARYYPASPDVNSRTPNKLIDLYDVRPPWYIQGAASPKDMLTLVDVS 261
Db 174 ALSWQYFGSDTGLIRHYPAQAOWTDRPNRDDADTYDCKRRSWIETATCSKDIVILLDHS 233
Qy 262 GSVGLTKLIRTSVSEMLETLSDDDFVYNVASFNSNAOD-VSCFO-HLVQAVNRNKKYLK 319
Db 234 CSMTGFRHHVAKFIRSIILDFSNDDFTILYSSSEVDIIPCFNGALVQATPENIEVFN 293
Qy 320 DAVNNI-TAKGITDYKKGFSFAFOLLNYSR-----ANCKIIMLTGDGEERAQEIF 373
Db 294 QQIEQLDDPEGYANLTLAYETAFOLLRRKYDSSRHCVTNSTCNOQIMLVTDGVAQNTTEVF 353
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Search completed: July 23, 2001, 07:47:28
Job time: 614 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 23, 2001, 07:36:44 ; Search time 92.97 Seconds
(without alignments)
693.162 Million cell updates/sec

Title: US-09-397-548-17

Perfect score: 5599

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries:

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5599	100.0	1091	16	AA1980
2	5599	100.0	1091	19	AA1981
3	5599	100.0	1091	21	AA1982
4	5599	99.9	1091	19	AA1983
5	5599	99.9	1091	14	AA1984
6	5599	99.9	1091	19	AA1985
7	5599	99.3	1086	16	AA1986
8	5599	99.3	1086	21	AA1987
9	5599	99.3	1086	19	AA1988
10	5542.5	99.0	1084	16	AA1989
11	5542.5	99.0	1084	19	AA1990

12	5542.5	99.0	1084	21	AA1991
13	5523	98.6	1103	16	AA1992
14	5523	98.6	1103	19	AA1993
15	5523	98.6	1103	21	AA1994
16	5503	98.3	1079	19	AA1995
17	5503	98.3	1079	21	AA1996
18	5497	98.2	1079	16	AA1997
19	5385.5	96.2	1106	18	AA1998
20	5385.5	96.2	1106	18	AA1999
21	5385.5	96.2	1106	21	AA2000
22	5364.5	95.8	1106	16	AA2001
23	5257.5	93.9	1100	10	AA2002
24	5257.5	93.9	1100	10	AA2003
25	5257.5	93.9	1100	10	AA2004
26	5257.5	93.9	1100	10	AA2005
27	5257.5	93.9	1100	10	AA2006
28	5257.5	93.9	1100	10	AA2007
29	5257.5	93.9	1100	10	AA2008
30	5257.5	93.9	1100	10	AA2009
31	5257.5	93.9	1100	10	AA2010
32	5257.5	93.9	1100	10	AA2011
33	5257.5	93.9	1100	10	AA2012
34	5257.5	93.9	1100	10	AA2013
35	5257.5	93.9	1100	10	AA2014
36	5257.5	93.9	1100	10	AA2015
37	5257.5	93.9	1100	10	AA2016
38	5257.5	93.9	1100	10	AA2017
39	5257.5	93.9	1100	10	AA2018
40	5257.5	93.9	1100	10	AA2019
41	5257.5	93.9	1100	10	AA2020
42	5257.5	93.9	1100	10	AA2021
43	5257.5	93.9	1100	10	AA2022
44	5257.5	93.9	1100	10	AA2023
45	5257.5	93.9	1100	10	AA2024

ALIGNMENTS

RESULT 1

AA1980
ID AA1980 standard; Protein; 1091 AA.
XX
AC AA1980;
XX
DT 01-DEC-1995 (first entry)
XX
DE Human neuronal calcium channel subunit alpha 2b.
XX
KW Calcium channel subunit; antagonist; agonist; diagnosis;
Lambert Eaton Syndrome.
XX
OS Homo sapiens.
XX
PN W09504822-A.
XX
PD 16-FEB-1995.
XX
PF 11-AUG-1994; 94WO-US09230.
XX
PR 11-AUG-1993; 93US-0105536.
PR 05-NOV-1993; 93US-0149097.
(SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
Ellis SB, Gillespie A, Harpold MM, Mccue AF, Williams ME;
WPI; 1995-090900/12.
DR N-PSDB; AA084664.
XX
PT DNA encoding human calcium channel sub-unit(s) - used for developing prods. for studying calcium channels, e.g. for obtaining agonists and antagonists

CC channel. Calcium channels are membrane-spanning, multi-subunit proteins
CC that allow controlled entry of calcium ions into cells. This leads
CC to depolarisation events required for muscle contraction. The recombinant
CC subunit, when expressed with nucleic acids encoding the complete calcium
CC channel, can be used in assays for the detection and characterisation of
CC compounds that modulate the channel. The DNA encoding the subunits can
CC be alternatively spliced when transcribed, giving more than one form of
CC the protein from the same transcript, each having slightly different
CC properties. In addition, the reactivity of the alpha 1 subunit with IgG
CC molecules from the serum of an individual with Lambert Eaton Syndrome
CC (LES) can be used as a diagnostic for the disease.

XX Sequence 1091 AA;

Query Match 100.0%; Score 5599; DB 19; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCILLATLTLLFQSLIGPSSEEPFSAVITKSWYDKMQEDLVTLAKTASGVNQLVDI 60
DB 1 maagcillaltltllfqsllgpsseefpsavtikswydkmqedlvtlaktasgvnqlvdi 60
QY 61 YEKYQDLYTVEPNARQLVEIARDIEKLLSNRSKALVSLALEAEKVQAQHQREDFASN 120
DB 61 yekyqdytvepnarqlveiaardiekllsnrskalvslaleaekvqaahqwedfasn 120
QY 121 EYVYNAKDDLPDPEKNDSPGSGRIKPFVIEDANFGRQISYHAAVHPIDYIEGSTIVL 180
DB 121 evyynakddldpekdndspgsgrikpvfiedanfrqisqhaavhiptdiyegstivi 180
QY 181 NELNWTALDEVPKKNREEDPSLLQVFGSATGLARYYPASPVWDNSRTPNKIDLYDVR 240
DB 181 nelnwtaldevpkknreedpsllqvfgsatglaryypaspvwdnsrtpnkidlydvr 240
QY 241 RPYVIGGAASPKDMLILVDVSGVSGILTKLIRTSVSEMLETSLDDDFVNVASFNSAQD 300
DB 241 rpyviggaspkdmlilvdvsgvsgiltklirtsvsemlletlssdddfnvvasfnasqd 300
QY 301 VSCFQHLVQANVRNKKVLDAVNNTAKGITYDKKGFSAFEOALLNVNVRANCKIIML 360
DB 301 vscfqlvqanvrnkvkldavnnitakgitydkkgsfafedllnynvsnrncnkiml 360
QY 361 FTDGGERAQEIPKYNKKVKVFRFSVQGHYERGIQWACENKGYIYEIPSGAIR 420
DB 361 ftdggeeraqeipkynkkkvfrfsvqghnyergiqwacenkgyiyeipsigair 420
QY 421 INTQEVLDVLRPMVLGDKAKQVQNTNVLDALEGLVITGLPVFNTGQFENKTNLK 480
DB 421 intqeyldvlgrpmvlgdkakqvqntnvyldaleglvitglpvnitgqfenktnlk 480
QY 481 NQILGVMGVDVSLDILKRLTPFTLCPNGIYFPAIDPNGVLLHPNLOPKNPKSQBPVTL 540
DB 481 nqilgvmgvdsledilkrltpftlcpngiyyfpaidpngvllhpnlopknpksqbpvtl 540
QY 541 DFLDAELNDIKVEIRNKMIDGESGKFTLTKVSDERYIDKGNRTYTWTVPNGTDYSL 600
DB 541 dfldaelndikveirnkmidgesgkftltkvsgderyidkgnrtytwtvpngtdysl 600
QY 601 ALVLPYISFYIKAKLEETIQARSKGKMKDSEITLKPONFESGYTFTIAPRDYCNLDKI 660
DB 601 alvlpysfyikakleetitarskgkkmkdselitkpdnfeesgytftiaprdycondlki 660
QY 661 SDNTEFLNNEFIDRKTPNPNPCNADLNRYLLDAGFTNELVQNVKSKOKIKGVKAR 720
DB 661 sdntefllnnefidrktpnppncnadlnryllldagftnelvqnvkskknkigvkar 720
QY 721 FVVTGGITRVYPKAENQENPETEYDFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
DB 721 fvvtdggitrvypkagenqenpeteydfykrslndndnyvftapyfnkspgpayesgi 780
QY 781 MYSKAVEIYIQGKLLKPAVVGIKIDVNSWIENTFTKTSIRDPACGAPVCDCKRNSDVMDCVI 840
DB 781 myskaveiyiqgkllkpaavgikidvnswnientftktsirdpacgapvcdckrnsdvmdcvi 840

Db 781 mvskaaveiyiqgkllkpaavgikidvnswnientftktsirdpacgapvcdckrnsdvmdcvi 840
QY 841 LDGSGFLLMANHDDYTNQIGRFFGEIDPSPSLMRHLVNSYAFNKSVDYQSVCEPGAAPKQ 900
DB 841 ldgsgfllmanhddytngqirffgeidpslmrhlvnsyafnksvdyqsvcepgaapkq 900
QY 901 GAGHRSAYVPSVADIIQIGWATAAASWILQOELLSTFPPRLLEAVEMEDDDFTASLSKQ 960
DB 901 gaghrsayvpsvadilqigwwataaawslilqellstfprlleavemedddftaslskq 960
QY 961 SCITEQYXFEFNDKSFSGVLDCGNCSTRIFHGEKLMNTNLIFTMVESKGTCPDCTRLLI 1020
DB 961 sciteqyxfefndksfsgvldcgcncstrifhgeklnmtnliftmvskgtcpdctrlli 1020
QY 1021 QABQTSDGPNPCDMVKQPRYRKGPVDFVFNVLVLEDTDCGGSV 1063
DB 1021 qaeqtsdgppncdmvkmqpryrgkpdvfcfnvldedytdcgvs 1063

RESULT 3

AAB10576
ID AAB10576 standard; Protein; 1091 AA.

AC AAB10576;

XX 22-DEC-2000 (first entry)

XX Human calcium channel alpha-2 subunit protein.

XX Human; calcium channel; calcium channel subunit; diagnosis;
XX Lambert Eaton Syndrome; calcium channel subunit alpha-2.

XX Homo sapiens.

XX US6096514-A.

XX 01-AUG-2000.

XX 25-MAY-1995; 95US-0450562.

XX 04-APR-1988; 88US-0176899.

XX 02-FEB-1990; 90US-0482384.

XX 08-NOV-1990; 90US-0603751.

XX 30-NOV-1990; 90US-0620250.

XX 15-AUG-1991; 91US-0745206.

XX 10-APR-1992; 92US-0868354.

XX 13-JUL-1992; 92US-0914231.

XX 11-AUG-1993; 93US-0105536.

XX 05-NOV-1993; 93US-0149097.

XX 07-FEB-1994; 94US-0193078.

XX 04-APR-1994; 94US-0223305.

XX 11-AUG-1994; 94US-0290012.

XX 23-SEP-1994; 94US-0311363.

XX 28-SEP-1994; 94US-0314083.

XX 07-NOV-1994; 94US-0336257.

XX 13-MAR-1995; 95US-0404950.

XX (SIBI-) SIBIA NEUROSCIENCES INC.

XX Ellis SB, Williams ME, McCue AF, Harpold MM;

XX WPI; 2000-548230/50.

XX N-PSDB; AAA71707.

PT Human calcium channel beta subunit polynucleotides, useful for
PT producing recombinant eukaryotic cells and for diagnosing Lambert Eaton
PT Syndrome

XX Example IV; Column 135-144; 153pp; English.

XX This invention describes a novel isolated DNA molecule (I) comprising a
XX sequence encoding a beta3-1 subunit of a human calcium channel.
XX Nucleic acid probes comprising 14-30 contiguous nucleotides of

CC beta_3 subunit encoding DNA are useful for isolation and cloning of
 CC calcium channel subunit-encoding DNA. Recombinant eukaryotic cells that
 CC express heterologous calcium channel are useful for identifying compounds
 CC that modulate calcium channel activity and in assays for identifying
 CC agonists and antagonists of calcium channel activity in humans. Human
 CC calcium channel subunit of eukaryotic cells expressing the channel are
 CC useful for diagnosing Lambert Eaton Syndrome (LES) in a human. This
 CC sequence represents the human calcium channel alpha-2 subunit which is
 CC described in the method of the invention.

XX Sequence 1091 AA;

Query Match 100.00; Score 5599; DB 21; Length 1091;
 Best Local Similarity 100.00; Pred. No. 0;
 Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLFOSLLIGPSEPPFSAVTVIKSWDKMQEDLVTLAKTAGSVNQLVDI 60
 Db 1 maagccllaltlfigsligpseepfssavtikswdkmqedlvltaktagsvnqlvdi 60
 QY 61 YEKYQDLTYVEPNNAQQLVEIAARDIEKLLNSRKALYSALAEKVAQAQWREDFASN 120
 Db 61 yekyqdltyvepnnaqqlveiaardieklkllnsrkalsalaeakvqaahqwedfasn 120
 QY 121 EVVYNAKDDLDPEKNDSEPGSRQIKPVFIEDANFGROIYSQHAHVHPTDIYEGSTIVL 180
 Db 121 evvyynakddldpekndsepgsrqikpvfiedanfgroisqhaahvhtptdiyegstivl 180
 QY 181 NELNWTSSALDEVEKKNREEDPSLLQWFGSATGLARYYPASPVWDSNTPNKIDLYDVR 240
 Db 181 nelnwtssaldevekknreedpsllqwfgsatglaryypaspvwdsntpnkidlydvr 240
 QY 241 RPWYIOGAASPKDMLILVDVSGVSGTLKLIKRTSVSEMLETLDSDDFVNVASNSNAQD 300
 Db 241 rpwyioqaaspkdmlilvdvsgvsgtlklirsvsemlletldsddfvnvasnsnaqd 300
 QY 301 VSCFQHLVQANVRNKKVLKDAVNNTAKGITDYKKGSFAFEQLNLYNVRANCNKLIIML 360
 Db 301 vscfqlhqvannrnkvkldavnnitakgitdykkgfsafefqlnlynvrancnkliiml 360
 QY 361 FTDGGEAQAEIFNKYKDKKVRFRVSVQHNVERGPIOMACENKGYIYEIPSGAIR 420
 Db 361 ftdggeeraqeifnkynkdkkvrfrsvqghnyergpiqwmacenkgyyeipsigair 420
 QY 421 INTQEYLDVLGRPMVLAKGAKOVQNTVYLDALGLVITGTLVPFNITGQFENKTNLK 480
 Db 421 intqeyldvlgrpmvlakgakovntvylldalglvitgtlvpfnitgqfenktnlk 480
 QY 481 NQLILGVMGVDSLEDIKRLTPRTFLCPNGYYFAIDPNGVYLLHPNLQPKNKSQEPVIL 540
 Db 481 nqlilgvmgvdsleedikrltprtflcpngyyfaidpngvyllhpnlpknksqepvtil 540
 QY 541 DFLDAELENDIKVEIRNKMDIGSGSEKTRTLVKSDERYIDKGRNTYTWTVPVNGDYSL 600
 Db 541 dfldaelendikveirnkmdigsgsekttrtlvksderyidkgrntywtvpvngdyisl 600
 QY 601 ALVLPYSFYIYKAKLEETITQARSKGKWKQSETLKPNFEESSGVTFIAPRDYCNLDKI 660
 Db 601 alvlpysfyyiakleetitqarskkgkwmksetlknfnfessgytffiaprdycondki 660
 QY 661 SDNTEFLNFEIDRKPNNPNSCNADLINRVLLDAGFTNELVQYNSKQNKIKGVKAR 720
 Db 661 sdnteflnfnfeidrknnpnscnadlinrvllldagftnelvqynskqknkigvkar 720
 QY 721 FVVTGGITRVTPKAGENWQBNPETEDSFYKRSILDNDNVYFTAPYFNKSGPGAYESGI 780
 Db 721 fvtvtdggitrvtpkagenwqbnpetedsfykrsildndnvftapyfnksgpgayesgi 780
 QY 781 MVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPACGVPCKRNSDVMDCVI 840
 Db 781 mvskaveiyiogkllkpaavgkikdvnswieenftktsirdpcagvpckrnsdvmdcvi 840

QY 841 LDDGGFLMANHDDYTNQIGRFFGEIDPSIMRHLVNISYAFNKSYDYQSVCEPGAAPKQ 900
 Db 841 lddggflmanhddytngigrffgeidpsimrhlvnisvafnkssydyqsvcepgaapkg 900
 QY 901 GAGHSAYVPSVADILQIGWATAAASILQOFLSLTFPRLLLEAVEMEDDDFTASLSKQ 960
 Db 901 gaghsayvpsvadilqigwataaawsilqflsltfprlleavemedddftaslskq 960
 QY 961 SCITBOTQVFFPNDKSPFSGVLDGNCSEIFHGEKLMNTNLIFIMVESKGTCPDPTLLI 1020
 Db 961 scitbotqvffpndkspsfsgvldcncsfrifhgeklmntnlifimveskgtcpdptrlli 1020
 QY 1021 QAEQTSQDGNPCDMVKQPRYKRGPDVCFDNNVLEDTDCGGVS 1063
 Db 1021 qaeqtsdgnpcdmvkqpryrgpdvcfdannvledtydcggvs 1063

RESULT 4

AAW37879

ID AAW37879 standard; Protein; 1091 AA.

XX AAW37879;

XX 28-AUG-1998 (first entry)

XX Human calcium channel a2d subunit.

XX Calcium channel; human; central nervous system disorder;
 XX Lambert-Eaton syndrome; diagnosis; therapy.

XX Homo sapiens.

XX WO9811131-A2.

XX 19-MAR-1998.

XX 11-SEP-1997; 97WO-US16146.

XX 16-SEP-1996; 96US-0713118.

XX (AMHP) AMERICAN HOME PROD CORP.

XX Chen ARS, Franco R, Shuey DJ;

XX WPI; 1998-207325/18.

XX N-PSDB; AAV29060.

XX DNA encoding human neuronal calcium channel subunit(s) - useful for
 XX diagnosis of and treatment of central nervous system disorders, e.g.
 XX Lambert-Eaton syndrome

XX Disclosure; Fig 2; 89pp; English.

XX This polypeptide comprises the a2d subunit of the human neuronal
 CC calcium channel. cDNA clones (see AAV29059-61) encoding the a1B
 CC subunit (see AAW37879), the a2d subunit and a b3 subunit (see AAW37880)
 CC have been isolated. These have been inserted into expression
 CC vectors and are stably expressed in transformed cell lines. The
 CC transformed cells show omega-conotoxin GVIA binding activity,
 CC and omega-conotoxin GVIA toxin sensitive potassium-stimulated
 CC calcium uptake, indicating that the proteins expressed by the
 CC clones are capable of forming a functioning calcium channel.
 CC Nucleic acids encoding the 3 subunits, as well as vectors, host
 CC cells and methods of isolating nucleic acids encoding related
 CC calcium channels are disclosed. Fusion proteins incorporating the
 CC subunit proteins, antibodies, and assays for identifying agents
 CC that modulate calcium channel activity are also provided. Such
 CC agents can be used to treat certain central nervous system
 CC disorders by altering calcium channel activity. Methods of
 CC diagnosing diseases associated with particular calcium channels,
 CC such as Lambert-Eaton syndrome, are disclosed.

XX Sequence 1091 AA;

XX SQ

Query Match 99.9%; Score 5595; DB 19; Length 1091;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1062; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAGCLLATLTLFQSLLIGPSSSEEPFPAVITKSWDKMOEDLVTLAKTASGVNOLVDI 60
DB 1 maagcllatltilfqslligpsseepfpaavtikswdkmqedlvltaktasgvnqlvdi 60

QY 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHOREDFASN 120
DB 61 yekyqdytvepnarqlveiaardiekllsnrskalvslaleaekvqaahqwfedfasn 120

QY 121 EYVYNAKDDLPDEKNDSPGSGORIKPVFIEDANFORQISYQAAVHIPDPIYEGSTIVL 180
DB 121 evvyynakddlpdekndspgsgrikpvfiedanforqisqhaavhiptdiyegstivl 180

QY 181 NELNWTSADEVFKKNEEDPSLLWQVFGSAGCLARYYPASPWVDNSRTPNKKIDLDYVRR 240
DB 181 nelnwtasadevfkneedpsllwqvfgsatglaryypaspwvdnsrtpnkkidldyvr 240

QY 241 RPWYIQGAASPKDMLILVDVSGVSLTLKLRITSVSEMLETSLDDDFNVASFNSNAOD 300
DB 241 rpwyiqgaaspkdmlilvdsvsgvsltlklritsvsemlletlsdddfnvvasfnasqd 300

QY 301 VSCFQHLVQANVRNKKVLKDAVNNIPAKGIDYKGFSAFEOQLNYSRANCNKIIML 360
DB 301 vscfqlvqanvrnkkvlkdavnnitakgidykgsfafeqllnynvsrancnkilmi 360

QY 361 FTDGGERAQEFNKYKDKKRVFRFSGVGHNYERGPTQWACENKGYIYEIPSGAIR 420
DB 361 fdggeeraqefnkykdkkrvfrfsgvghnyergptqwmacenkgyyieipsigair 420

QY 421 INTQEYLDVLGRPMVLGAKQOVQNTVYLDALGLVITGTPVENITGQFENKTNLK 480
DB 421 intqeyldvlgrpmvlgakqovqntvnyldaleglvitgtplvenitgqfentnklk 480

QY 481 NQILGVMGVDSLEDIKRLTPRFTLCPNGYFPAIDPNGYVLLHPLNLPKNKPSQBPVTL 540
DB 481 nqilgvmgvdsleedikrltpftlcpngyfaidpngyallhplnlpknkpsqbpvtl 540

QY 541 DFLDAELNDIKVIRNKNMIDGESGKTRTLVKSDERYIDKGNRTYTWTPVNGTDYSL 600
DB 541 dfldaelndikvirnknmidgesgktrtlvksderyidkgnrtytwtvpvngtdysl 600

QY 601 ALVLPYSFYITAKLEETITQARSKGKMDSETLKPNEESGYTFAPRDYCNDLKI 660
DB 601 alvlpysfyyiakleetitqarskkgkmdsetlkpndeesgytfflaprdywndlki 660

QY 661 SDNTEFLNFEFIDRKTNNPNSCADLINRVLLDAGFTNELVQVWSKQKNIGVKAR 720
DB 661 sdnteflnfnefidrktnnpnsnadlinrvlldagftnelvqvwsqknigvkar 720

QY 721 FVVTGGIRVYPKEAGENQWENPEYEFYKRSLDNDNYFTAPYFNKSGPAYESGI 780
DB 721 fvtvggirtvypkeagenqwenpetyefykrslndnyftapyfnksppayesgi 780

QY 781 MYSKAVEIYIQGLKLPVAVGIIKIDVNSNIENFTKTSIRDPACGPVCDCKRNSDVMDCVI 840
DB 781 myskaveiyiqglklpavvgiikidvnsnienfktksirpdcagpvcdckrnsdvmdcv 840

QY 841 LDGGFLLMANHDDYNNQIGRFFGEIDPSLMRHLNVNISYAFNKSXYDSVCEPAGAPKQ 900
DB 841 ldggfllmanhddynnqigrffgeidpslmrhlvnvisyafnksydyqvcepgaapkq 900

QY 901 GAGHRSAYPSVADIIQIGWATAAASWILQOFLSLTFRLLLEAVEMEDDDFTASLSKQ 960
DB 901 gaghrsayspsvadliqigwataaaswlqofllsltfrllleavemedddftaslskq 960

QY 961 SCTTEQTYFFDNDSKSFSGVLDCGNCRIHFHGEKLMNTNLFIMVESKGTCTCPDRLII 1020
DB 961 sctteqtyffdnndsksfsgvlcdgncsrifhgeklnmtnlffimveskgctcpdcrlli 1020

QY 1021 QABQTSQDGNPCDMVKQPRYKGPVCFDNNVLEDYTDGGSV 1063
DB 1021 qaetsdgnpcdmvkgpryrgkpdvcfdnnvledytdcgvs 1063

RESULT 5
AAR33553
ID AAR33553 standard; Protein; 1091 AA.
XX
AC AAR33553;
XX
DT 30-JUN-1993 (first entry)
XX
DE Sequence of the alpha 2 human calcium channel subunit.
XX
KW Human calcium channel subunit; diagnosis; agonist; antagonist;
KW Lambert Eaton syndrome.
XX
OS Homo sapiens.
XX
PN W09304083-A.
XX
PD 04-MAR-1993.
XX
PF 14-AUG-1992; 92WO-US06903.
XX
PR 15-AUG-1991; 91US-0745206.
PR 10-APR-1992; 92US-0868354.
XX
PA (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
XX
PI Brenner R, Ellis SB, Feldman DH, Harpold MM, Mocue AF;
PI Williams ME;
XX
WPI: 1993-093936/11.
DR N-PSDB; AAQ37821.
XX
PT DNA encoding specific human calcium channel sub-units - used for
PT identifying calcium channel agonists and antagonists and
PT diagnosing Lambert Eaton syndrome
XX
PS Disclosure; Page 134-138; 150pp; English.
XX
CC DNA encoding a human neuronal calcium channel alpha 2 subunit was
CC isolated from a human genomic DNA library probed under low and high
CC stringency conditions with a fragment of DNA encoding the rabbit
CC skeletal muscle calcium channel alpha 2 subunit. The fragment
CC included nucleotides having a sequence corresponding to the
CC nucleotide sequence between nucleotides 43 and 272 inclusive of
CC rabbit back skeletal muscle calcium channel alpha 2 subunit cDNA.
CC PCR analysis identified splice variants of the human calcium alpha
CC 2 subunit transcript. In particularly preferred embodiments, the
CC DNA encoding the alpha 2 subunit is produced by alternative
CC processing of a primary transcript that includes DNA encoding the
CC amino acids set forth in AAR33553 and the DNA of AAQ37823 inserted
CC between nucleotides 1624 and 1625 of AAQ37821.
XX
SQ Sequence 1091 AA;

Query Match 99.9%; Score 5593; DB 14; Length 1091;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1062; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAGCLLATLTLFQSLLIGPSSSEEPFPAVITKSWDKMOEDLVTLAKTASGVNOLVDI 60
DB 1 maagcllatltilfqslligpsseepfpaavtikswdkmqedlvltaktasgvnqlvdi 60

QY 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHOREDFASN 120
DB 61 yekyqdytvepnarqlveiaardiekllsnrskalvslaleaekvqaahqwfedfasn 120

QY 121 EVVYNAKDDLDPEKNDSEPSQRIKPVFIEDANFGROISYQHAHVHPTDIYEGSTIVL 180
Db 121 evvynakddldpekndsepsqrikpvfiedanfgroisqyhaavhiptdiyegstivl 180
QY 181 NELNWTSSALDEVFKKREEDPSLLQVFGSATGLARYYPASPWVDNRTNPKIDLYDVR 240
Db 181 nelnwtssaldevfkknreedsllqvfgsatglaryypaspwvdnrtnpkidyvrr 240
QY 241 RPWTQGAASPKDMLILVDVSGVSGITLKIIRTSVSEMLETLSDDDFVNVASFNQAQD 300
Db 241 rpwtqgaaspkdmlilvdvsgvsgitlkiirtsvsemletlsdddfvnvasfnnaqd 300
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGTIDYKKGFSFAFEQLLNVRANCNKIIML 360
Db 301 vscfqhlvqanvrnkvlkavnnitakgtidykkgfsfafeqllnvrancnkliiml 360
QY 361 FTGGGERAEIENKYNKKVRVFSVQGHYERGIQWACENKGYEYIEPSTGAIR 420
Db 361 ftdggeeraeiefnkynkkvrvfsvqghyergiqwacenkgyeiepstgaair 420
QY 421 INTQEYLDVLRPMVLGAKAKOVQWTVNYLDLEGLVITGLPVFNITQPFENKTNLK 480
Db 421 intqeyldvlrmpvlgakakovqwtvnyldlelglvitglpvnitqpfenktnlk 480
QY 481 NQILGVMGVDSLEDIKRLTPRTLCPLNGYFPAIDPNCVYLLHPNLQPKNKSQEPVTL 540
Db 481 nqilgvmgvdsleedikrltprtlcpngyfpaidpncvyllylhpnlqpknsksepvtl 540
QY 541 DFLDAELENDIKVEIRNKMIDGESGEKTFRTLVKSDERYIDKGNRTYTWTPVNGTDYSL 600
Db 541 dfldaelendikveirnkmidgesgektftrtlvksderyidkgnrtytwtvpngtdysl 600
QY 601 ALVLPYSPYITAKLEETITQARSKKMKKSEITLKPONFEESGYTFIAPRDYCNLDKI 660
Db 601 alvlpyspyitakleetitqarskkmksetltpkpnfeesgytfiaprdydcndiki 660
QY 661 SDNTEFLNFEIDRTPNPNPCNADLINRVLLDAGTNELVQNYWSKQNKIKGVAR 720
Db 661 sdntefllnfeidrtppnpsncadlinrvlldagtneelvqnywskgnkikgvark 720
QY 721 FVVTGGITRVYPKAGENQENPTYEDSFYKRSLDNDNVFTAPYFNKSGPGAYESGI 780
Db 721 fvtvtdggitrvypkagenqenptyedsfyrksldndnvftapyfnkspgpaysesi 780
QY 781 MVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFYKTSIRDPACGVCCKRNSVMDCVI 840
Db 781 mvskaveiyiogkllkpvvgkldvnswienvfyktsirdpcagvcckrnsvmdcvi 840
QY 841 LDDGGFLMANHDDYTNIQIGRFFGEIDPISLMRLHVNISVYAFNKSXYQSCVCEPAAPKQ 900
Db 841 lddggflmanhddytngirffgeidpislmrhvnisvyafnksxyqscvcepaapkq 900
QY 901 GAGHRSAYVPSVADILQIGWATAAANSILOQFLSLTFPRLLLEAVEMEDDDFTASLSKQ 960
Db 901 gaghrsayvpsvadilqigwataaansilqlfllstfprlleavemedddftaslskq 960
QY 961 SCITEQYQYFFDNDKSFSGVLDGCGNSRIFPHGKLMNTNLIFIMVESKGTCPDTRLLI 1020
Db 961 sciteqyqyffndksfsgvldgcgnsrifphgklnmntnlifimveskgtcpdtrlli 1020
QY 1021 QAETSQGNPCDMVKQPRYKRGPDVCFDNNVLEDYDCGGVS 1063
Db 1021 qaetsqgnpcdmvkprykrqpdvcfdnnvledydcggvs 1063

RESULT 6
AAW63148
ID AAW63148 standard; Protein; 1110 AA.
XX
AC AAW63148;
XX
DF 12-OCT-1998 (first entry)
XX

DE Human calcium channel alpha-2 subunit.
XX
KW Alpha-2 subunit; human; calcium channel; assay; detection;
KW characterisation; Lambert Eaton Syndrome; LES; diagnosis.
XX
OS Homo sapiens.
XX
PN US5792846-A.
PD 11-AUG-1998.
PF 31-MAY-1995; 95US-0455543.
PR 04-APR-1994; 94US-0223305.
PR 04-APR-1988; 88US-0176899.
PR 04-APR-1989; 89US-0603751.
PR 20-FEB-1990; 90US-0482384.
PR 30-NOV-1990; 90US-0620250.
PR 15-AUG-1991; 91US-0745206.
PR 31-MAY-1995; 95US-0455543.
XX (SIBI-) SIBIA NEUROSCIENCES INC.
PA Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;
PI Williams WE;
PI
XX WPI; 1998-456192/39.
DR N-PSDB; AAV42694.
XX
XX DNA encoding human calcium channel alpha 1B subunit protein -
PT useful for recombinant production of the channel for screening of
PT its modulators, and diagnosis of Lambert Eaton Syndrome
XX
PS Disclosure: Columns 131-138; 166pp; English.
XX
CC The present sequence represents the alpha-2 subunit of a human calcium
CC channel. Calcium channels are membrane-spanning, multi-subunit proteins
CC that allow controlled entry of calcium ions into cells. This leads
CC to depolarisation events required for muscle contraction. The recombinant
CC subunit, when expressed with nucleic acids encoding the complete calcium
CC channel, can be used in assays for the detection and characterisation of
CC compounds that modulate the channel. The DNA encoding the subunits can
CC be alternatively spliced when transcribed, giving more than one form of
CC the protein from the same transcript, each having slightly different
CC properties. In addition, the reactivity of the alpha 1 subunit with IgG
CC molecules from the serum of an individual with Lambert Eaton Syndrome
CC (LES) can be used as a diagnostic for the disease.
XX
SQ Sequence 1110 AA;

Query Match 99.7%; Score 5579.5; DB 19; Length 1110;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 1063; Conservative 0; Mismatches 0; Indels 19; Gaps 1;
QY 1 MAAGCLLALTLTLFQSLIIGPSSSEPPSAVTIKSWYDKMQEDLVTLAKTASGVNQLVDI 60
Db 1 maagcllaltltlfgslilgppsseepfsvatikswydkmqedlvtlaktasgvnqlvdi 60
QY 61 YEKYQDLYTVEPNNAQLVEIAARDTEKLLSNRSKALVSLAEAKVQAAHQWREDFASN 120
Db 61 yekyqdytvepnnarqlveiaardteklslsnrskalvslaeakvqaahqwrdfasn 120
QY 121 EVVYNAKDDLDPEKNDSEPSQRIKPVFIEDANFGROISYQHAHVHPTDIYEGSTIVL 180
Db 121 evvynakddldpekndsepsqrikpvfiedanfgroisqyhaavhiptdiyegstivl 180
QY 181 NELNWTSSALDEVFKKREEDPSLLQVFGSATGLARYYPASPWVDNRTNPKIDLYDVR 240
Db 181 nelnwtssaldevfkknreedsllqvfgsatglaryypaspwvdnrtnpkidyvrr 240
QY 241 RPWTQGAASPKDMLILVDVSGVSGITLKIIRTSVSEMLETLSDDDFVNVASFNQAQD 300

||||| 241 rpyigaaapkmllilvdvsgsvgltklirtsvaemletisdddfnvvaafnsnaq 300
QY 301 VSCFQHLVQANVRNKKVLDKADANNITAKGITYKGFSAFQOLLNYSRANCNKIIML 360
Db 301 vscfqlvqanvrnkkvldkadvnnitakgitykgsfafedqllnynvrancnkilml 360
QY 361 FTGGGERAQEIEFNKNDKVRFRFSVGOHNYERGPTQWACENKGYEYIEPSTCAIR 420
Db 361 ftdgggeerqeiFNKNDKVRFRFSVGOHNYERGPTQWACENKGYEYIEPSTCAIR 420
QY 421 INTQEDYLDVLRPMVLGAKAKOVQNTVYLDALGLVITGTPVFNITGQFENKTNLK 480
Db 421 intqeyldvLRPMVLGAKAKOVQNTVYLDALGLVITGTPVFNITGQFENKTNLK 480
QY 481 NQILGVMDVSDLEIKRLTPFTICPNGYFAIDPNGVYLHLPNLQPK----- 530
Db 481 nqilgvmdvSDLEIKRLTPFTICPNGYFAIDPNGVYLHLPNLQPK----- 530
QY 531 -----NPKSOEPTVLDLDAELENDIKVEIRKMDGESGEKTFRTLVKSQDERYI 581
Db 531 -----NPKSOEPTVLDLDAELENDIKVEIRKMDGESGEKTFRTLVKSQDERYI 581
QY 541 lrkrrpnlgpksqepvtldfdaeendkveirnkmdgesgektfirtlvksqgeryi 600
Db 541 lrkrrpnlgpksqepvtldfdaeendkveirnkmdgesgektfirtlvksqgeryi 600
QY 582 DKGRTYTPVNGTDSLALVLTPTYSFYIRAKLEETITQARSKGKMKDSITLKPDNF 641
Db 601 dkgrrtytpvngtdyslalvltptysfyirakleetitqarskgkmdsetilpknf 660
QY 642 EESGYTFIAPRDYNDLKISDNTEFLNPFIDRKTPNPNPCNADLINRVLLDAGFTN 701
Db 661 eesgytfiaprdycndlkisdnteflnpfidrktpnnpncnadlinrvlldagftn 720
QY 702 ELVONYWSKQNKIGVKARFVYTDGCTRVYPKEAGENQENPETYEDSFYKESLNDNY 761
Db 721 elvqnywsqknlgvkarfvvtdgctrvypkeagenqenpetyedsfykrsldndy 780
QY 762 VETAPFNKSGGAYESGIMSKAVIYIQGKLLKPAVVGKIDVANSWIENFTKTSIRD 821
Db 781 vftapyfnsksggayesgimskaveiyiqgkllkpaavgikidvnswieftktsird 840
QY 822 CAGPVCDCRNSDMDCVILDGGFLLMANHDDYTQIGRFFGQIEDPSLMRHLVNSVYA 881
Db 841 cagpvcdcrnsdmvdcvildggfllmanhddytqigrffgqiedpslmrhlvnsvya 900
QY 882 FNKSYDQVCEPAGAPKOGAGHRSAYVPSVADILQIGWATAAASILQOFLLSLTFPR 941
Db 901 fnksydyqsvcepagapkgaghrsayvpsvadilqigwataaasilqgflsltfpr 960
QY 942 LLEAVEMEDDDFTASLSKQSCITEQTYQYBFDNDKSGFSGLDCGNGSRIFPHGKLMNTNL 1001
Db 961 lleavemedddftaslskqsciteqtyqyffndsksfsgvldcngcsrifhgeklmntnl 1020
QY 1002 IFIMVESKTCPCDTRLLLOAQSOTSGPNPCDMKVPKRGPDVCFDNNVLEDYDCGG 1061
Db 1021 ifimveskgtcpcdtrlllqaetsgpnpcdmvkgpkyrgpdvcfdnnvledydcgg 1080
QY 1062 VS 1063
Db 1081 VS 1082

RESULT 7
AAR71013
ID AAR71013 standard; Protein; 1086 AA.
XX
XX
AC AAR71013;
XX
DT 01-DEC-1995 (first entry)
XX
DE Human neuronal calcium channel subunit alpha 2c.
XX
KW Calcium channel subunit; agonist; antagonist; diagnosis;
KW Lambert Eaton Syndrome.
XX

OS Homo sapiens.
XX
PN W09504822-A.
XX
PD 16-FEB-1995.
XX
PF 11-AUG-1994; 94WO-US09230.
XX
PR 11-AUG-1993; 93US-0105536.
PR 05-NOV-1993; 93US-0149097.
XX
PA (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
XX
PI Ellis SB, Gillespie A, Harpold MM, Mccue AF, Williams ME;
XX
DR WPI; 1995-090900/12.
XX
XX N-PSDB; AAQ84667.
PT DNA encoding human calcium channel sub-unit(s) - used for
PT developing prods. for studying calcium channels, e.g. for
PT obtaining agonists and antagonists
XX
PS Disclosure; Page 237-242; 285pp; English.
XX
CC Human neuronal alpha 2 coding sequence (AAQ84664) transcript is
CC differentially processed in skeletal muscle, aorta, and CNS in
CC the region corresp. to nt 1595-1942 of AAQ84664 in each of the
CC tissues. Five alternatively spliced variant transcripts that differ
CC in the presence or absence of one to three different portions of
CC this region. There are three sequences involved (see AAQ84664 FT
CC and AAQ84665 FT), sequence 1, sequence 2 and sequence 3. The five
CC alpha 2 encoding transcripts from the different tissues include
CC different combinations of the three sequences, except for one of
CC the alpha 2 transcripts expressed in aorta which lacks all three
CC sequences. The five alpha 2 forms identified are (1) a form that
CC lacks sequence 3 called alpha 2a, expressed in skeletal muscle
CC (2) one that lacks sequence 1 called alpha 2b, expressed in CNS
CC (3) one that lacks sequences 1 and 2 called alpha 2c, expressed in
CC aorta (4) one that lacks sequences 1, 2 and 3 called alpha 2d,
CC expressed in aorta and (5) one that lacks sequences 1 and 3
CC called alpha 2e. The DNA and AA sequences of alpha 2a - alpha 2e
CC are set forth in AAQ84666-Q84669 and AAR71012-R71015 respectively.
XX
SQ Sequence 1086 AA;

Query Match 99.3%; Score 5559.5; DB 16; Length 1086;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1058; Conservative 0; Mismatches 0; Indels 5; Gaps 1;
QY 1 MAAGCLLALTTLTFLQSLITGPSSEEPFPPSAVTIKSWDKMQEDLVTLAKTAGVNLVDI 60
Db 1 maagcllalttlftlqslitgpsseepfppsavtikswdkmqedlvtlaktasvngqlvd 60
QY 61 YEKYQDLYTVEPNARQLVEIAARDIEKLNSRKSALVSLALEAEKVQAAHQRNEDFASN 120
Db 61 yekyqdytvepumarqlveiaardieklnsrksalvslaleaeqvaaqhqrnfasn 120
QY 121 EYVYNKADDLDPKNDSEPGSQRIKPVFTEDANFRQISQYHAAVHIPTDIYEGSTIVL 180
Db 121 evvynakaddlpekdndsepgsqrikpvftedanfrqisqyhaavhiptdiyegstivl 180
QY 181 NELNWTSAIDDEVFKNREEDPSLLWQVFGSATGLARYYPASPWVDSRTPNKIDLDYVRR 240
Db 181 nelnwtasaiddevfknreedsllwqvfgsatglaryypaspwvdsrtpnkidldyvrr 240
QY 241 RPWYIOGAASPKDMLILVDVSGVSGLTILRTSYSEMLETLSDDDFVNVASFNSNAQD 300
Db 241 rpwyiogaaspkdmlilvdvsgsvgltklirtsvsemetltsdddfnvvaafnsnaqd 300
QY 301 VSCFQHLVQANVRNKKVLDKADANNITAKGITYKGFSAFQOLLNYSRANCNKIIML 360
Db 301 vscfqlvqanvrnkkvldkadvnnitakgitykgsfafedqllnynvrancnkilml 360

QY 361 FTDGGEERAQEIFNKNYKDKKVRVERFSGVGHNYERGPQWACENKGYEIPISGAIR 420
Db 361 ftdggeeeraqeifnknkdkkvrverfsvgnnyergpqlwmacenkgyyieipsigair 420
QY 421 INTQYLDVLRGPMVLADGKAKQVQWNTVYLDLGLVITGTLVPVFNITGQFENKTNLK 480
Db 421 intqeyldvlgprpmvlagdkakqvtwnvyldalelglvitgtlpvfnitgqfenktnlk 480
QY 481 NQILGVNGVDVSLIEDIKRLTPRTLCPLNGYFAIDPNGYVLLHPNLQPNKPSQEPVTL 540
Db 481 nqilgvngvdsvedikrltprtlcpngyfaidpngyvvllhpnlpqk-----epvtl 535
QY 541 DFLDAELNDIKVEIRNMIDGEGEFTFRLVKSQDERYIDKGNRRYTWTPVNGTDYSL 600
Db 536 dfldaelndikveirnmidgesegftftrlvksqderydkgndrtytwtpvngtdysl 595
QY 601 ALVLPYTFYIYAKLBETITQARSKGKMDSETLKPDPNFESGYTFIAPRDYCNLDKI 660
Db 596 alvlpysfyiyaklbetitqarskkgkmdsetlkpdpnfesgytfiaprdycndlki 655
QY 661 SDNTEFLNFEIDRKTNPNSCNADLINRVLLDAGFTNELVQWYKQNKIGVKAR 720
Db 656 sdnteflnfnefidrktnpnpscnadlinrvlldagftnelvqywsqknigvkaykar 715
QY 721 FVVDGGITRVYKPEAGENQENPETEYDSFYKRSLDNDNYFTAPYFNKSGPGAYESGI 780
Db 716 fvvtdggitrvykpeagenqenpeteydsfykrsldndnyftapyfnkspggayesgi 775
QY 781 MYSKAVEIYIOGKLLPAPVVGKIDVNSWIENTFTKTSIRDPCAGPVCDCKRNSDVMDCVI 840
Db 776 mvskaaveiyiogkllpavvgkldvnswnentftktsirdpcagpvcdckrnsdvmcvi 835
QY 841 LDGSGFLMANHDDYNTQIGRFGEDTSPSLRHLVNSISYAFNKSVDYQSVGCEPAAPKQ 900
Db 836 ldgsgflmanhddyngtqigrfgedtspslrhlvnsisyafnksvdyqsvgcepaapkq 895
QY 901 GAGHSAYVPSVADIIQIGWATAAAWSTLQOFLSLFPRLLLEAVEMDDFTASLSKQ 960
Db 896 gaghsayvpsvadilqigwataaawstlqflslfprllleavemddftaslskq 955
QY 961 SCITQOTQFFDNDKSGSVGLDCGNCRIHFGEKLMNTNLIFFIMVESKGTCPDTRILLI 1020
Db 956 sciteqtqotffndksksgvldcncsrifhgeklmntnliffimveskgtcpdtrilli 1015
QY 1021 QAEQTSDCPNCDMVKQPRYKGGPDVCFDNNVLEDYTDGCGVS 1063
Db 1016 qaeqtsdgnpcdmvkprrykggpdvcfdnnvledytdcgvs 1058

RESULT 8
AAW63153
ID AAW63153 standard; Protein; 1086 AA.
XX AC AAW63153;
XX AC AAW63153;
DT 12-OCT-1998 (first entry)
XX DE Human calcium channel alpha-2c subunit.
XX DE Alpha-2 subunit; human; calcium channel; assay; detection;
KW characterisation; Lambert Eaton Syndrome; LES; diagnosis.
KW Homo sapiens.
XX OS US5792846-A.
XX PN 11-AUG-1998.
XX PD 31-MAY-1995; 95US-0455543.
XX PF 04-APR-1994; 94US-0223305.
XX PR 04-APR-1988; 88US-0176899.

PR 04-APR-1989; 89US-0603751.
PR 04-APR-1989; 89WO-US01408.
PR 20-FEB-1990; 90US-0482384.
PR 30-NOV-1990; 90US-0620250.
PR 15-AUG-1991; 91US-0745206.
PR 31-MAY-1995; 95US-0455543.
XX (SIBI-) SIBIA NEUROSCIENCES INC.
XX Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;
PI Williams ME;
FI WPI; 1998-456192/39.
DR N-PSDB; AAV42702.
XX DNA encoding human calcium channel alpha 1B subunit protein -
PT useful for recombinant production of the channel for screening of
PT its modulators, and diagnosis of Lambert Eaton Syndrome
XX Claim 3; Columns 293-300; 166pp; English.
XX The present sequence represents the alpha-2c subunit of a human calcium
CC channel. Calcium channels are membrane-spanning, multi-subunit proteins
CC that allow controlled entry of calcium ions into cells. This leads
CC to depolarisation events required for muscle contraction. The recombinant
CC subunit, when expressed with nucleic acids encoding the complete calcium
CC channel, can be used in assays for the detection and characterisation of
CC compounds that modulate the channel. The DNA encoding the subunits can
CC be alternatively spliced when transcribed, giving more than one form of
CC the protein from the same transcript, each having slightly different
CC properties. In addition, the reactivity of the alpha 1 subunit with IgG
CC molecules from the serum of an individual with Lambert Eaton Syndrome
CC (LES) can be used as a diagnostic for the disease.
XX Sequence 1086 AA;
SQ

Query Match 99.3%; Score 5559.5; DB 19; Length 1086;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1058; Conservative 0; Mismatches 0; Indels 5; Gaps 1;
QY 1 MAAGCLLALTTLFQSLIGPSSPEPPSAVTIKSWDKMQEDLYTLAKTAGVNLVDI 60
Db 1 maagcllalttlfqslligpsseepipsavtikswdkmqedlytlaktasgvnlvdi 60
QY 61 YEKYQDLYTVEPNNAQLVEIARDEIKLLSNRKAIVSLAEAEKVQAAHQWREDFASN 120
Db 61 yekyqdytvepnnarqlveiaardieklisnrkalvslaeakvqaahqwrdefasn 120
QY 121 EVVYNAKDDLDPKNDSEPGSQRIKPVFIEDANFGROIYQHAHVHPTDIYEGSTIVL 180
Db 121 evvyynakddl dpeknndsepgsqrikpvfiedanfgroiyqhaavhptdiyegstivl 180
QY 181 NELNWTSALEDEVFKKNEEDPSLLWQVFGSATGLARYPPSPWVDNRTPNKIDLYDVR 240
Db 181 nelnwtaledevfkknreedpsllwqvfsgatglaryppspwvdsnrtpnkildyavr 240
QY 241 RPWYIOGAASPKDMLILVDYSGVSGTLTKLIRTSVSEMLETISDDDFVNVASPNNAQD 300
Db 241 rpwyiggaaspkdmllilvdsgsvgtlklirtsvsemletisdddfvnavspnnaqd 300
QY 301 VSCFOHLVQANVENKKVLDKAVNNITAKGITYDKKGFSAFEQLLNNVSRANCKIIML 360
Db 301 vscfhlvqanvrnkklvldkavnnitakgitydkkgsfafeqllnnyvranckkiiml 360
QY 361 FTDGGEERAQEIFNKNYKDKKVRVERFSGVGHNYERGPQWACENKGYEIPISGAIR 420
Db 361 ftdggeeeraqeifnknkdkkvrverfsvgnnyergpqlwmacenkgyyieipsigair 420
QY 421 INTQYLDVLRGPMVLADGKAKQVQWNTVYLDLGLVITGTLVPVFNITGQFENKTNLK 480
Db 421 intqeyldvlgprpmvlagdkakqvtwnvyldalelglvitgtlpvfnitgqfenktnlk 480

QY 661 SDNTEFLNFEIDRKTTPNPSCNADLINRVLLDAGFTNELVQNYWSKQNKIGVKAR 720
DB 654 sdntefllnfeidrktpnpnscnadlinrvlldagftnelvqnywsqknigvkqr 713
QY 721 FVVTGGITRVYPKEAGENWQENPEYEDSFYKRSIDNDNYVFTAPYFNKSGPGAYESGI 780
DB 714 fvvtdggitrvyypkeagenwqenpetyedsfyrksidndnyvftapyfnkspgayesgi 773
QY 781 MYSKAVEIYIQGLKLPAYVIGIKIDVNSWIENTFTKTSIRDPCAGPVCDCKRNSDVMDCVI 840
DB 774 mvskaiveiyiqglklpavvlgikidvnswnientftktsirdpcagpvcdckrnsdvmdcvi 833
QY 841 LDGGFLLMANHDDYTNQIGRWATAAASWILQOFLLSLTPRLLEAVEMEDDDFTASLSKQ 960
DB 834 lddggfllmanhddytngqigrwataaawslqgflsltprrlleavemeddftaslskq 893
QY 901 GAGHRSAYPSVADILQIGRWATAAASWILQOFLLSLTPRLLEAVEMEDDDFTASLSKQ 960
DB 894 gaghrsaypsvadilqigrwataaawslqgflsltprrlleavemeddftaslskq 953
QY 961 SCITEQTYFFDNDKSFSGVLDGCGNCSRFHGEKLMNTNLIFIMVESKGTCPDTRLLI 1020
DB 954 sciteqtgyffndksfsgvldgcnscrfhgeklmntnlifimveskgtcpdtrlli 1013
QY 1021 QAEQTSQGNPCDMVKQPYRKGPDVCFDNNVLEDYTDGCGVVS 1063
DB 1014 qaeqtsqgnpcdmvkqpyrkgpdvcfdnnvledytdcgvgvs 1056

RESULT 11
AAW63155
ID AAW63155 standard; Protein; 1084 AA.
XX AAW63155;
XX AC
XX DT 12-OCT-1998 (first entry)
XX DE Human calcium channel alpha-2e subunit.
XX KW Alpha-2 subunit; human; calcium channel; assay; detection;
KW characterisation; Lambert Eaton Syndrome; LES; diagnosis.
XX OS Homo sapiens.
XX PN US5792846-A.
XX PD 11-AUG-1998.
XX PF 31-MAY-1995; 950S-0455543.
XX PR 04-APR-1994; 94US-0223305.
PR 04-APR-1988; 88US-0176899.
PR 04-APR-1985; 89US-0603751.
PR 04-APR-1985; 89WO-US01408.
PR 20-FEB-1990; 90US-0482384.
PR 30-NOV-1990; 90US-0620250.
PR 15-AUG-1991; 91US-0745206.
PR 31-MAY-1995; 95US-0455543.
XX (SIBI-) SIBIA NEUROSCIENCES INC.
XX PI Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;
PI Williams ME;
XX WPI: 1998-456192/39.
DR N-PSDB; AAW42704.
XX DNA encoding human calcium channel alpha 1B subunit protein -
PT useful for recombinant production of the channel for screening of
PT its modulators, and diagnosis of Lambert Eaton Syndrome
XX Claim 3; Columns 305-310; 166pp; English.
XX

CC The present sequence represents the alpha-2e subunit of a human calcium
CC channel. Calcium channels are membrane-spanning, multi-subunit proteins
CC that allow controlled entry of calcium ions into cells. This leads
CC to depolarisation events required for muscle contraction. The recombinant
CC subunit, when expressed with nucleic acids encoding the complete calcium
CC channel, can be used in assays for the detection and characterisation of
CC compounds that modulate the channel. The DNA encoding the subunits can
CC be alternatively spliced when transcribed, giving more than one form of
CC the protein from the same transcript, each having slightly different
CC properties. In addition, the reactivity of the alpha 1 subunit with IgG
CC molecules from the serum of an individual with Lambert Eaton Syndrome
CC (LES) can be used as a diagnostic for the disease.
XX Sequence 1084 AA;
SQ

Query Match 99.0%; Score 5542.5; DB 19; Length 1084;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1055; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY 1 MAAGCCLALTLTFLQSLIGPSSEEPFSAVTIKSWDKMQEDLVTLAKTAGVGNOLVDI 60
DB 1 maagcclaltltlfgsligpsseepfpsavtikswdkmqedlvtlaktasgvnqlvdi 60
QY 61 YEKYQDLYTVEPNNAQOLVEIAARDIEKLLSNRSKALVSLAEAEKVQAAHQHREFASN 120
DB 61 yekyqdytvepunnarqlveiaardiekllsnrskalvslaeaeekvqaahqhvredfasn 120
QY 121 EVVYVNAKDDLDPEKNDSEPGSORIKPVFTEDANFRQISQYHAAVHIPDIDYEGSPVL 180
DB 121 evvyvnaakddldpekndsepgsgrikpvfiedanfrqisqyhaavhipdidiyegstivl 180
QY 181 NELNWTSAIDVEFKNREEDPSLLWQVFGSATGLARYYPASPWVDNSRTPNKIDLYDVR 240
DB 181 nelnwtalidvefknreedpsllwqvfgsatglaryypaspwvdnsrtpnkidlydvrr 240
QY 241 RPWYIOGAASPDKMLILVDVSGVSGLTCLKIRTSVSEMLETSLDDDFVNVASFNSAQD 300
DB 241 rpwyiogaaspkdmllldvsgsvsgltklirtsvsemlletlsdddfvnvasfnasq 300
QY 301 VSCFQHLVQANVRNKKVLDVANNITAKGITYDKGFSFAFEOALLNYSRANCNKIIML 360
DB 301 vscfqlvqanvrnkvldavnnitakgitydkgfsfafedallnysrancnkliml 360
QY 361 FTDGGEERAQEIFENKYNKDKKRVFRFVSGQHNRYERGIQWACENKGYIYEIPSGAIR 420
DB 361 ftdggeeraqefinkynkdkkvrfrfsvqghnyergiqwacenkgyiyeipsigair 420
QY 421 INTQEYLDVLGRPMVLADKAKOVQNTNLYDLALEGLVITGLTPVFNITGQENKTNLK 480
DB 421 intqeyldvlgrpmvlagdkakovqntnlydaleiglvitgltpvfnitgqenknlnk 480
QY 481 NQLILGVMGVDSLEDIKRLTPRFTLCPNGYIFAIDPNQYVLLHPNLPKNPKSQEPVTL 540
DB 481 nqlilgvmgvdsledikrltpfrftlcpngyifaidpnqyvvllhpnlpknpsqepvtl 540
QY 541 DFLDAELENDIKVEIRNKMIDGESGEKTFRTLVKSDERYIDKGNRTYTTPVNGTDSL 600
DB 541 dfldaelendikveirnkmidgesgektftrtlvksqderiydkgnrtytvtvpngtdysl 600
QY 601 ALVLPYSFYIYKAKLEETITQARSKKGMKDSSETLKPDPNFESGYTFIAPROYCNDLKI 660
DB 601 alvlpysfyiykakleetitqary-----setlkdndfreesgytfiaproycndlki 653
QY 661 SDNTEFLNFEIDRKTTPNPSCNADLINRVLLDAGFTNELVQNYWSKQNKIGVKAR 720
DB 654 sdntefllnfeidrktpnpnscnadlinrvlldagftnelvqnywsqknigvkqr 713
QY 721 FVVTGGITRVYPKEAGENWQENPEYEDSFYKRSIDNDNYVFTAPYFNKSGPGAYESGI 780
DB 714 fvvtdggitrvyypkeagenwqenpetyedsfyrksidndnyvftapyfnkspgayesgi 773
QY 781 MYSKAVEIYIQGLKLPAYVIGIKIDVNSWIENTFTKTSIRDPCAGPVCDCKRNSDVMDCVI 840

Db 774 mvskavelyigkilkpavvgikidvswienfktksirpcagpvcckrnsvmdcvl 833
 Qy 841 LDDGGFLIMAHNDYTNQIGRFFGEIDPSLMRHLNLSVYAFNKSVDYQSVCEPAAKQ 900
 Db 834 lddggfllmanhdytnqirffgeidpslmrhlvnlsvyafnksydyqsvcepaaqk 893
 Qy 901 GAGHRSAYVSVADILQIGWATAAASILQOFLLSLTFFPRLLAEVEMEDDDFTASLSKQ 960
 Db 894 gaghrrsayvsvadilqigwataaawilqqfllstfprllaeavemedddftaslskq 953
 Qy 961 SCITEQYQYFFDNDKSFSGVLDCGNCSTRIFPHGCKLMTNLIPIFIMVESKGTCTPCDTRLII 1020
 Db 954 sciteqyqyffndksfsgvldcgcncsrifhgeklmntnlifimveskgtcptcdtrlll 1013
 Qy 1021 QABQSDGPNPCDMVQPRYKGPVDFVCFDNNVLEDYDCGGVS 1063
 Db 1014 qabqsdgpnpcdmvqprykgpdcvdfdnvledydcggvs 1056

RESULT 12

AAB10589
 ID AAB10589 standard; Protein; 1084 AA.

AC AAB10589;
 DT 22-DEC-2000 (first entry)

DE Human calcium channel alpha-2e subunit protein.
 KW Human; calcium channel; calcium channel subunit; diagnosis;
 KW Lambert Eaton Syndrome; calcium channel subunit alpha-2e.
 OS Homo sapiens.
 XX US6096514-A.
 PN 01-AUG-2000.
 PD 25-MAY-1995; 95US-0450562.
 PF 04-APR-1988; 88US-0176899.
 PR 02-FEB-1990; 90US-0482384.
 PR 08-NOV-1990; 90US-0603751.
 PR 30-NOV-1990; 90US-0620250.
 PR 13-APR-1991; 91US-0745206.
 PR 10-APR-1992; 92US-0868354.
 PR 13-JUL-1992; 92US-0914231.
 PR 11-AUG-1993; 93US-0105536.
 PR 05-NOV-1993; 93US-0149097.
 PR 07-FEB-1994; 94US-0193078.
 PR 04-APR-1994; 94US-0223305.
 PR 11-AUG-1994; 94US-0290012.
 PR 23-SEP-1994; 94US-0311363.
 PR 28-SEP-1994; 94US-0314083.
 PR 07-NOV-1994; 94US-0336257.
 PR 13-MAR-1995; 95US-0404950.

(SIBI-) SIBIA NEUROSCIENCES INC.

Ellis SB, Williams ME, McCue AF, Harpold MM;
 WPI; 2000-548230/50.
 N-PSDB; AAA71727.

Human calcium channel beta subunit polynucleotides, useful for
 producing recombinant eukaryotic cells and for diagnosing Lambert Eaton
 Syndrome

Disclosure; Column 253-260; 153pp; English.

This invention describes a novel isolated DNA molecule (1) comprising a
 sequence encoding a beta3-1 subunit of a human calcium channel.

CC Nucleic acid probes comprising 14-30 contiguous nucleotides of
 beta.3 subunit encoding DNA are useful for isolation and cloning of
 calcium channel subunit-encoding DNA. Recombinant eukaryotic cells that
 express heterologous calcium channel are useful for identifying compounds
 that modulate calcium channel activity and in assays for identifying
 agonists and antagonists of calcium channel activity in humans. Human
 calcium channel subunit or eukaryotic cells expressing the channel are
 useful for diagnosing Lambert Eaton Syndrome (LES) in a human. This
 sequence represents the human calcium channel alpha-2e subunit which is
 described in the method of the invention.

XX Sequence 1084 AA;

Query Match 99.0%; Score 5542.5; DB 21; Length 1084;
 Best Local Similarity 99.2%; Pred. No. 0;
 Matches 1055; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

Qy 1 MAAGCLLALTTLTFLQSLLITGPSSEPPFSAVTIKSWDKMQEDLVTAKTASGVNQLVDI 60
 Db 1 maagcillaaltltlfgslligpsseepfseavtikswdkmqedlvtlaktasgvnqlvdi 60
 Qy 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDFASN 120
 Db 61 yekyqdytvepnnarqlveiaardieklslsnrskalvslaleaeqvaaqhqrdfasn 120
 Qy 121 EYVYNKADLDPEKNDSEPGSORIKPFIEDANPGROISQHOAAVHIPTDIYEGSTIVL 180
 Db 121 evvynakddlpeknndsepgsorkipvfiedanfgriqsyqhaavhiptdiyegstivl 180
 Qy 181 NELNWTSALEDEVFKNREEDPSLLWQVFGSATGLARYYPASPWVDSRTPNKIDLYDVR 240
 Db 181 nelnwtalsaldevfknreedsllwqvfgsatglaryypaspwvdsrtpnkidlydvr 240
 Qy 241 RPWYIQGAASPKDMLILVDVSGSVSGTLKLI RTSVSSEMLETSDDDFVNVASFNSNAOD 300
 Db 241 rpwyiqgaaspkdmllilvdvsgsvsgtlklirtsvesemletdaddfvnvafnsnaod 300
 Qy 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGSAFEPQLLNYSKANCNKITML 360
 Db 301 vscfqlhvqanvrnkvlkdavnnitakgitydkkgfsafeqlnynvarancnkli 360
 Qy 361 FTDGGERAQEIFNKYKDKRVFRFSGVQHNYERGPQIOWMACENKGYEYEPSIGAIR 420
 Db 361 ftdggeeraqeifnkynkdkrvfrfsgvqhnyergpqiowmacenkgyeypsiga 420
 Qy 421 INTQEVLDVLGRPMVLGADKAKQVQMTNLYDLALEGLVITGLPVENITGQFENKTNLK 480
 Db 421 intqeyldvlgrpmvlagdkakqvqmntnlydaleglvitglpvenitgqfenktnlk 480
 Qy 481 NOLILGVMGVDSLEDIKRLTPRFTLCPNGYYPADIPNGYVLLHPLNLPKPKSQBPVTL 540
 Db 481 nqllilgvmgvdsledikrltpftlcpngyyfaldpnyvllhplnlpkpkqsqbpv 540
 Qy 541 DFLDAELENIDKVEIRNKMIDGESGKTFRTLVKSODERYIDKNRTYTWTPVNGPDYSL 600
 Db 541 dfldae lenidkveirnkmidgesgktrtlvksoderyidknrtytwtvpngpdy 600
 Qy 601 ALVLPTYSPYIKALEETITQARSKKGMKMDSEITLKPDNFEESGYTFTAPRDCNDLKI 660
 Db 601 alvlptysfyikaleetitqary-----setlkdpnfeesgytftaprdy cndlki 653
 Qy 661 SDNNTFELLNFEFIDRTPNPNPSCNADLINRVLLDAGFTNELVQNSKQNKIKGVKAR 720
 Db 654 schntefllnfnefidrtpnnpncnadlinrvlldagftnelvqnywskqknkikgvkar 713
 Qy 721 FVVDGGITRVYPKEAGENWQENPETYEDSFVKRSLDNDNYFTTAPYFNKSGPGAYESGI 780
 Db 714 fvvtdggitrvykpeagenwqenpetyedsfvykrsldndnyvftapyfnksgpgayesgi 773
 Qy 781 MVSKAVEYIIGKLLKPAVVGIKIDVNSWIENFTKTSIRDPACGVCCKRNSDVMDCVI 840
 Db 774 mvskaveiyigkilkpavvgikidvnswie nftktsirdpcagvcdckrnsvmdcvl 833

QY 841 LDGGFLMANHDDYTNQIGRFFGEIDPSLMRLHVNISYAFNKSYDYOSVCEPGAAPKQ 900
 Db 834 ldggflmanhddytngirffgeidpslmrlhvnlsyafnksydyosvcepgaapkq 893
 QY 901 GAGHSAYPSVADILQIGWATAAASLIQOFLSLTFRLLLEAVEMEDDFTASLSKQ 960
 Db 894 gaghsaypsvadilqigwataaasllqofllstfrllleavemeddftaslskq 953
 QY 961 SCITEQOQFFONDSSFGVLDGNCISRFHGEKLMNTNLFIMYESKGTCPDTRLLI 1020
 Db 954 sciteqoqffondssfgvldgncisrfhgeklmntnlfimveskgtcpdtrlll 1013
 QY 1021 QAEQTSNGNPMQVQPKRYKGPVCFNNVLEDTDCGGVS 1063
 Db 1014 qaeqtsdgnpdmvqpyrykpgdvcfnnvledydcggvs 1056
 RESULT 13
 AAR71012
 ID AAR71012 standard; Protein; 1103 AA.
 AC AAR71012;
 XX
 DT 01-DEC-1995 (first entry)
 XX Human neuronal calcium channel subunit alpha 2a.
 DE
 XX
 KW Calcium channel subunit; antagonist; agonist; diagnosis;
 KW Lambert Eaton Syndrome.
 XX
 OS Homo sapiens.
 XX
 PN W09504822-A.
 XX
 PD 16-FEB-1995.
 XX
 PF 11-AUG-1994; 94UO-0509230.
 XX
 PR 11-AUG-1993; 93US-0105536.
 PR 05-NOV-1993; 93US-0149097.
 XX
 PA (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
 XX
 PI Ellis SB, Gillespie A, Harpold MW, Mccue AF, Williams ME;
 DR WPI: 1995-090900/12.
 DR N-PSDB; AAQ84666.
 XX
 PT DNA encoding human calcium channel sub-unit(s) - used for
 PT developing prods. for studying calcium channels, e.g. for
 PT obtaining agonists and antagonists
 XX
 PS Disclosure; Page 231-236; 285pp; English.
 XX
 CC Human neuronal alpha 2 coding sequence (AAQ84664) transcript is
 CC differentially processed in skeletal muscle, aorta, and CNS in
 CC the region corresp. to nt 1595-1942 of AAQ84664 in each of the
 CC tissues. Five alternatively spliced variant transcripts that differ
 CC in the presence or absence of one to three different portions of
 CC this region. There are three sequences involved (see AAQ84664 FT
 CC and AAQ84665 FT), sequence 1, sequence 2 and sequence 3. The five
 CC alpha 2 encoding transcripts from the different tissues include
 CC different combinations of the three sequences, except for one of
 CC the alpha 2 transcripts expressed in aorta which lacks all three
 CC sequences. The five alpha 2 forms identified are (1) a form that
 CC lacks sequence 3 called alpha 2a, expressed in skeletal muscle
 CC (2) one that lacks sequence 1 called alpha 2b, expressed in CNS
 CC (3) one that lacks sequences 1 and 2 called alpha 2c, expressed in
 CC aorta (4) one that lacks sequences 1, 2 and 3 called alpha 2d,
 CC expressed in aorta and (5) one that lacks sequences 1 and 3
 CC called alpha 2e. The DNA and AA sequences of alpha 2a - alpha 2e
 CC are set forth in AAQ84666-084669 and AAR71012-R71015 respectively.

XX SQ Sequence 1103 AA;
 Query Match 98.6%; Score 5523; DB 16; Length 1103;
 Best Local Similarity 97.5%; Pred. No. 0;
 Matches 1055; Conservative 0; Mismatches 1; Indels 26; Gaps 2;

QY 1 MAAGCIIALTITLTFQSLILGPSSEEPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
 Db 1 maagcIIaltltlfgslilgpsseepfpsavtikswdkmqedlvtlaktasgvnqlvdi 60
 QY 61 YEKYQDLYVEPNNAQOLVEIAARDIEKLLSNRSKALVSLAEAKVQAAHQHREFASN 120
 Db 61 yekyqdlytvepnnaqolveiaardiekllsnrskalvslaeakvqaahqrefasn 120
 QY 121 EVVYVNAKDDLDPKNDSPGSGRIKPVFIEDANFGRQISYQHAHVHPTDIYEGSTIVL 180
 Db 121 evvyvnaKddlDPKndspgsgriKpVfiEdanfGRqISyQHAAVhHPTdiYegstivl 180
 QY 181 NELNMTSALDEYFKKNREEDPSLLQWFGSATGLARYYPASPWVDNSRTPNKKIDLYDVR 240
 Db 181 nelnmtsAldeYfKknReEDpsllQwfgsAtglARyYPaspWvdnsRtpnKkiDlydvr 240
 QY 241 RPWYIOGAASPDKMLILVDVSGVSGILTLKIRTSVSEMLETSLDDDFVNVASFNSNAQD 300
 Db 241 rpwyIogAaspdkmLilvdvsgvsgilTLkIRtsVseMLEtSLdddfVnvAsfNsnaqd 300
 QY 301 VSCFOHLVQANVKNKKVLDAVNNITAKGITDYKKGFSFAFELLNANVNSRANCNKIIML 360
 Db 301 vscfOhlvQanvKnKkVldAvnnITaKgiTDyKkgFSfAFellNaNvNsRancnKiImL 360
 QY 361 FTDGGEERAQEIFNKYNKDKKVRVFRFSVQGHNYERGPQWACENKGYIYEIPSGAIR 420
 Db 361 ftdggeeraqeiFNkYNkDKKvrvFRfsVqGhnyERgpQwAcenKgyIyeIPsgair 420
 QY 421 INTQEYLDVLGRPMVLGADKAKOVQNTNVLDALELGLVITGTPVFNITGQENKTNLK 480
 Db 421 intqeyldvlgrpmvlgadKakOvqNtnVldAlelGLvITgTpVfnITgQenKtnlk 480
 QY 481 NQLILGVMGVDVSLIEDIKRLTPRTICPNGYEFAIDPNGVYLLHPNLQPK----- 530
 Db 481 nqlilgvmgvdsleDiKrlTpRtIcPngyYfaIdPngvYllhPnlqPkIgvIptIn 540
 QY 531 -----NPKSOEPVTLDFDAELENDIKVEIRKNMDGSEGEKTFRLVKSQDERYI 581
 Db 541 lkrtrpniqnksqepvtIdfaelendikVeirKnMDgseGEKtFrlVksQderyI 600
 QY 582 DKGNRRTYTPVNGTDYSLALVLPYTSFYIYKAKLEETITQARSKKGKMKDSSTLKPDNF 641
 Db 601 dkgnrtytvpngtdyslalvlpTysfyYiYkAkLeEtITqARsKKGkMKdsStlKpDnf 653
 QY 642 EESGYTFIAPROXCNCLKISDNNTPELLNPEIDRKTNNPCSNADLINRVLLDAGFTN 701
 Db 654 eesgytfiaprdyCndlkIsdnntellNpeIdRktNnpCsnadlinrvllDagftn 713
 QY 702 ELVQNVWSKQNKIKGVKARFVVTGDTTRVYKPEAGENWOENPETVEDSFYKRSLDNDNY 761
 Db 714 elvqnVwsKqnKikgvkArfvvtGdttrVykPeaGenwoenPetvedsfYkrsldndny 773
 QY 762 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDP 821
 Db 774 vftapyfNksGpgayesGimvSkaveIyIOgKllKpavvgKiDvnsWienftKtsirDp 833
 QY 822 CAGPVCDCRNSDVMDCVILDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRLHVNLSVYA 881
 Db 834 cagpvcdcRnsdvmdcvilddggfllmanhddytngirffgeidpslmrlhvnlsvya 893
 QY 882 FNKSYDQSVCEPGAAPKOGAGHRSAYVPSVADILQIGWATAAASLIQOFLSLTFR 941
 Db 894 fnksydyqsvcepgaapkogaghrsayvpsvadilqigwataaasllqofllstfr 953
 QY 942 LLEAVEMEDDDFTASLSKQSCITEQOYTFDNDNSKSFSGVLDGNCISRFHGEKLMNTN 1001

Db 1014 ifimveskgtcpdtrlllqaeqtsdgnpcdmvkgprykrpdpvcfdnnvledydcgg 1073

QY 1062 VS 1063

Db 1074 vs 1075

RESULT 15

ID AAB10586 standard; Protein; 1103 AA.

AC AAB10586;

DT 22-DEC-2000 (first entry)

DE Human calcium channel alpha-2a subunit protein.

KW Human; calcium channel; calcium channel subunit; diagnosis;
Lambert Eaton Syndrome; calcium channel subunit alpha-2a.

OS Homo sapiens.

PN US6096514-A.

PD 01-AUG-2000.

PF 25-MAY-1995; 95US-0450562.

PR 04-APR-1988; 88US-0176899.

PR 02-FEB-1990; 90US-0482384.

PR 08-NOV-1990; 90US-0603751.

PR 30-NOV-1990; 90US-0620250.

PR 15-AUG-1991; 91US-0745206.

PR 10-APR-1992; 92US-0868354.

PR 13-JUL-1992; 92US-0914231.

PR 11-AUG-1993; 93US-0105536.

PR 05-NOV-1993; 93US-0149097.

PR 07-FEB-1994; 94US-0193078.

PR 04-APR-1994; 94US-0223305.

PR 11-AUG-1994; 94US-0290012.

PR 23-SEP-1994; 94US-0311363.

PR 28-SEP-1994; 94US-0314083.

PR 07-NOV-1994; 94US-0336257.

PR 13-MAR-1995; 95US-0404950.

XX (SIBI-) SIBIA NEUROSCIENCES INC.

XX Ellis SB, Williams ME, McCue AF, Harpold MM;

XX WPI; 2000-548230/50.

XX N-PSDB; AAA71724.

XX Human calcium channel beta subunit polynucleotides, useful for
producing recombinant eukaryotic cells and for diagnosing Lambert Eaton
Syndrome

XX Disclosure; Column 229-236; 153pp; English.

XX This invention describes a novel isolated DNA molecule (I) comprising a
sequence encoding a beta3-1 subunit of a human calcium channel.
XX Nucleic acid probes comprising 14-30 contiguous nucleotides of
XX beta3 subunit encoding DNA are useful for isolation and cloning of
XX calcium channel subunit-encoding DNA. Recombinant eukaryotic cells that
XX express heterologous calcium channel are useful for identifying compounds
XX that modulate calcium channel activity and in assays for identifying
XX agonists and antagonists of calcium channel activity in humans. Human
XX calcium channel subunit or eukaryotic cells expressing the channel are
XX useful for diagnosing Lambert Eaton Syndrome (LES) in a human. This
XX sequence represents the human calcium channel alpha-2a subunit which is
XX described in the method of the invention.

SQ Sequence 1103 AA;

Query Match 98.8%; Score 5523; DB 21; Length 1103;
Best Local Similarity 97.5%; Pred. No. 0;
Matches 1055; Conservative 0; Mismatches 1; Indels 26; Gaps 2;

QY 1 MAAGCILLATLTLLFOSLLIGPSSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
Db 1 maagcillaltltlfgslilgssseepipsavtlkswdkmqedlvtlakcsgvnqlvdi 60

QY 61 YEKYQDLYTVEPNNAQOLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAAHQWREDFASN 120
Db 61 yekyqdltyvepnnarqlveiaardieklksnrskalvslaleaeqvaaahqwrdfasn 120

QY 121 EYVYNAKDDLPEKNDSEPGSQRIKPVFIEDANFGQISYQHAHVIPDITVEGSTIVL 180
Db 121 evvynakddlpeknndsepgsqrikpvfiedanfgqisqyhaavhiptdiyegstivl 180

QY 181 NELNWTSALEDEVRKKNREEDPSLLWVFGSATGLIARYYPASPVVDNSRTNKIDLYDVR 240
Db 181 nelnwtasaldevrkknreedsllwvfgsatglaryypaspvwdnsrtnpkidydvrr 240

QY 241 RPWYIOGAASPDKMLILVDYSGVSGITLKLIRTSVSEMLETSDDDFVNVSFNSNAQD 300
Db 241 rpywiggaaspkdmllilvdysgsvsgitklirtsvsemltssdddfvnvasfnsnaqd 300

QY 301 VSCFQHLVQANVRNKKVILKDAVNNTAKGITDYKKGSPAFEPQLLNYNVRANCKIIML 360
Db 301 vscfqlhqvsnvrnkvlkdavnntakgitdykkgfafefqllnynvrancnkliiml 360

QY 361 FTDGGERAQEIEFNKYNKKRVFRFESVGHNVYERPIOMACENKGYGYEIPISGAIR 420
Db 361 ftdggeeraqeiefnkynkkrvfrfsvghnyerpiqwmacenkgyyeipsigair 420

QY 421 INTQEYLDVLGRPMVLAGDKAKQVQWNTNVLDALEGLVITGTLVPFNITQGFENKTNLK 480
Db 421 intqeyldvlgrpmvlagdkakqvwnvnyldaleglvitgtlvpfnitqgfenktnlk 480

QY 481 NQLILGVMGVDSLEDIKRLTPFTICPNGYFAIDPNGYVLLHPNLOPK----- 530
Db 481 nqililgvmgvdsledikrltpfticpnygyfaidpnyvllhpnlpk----- 530

QY 531 -----NPKSQEPVTLDFDAELENDIKVEIRNMIDGESGEKTRTLVKSDERYI 581
Db 531 -----npskqepvtdlfdaelendikveirnmidgesgektftrlvksderyi 581

QY 581 LKRRPNIQPKSQEPVTLDFDAELENDIKVEIRNMIDGESGEKTRTLVKSDERYI 600
Db 581 lkrprniqpkseqepvtdlfdaelendikveirnmidgesgektftrlvksderyi 600

QY 601 DKGRTYTWTVPNGTDYSLALVLPYTYFYIKAKLEETITQARKSKGKMKDSETLKPDNF 641
Db 601 dkgnrtytwtvpngtdyslalvlpptyfyikakleetitqarkskgkmdsetlkdndf 641

QY 642 EESGYTFIAPRDYCNLDKISDNNTFELNFEFIDRTKTPNPNPCNADLINRVLLDAGFTN 701
Db 642 eesgytfiaprdycnldkisdntfelnfnfdrtktpnpncnadlinrvlldagftn 701

QY 702 ELVQNYWSKOKNTKGKARFVWTDGGITRVYKPEAGENMOENPETYEDSFYKRLSDNDNY 761
Db 702 elvqnywsokntkgkarfvwtddggitrvykpkeagenmoenpetyedsfykrldndny 761

QY 761 VFTAPYFNKSGPAGYSGIMVSKAVEIYIQGLKLPVAVGKIDVNSWIENFTKTSIRD 821
Db 761 vftapyfnkspgaysgimvskaveiyiqgllkpavvgikidvnswieftktsirdp 821

QY 822 CAGPVCCKNSQVMDCVILDDGGFLLMANHDDYTNQIGRFFGIDPSLRHLVNSIYVA 881
Db 822 cagpvccknsqvmcviiddggfllmanhddytnqigrffgidpslrhlvnsiyyva 881

QY 882 FNSYDYQSCVCEPAAKQAGHRSAYVPSVADILQIGWATAAAWSTLOQFLLSLFPR 941
Db 882 fnsydyqscvcepaaqkqaghrrsayvpsvadilqigwataaaawstlloqfllslfpr 941

QY 894 FNSYDYQSCVCEPAAKQAGHRSAYVPSVADILQIGWATAAAWSTLOQFLLSLFPR 953
Db 894 fnsydyqscvcepaaqkqaghrrsayvpsvadilqigwataaaawstlloqfllslfpr 953

QY 942 LLEAVEMEDDDFFASLSKQSCITEQTQYFFDNDNSKFSVGLDCGNCSTRIFHEGKIMTNL 1001
Db 942 lleavemedddffaslskqsciteqtqyffndnskfsvglcgcncstrifhegkimtnl 1001

QY 954 LLEAVEMEDDDFFASLSKQSCITEQTQYFFDNDNSKFSVGLDCGNCSTRIFHEGKIMTNL 1013
Db 954 lleavemedddffaslskqsciteqtqyffndnskfsvglcgcncstrifhegkimtnl 1013

QY 1002 IFIMVESKGTCPDTRLLIQAEQTSQGNPCDMVKQPRYKGPDPVCFDNNVLEDYTDGG 1061
Db 1014 ifimveskgtcpdtrlllqaeqtsdgnpcdmvkgprykgpdpvcfdnnvledytdcgg 1073
QY 1062 VS 1063
Db 1074 VS 1075

Search completed: July 23, 2001, 07:37:05
Job time: 506 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 23, 2001, 07:39:05 ; Search time 37.55 seconds
(without alignments)
570.273 Million cell updates/sec

Title: US-09-397-548-17

Perfect score: 5599

Sequence: 1 MAAGCLLALTFLFOSLLIG.....PDVCFDNNVLEDTDCGGVS 1063

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA.*

1: /cgnl_7/ptodata/1/iaa/5A.COMB.pep.*

2: /cgnl_7/ptodata/1/iaa/5B.COMB.pep.*

3: /cgnl_7/ptodata/1/iaa/6A.COMB.pep.*

4: /cgnl_7/ptodata/1/iaa/6B.COMB.pep.*

5: /cgnl_7/ptodata/1/iaa/PTUS.COMB.pep.*

6: /cgnl_7/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5599	100.0	1091	1	US-07-745-206A-25
2	5599	100.0	1091	1	US-08-455-543A-52
3	5599	100.0	1091	2	US-08-223-305C-52
4	5599	100.0	1091	2	US-08-311-363-25
5	5595	99.9	1091	3	US-08-713-118-4
6	5595	99.9	1091	4	US-09-452-007-4
7	5599.5	99.3	1086	1	US-08-455-543A-54
8	5599.5	99.3	1086	2	US-08-223-305C-54
9	5542.5	99.0	1084	1	US-08-455-543A-56
10	5542.5	99.0	1084	2	US-08-223-305C-56
11	5523	98.6	1103	1	US-08-455-543A-53
12	5523	98.6	1103	2	US-08-223-305C-53
13	5503	98.3	1079	1	US-08-455-543A-55
14	5503	98.3	1079	2	US-08-223-305C-55
15	5385.5	96.2	1106	1	US-08-435-675B-5
16	5367.5	95.9	1106	1	US-08-435-675B-5
17	5134.5	91.7	1086	6	US-08-336-257A-8
18	2581.5	46.1	508	1	US-08-435-675B-6
19	182	3.3	885	3	US-09-074-579-5
20	182	3.3	885	4	US-09-388-774-5
21	159.5	2.8	946	3	US-09-074-579-3
22	159.5	2.8	946	4	US-09-388-774-3
23	154	2.8	903	1	US-08-021-601-12
24	154	2.8	903	1	US-08-082-849B-12
25	154	2.8	903	5	PCT-US94-01624-12
26	152.5	2.7	789	1	US-08-471-033-32
27	152.5	2.7	789	2	US-08-471-044-32

28	152.5	2.7	789	2	US-08-463-483A-32	Sequence 32, Appl
29	152.5	2.7	789	2	US-08-471-046A-32	Sequence 32, Appl
30	152.5	2.7	789	2	US-08-470-566B-32	Sequence 32, Appl
31	152.5	2.7	789	2	US-08-838-219B-4	Sequence 4, Appl
32	152.5	2.7	789	2	US-08-469-334-32	Sequence 32, Appl
33	152.5	2.7	789	3	US-09-300-529-32	Sequence 32, Appl
34	152.5	2.7	789	3	US-09-233-336A-4	Sequence 4, Appl
35	152.5	2.7	789	4	US-09-233-752A-4	Sequence 4, Appl
36	150.5	2.7	789	4	US-08-960-780-6	Sequence 6, Appl
37	150.5	2.7	789	4	US-09-073-898-6	Sequence 6, Appl
38	148.5	2.7	790	4	US-08-960-780-4	Sequence 4, Appl
39	148.5	2.7	790	4	US-09-073-898-4	Sequence 4, Appl
40	147.5	2.6	746	2	US-08-838-219B-6	Sequence 6, Appl
41	147.5	2.6	746	3	US-09-233-336A-6	Sequence 6, Appl
42	147.5	2.6	746	4	US-09-233-752A-6	Sequence 6, Appl
43	145.5	2.6	790	4	US-08-960-780-8	Sequence 8, Appl
44	145.5	2.6	790	4	US-09-073-898-8	Sequence 8, Appl
45	141.5	2.5	789	1	US-08-471-033-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-07-745-206A-25
; Sequence 25, Application US/07745206A
; Patent No. 5429921
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: McCue, Ann
; APPLICANT: Feldman, Daniel
; TITLE OF INVENTION: Human Calcium Channel Compositions and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitch, Even, Tabin & Flannery
; STREET: 135 S. LaSalle
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07745.206A
; FILING DATE: 19910815
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Feder, Scott B
; REFERENCE/DOCKET NUMBER: 51504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-372-7842
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1091 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-745-206A-25

Query Match 100.0%; Score 5599; DB 1; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTFLFOSLLIGPSSEPPFSAVTIKSWDKMQEDVTLAKTASGVNQLVDI 60
DB 1 MAAGCLLALTFLFOSLLIGPSSEPPFSAVTIKSWDKMQEDVTLAKTASGVNQLVDI 60

QY 61 YEKYQDLTYVEPNARQVIAARDIEKLLSNRSKALVSALAEKVAQAAHQHREDFASN 120
Db 61 YEKYQDLTYVEPNARQVIAARDIEKLLSNRSKALVSALAEKVAQAAHQHREDFASN 120
QY 121 EVVYNAKDDLPKNDSEPGSQRIKPVFIEDANFGQISYQAAVHIPTDIIYEGSTIVL 180
Db 121 EVVYNAKDDLPKNDSEPGSQRIKPVFIEDANFGQISYQAAVHIPTDIIYEGSTIVL 180
QY 181 NELNWTSADEVEKKREEDPSLLQVFGSATGLARYYPASPVWDNSRTPNKIDLYDVR 240
Db 181 NELNWTSADEVEKKREEDPSLLQVFGSATGLARYYPASPVWDNSRTPNKIDLYDVR 240
QY 241 RPWYIOGAASPKDMLILVDVSGVSGLTGLKLTISVSEMLETSSDDDFVNVASFNSNAO 300
Db 241 RPWYIOGAASPKDMLILVDVSGVSGLTGLKLTISVSEMLETSSDDDFVNVASFNSNAO 300
QY 301 VSCFHLVQANVRNKKVLDAVNITAKITDYKGFSAFQOLLNYSRANCNKIIML 360
Db 301 VSCFHLVQANVRNKKVLDAVNITAKITDYKGFSAFQOLLNYSRANCNKIIML 360
QY 361 FTDGGERAEQIFNKYKDKVVRFPFSGVQHYNERGPIQWACENKGYIYIPISGAIR 420
Db 361 FTDGGERAEQIFNKYKDKVVRFPFSGVQHYNERGPIQWACENKGYIYIPISGAIR 420
QY 421 INTQEVLDVLRPMVLGAKAKOVQNTVYLDALGLVITGLTPVFNITGQFENKTNLK 480
Db 421 INTQEVLDVLRPMVLGAKAKOVQNTVYLDALGLVITGLTPVFNITGQFENKTNLK 480
QY 481 NOLILGVMGVDSLEDIKRLTPRFTLCPNYGYFAIDPNGYVLLHLPNLOPKNPKSOEPTVL 540
Db 481 NOLILGVMGVDSLEDIKRLTPRFTLCPNYGYFAIDPNGYVLLHLPNLOPKNPKSOEPTVL 540
QY 541 DFLDAELENIDKVEIRNKMIDGSEKERTFLVKSQDERYIDKGNRTYTWTVPNGTDSL 600
Db 541 DFLDAELENIDKVEIRNKMIDGSEKERTFLVKSQDERYIDKGNRTYTWTVPNGTDSL 600
QY 601 ALVLPYTFYIKAKLEETIQARSKKGMKDETLKPDNFEESYTIAPRDYCNLDKI 660
Db 601 ALVLPYTFYIKAKLEETIQARSKKGMKDETLKPDNFEESYTIAPRDYCNLDKI 660
QY 661 SDNTEFLNFEIDRTKTPNPNPCNADLINRVLLDAGFTNQLVQYWSKOKNKGKVAR 720
Db 661 SDNTEFLNFEIDRTKTPNPNPCNADLINRVLLDAGFTNQLVQYWSKOKNKGKVAR 720
QY 721 FVWTDGGITRYVPKEAGENWQENETEDSYKRSLONDNVTFTAPYFNKSGPGAYESGI 780
Db 721 FVWTDGGITRYVPKEAGENWQENETEDSYKRSLONDNVTFTAPYFNKSGPGAYESGI 780
QY 781 MVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPACGVCDCRNSDVMDCVI 840
Db 781 MVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPACGVCDCRNSDVMDCVI 840
QY 841 LDDGGFLMANHDDYTQIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGAAPKQ 900
Db 841 LDDGGFLMANHDDYTQIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGAAPKQ 900
QY 901 GAGHRSAYVPSVADILQGWATAAANSILQOFLSLTFFRLLEAVEMEDDDFTASLSKQ 960
Db 901 GAGHRSAYVPSVADILQGWATAAANSILQOFLSLTFFRLLEAVEMEDDDFTASLSKQ 960
QY 961 SCITEQTYFFDNDKSFSGVLDGCGNSRIFHGEKLMNTNLIIFIMVESKTCPCDTRLLI 1020
Db 961 SCITEQTYFFDNDKSFSGVLDGCGNSRIFHGEKLMNTNLIIFIMVESKTCPCDTRLLI 1020
QY 1021 QAEQTSQDPNPNCDWVKQPRYKGPVDCFDNNVLEDYTDGCGVS 1063
Db 1021 QAEQTSQDPNPNCDWVKQPRYKGPVDCFDNNVLEDYTDGCGVS 1063

RESULT 2
US-08-455-543A-52
; Sequence 52, Application US/08455543A

; Patent No. 5792846
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,543A
; FILING DATE: May 31, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/223,305
; FILING DATE: April 4, 1994
; APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,250
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-52517
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1091 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-455-543A-52

Query Match 100.0%; Score 5599; DB 1; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAGCLLALTTLTLFQSLILGPSSEEPFPPSAVTKSWDKMQEDLVTLAKTAGSVNQLVDI 60

Db 1 MAAGCLLATLTLFQSLGPGSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
QY 61 YEKYQDLYTVEPNNAQVLEIAARDIEKLLSNRSLKALVSLAEAEKVQAAHQWREDFASN 120
Db 61 YEKYQDLYTVEPNNAQVLEIAARDIEKLLSNRSLKALVSLAEAEKVQAAHQWREDFASN 120
QY 121 EVVYVNAKDDLPKNDSPGSGQRKPVFIEDANFGRQISYQAAVHIPTDIYEGSTIVL 180
Db 121 EVVYVNAKDDLPKNDSPGSGQRKPVFIEDANFGRQISYQAAVHIPTDIYEGSTIVL 180
QY 181 NELNWTLSALDEYFKKNREDPSLLQVFGSATGLARYYPASVWDNSRTPNPKIDLYDVR 240
Db 181 NELNWTLSALDEYFKKNREDPSLLQVFGSATGLARYYPASVWDNSRTPNPKIDLYDVR 240
QY 241 RPWYIQAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300
Db 241 RPWYIQAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300
QY 301 VSCFOHLVQANRKNKVLKDAVNNITAKGITDYKKGFSFAFOLLNLYNVRANCNKIIML 360
Db 301 VSCFOHLVQANRKNKVLKDAVNNITAKGITDYKKGFSFAFOLLNLYNVRANCNKIIML 360
QY 361 FTDGGEERAQEIFNKYNDKKVRFVSFGVQHNRYERGPQWACENKGYIYEIPSGAIR 420
Db 361 FTDGGEERAQEIFNKYNDKKVRFVSFGVQHNRYERGPQWACENKGYIYEIPSGAIR 420
QY 421 INTQBYDLVGRPMVLGAKAKQVQNTVYLDALGLVITGTLPVNITGQFENKTNLK 480
Db 421 INTQBYDLVGRPMVLGAKAKQVQNTVYLDALGLVITGTLPVNITGQFENKTNLK 480
QY 481 NOLILGVAGVDVSLIEDIKRLTRFRLCPNGYFFADPNQYVLLHPNLPKPKSQEPVTL 540
Db 481 NOLILGVAGVDVSLIEDIKRLTRFRLCPNGYFFADPNQYVLLHPNLPKPKSQEPVTL 540
QY 541 DFLDAELENDIKVEIRNKMIDGESKEKFTLVKSQDERYIDKGNRTYTWTVPNGTDYSL 600
Db 541 DFLDAELENDIKVEIRNKMIDGESKEKFTLVKSQDERYIDKGNRTYTWTVPNGTDYSL 600
QY 601 ALVLPYTFYIYKALEETITQARSKKGMKDSSETLKPONFEESGYTFIAPRDYCNLDKI 660
Db 601 ALVLPYTFYIYKALEETITQARSKKGMKDSSETLKPONFEESGYTFIAPRDYCNLDKI 660
QY 661 SONNTEFLNFEFTDRKTPNPNPCNADLINRVLLDAGFTNELVQVNSKQKNIRGVKAR 720
Db 661 SONNTEFLNFEFTDRKTPNPNPCNADLINRVLLDAGFTNELVQVNSKQKNIRGVKAR 720
QY 721 FVVTGGITRVYPKEAGENWQENPETYEDSFYKRLDNDNYYFTAPYFNKSGPGAYESGI 780
Db 721 FVVTGGITRVYPKEAGENWQENPETYEDSFYKRLDNDNYYFTAPYFNKSGPGAYESGI 780
QY 781 MYSKAVEIYIQGLKLPVAVGKIDVNSWIENTFTSIRDPACGVCDCRNSDYMDCVI 840
Db 781 MYSKAVEIYIQGLKLPVAVGKIDVNSWIENTFTSIRDPACGVCDCRNSDYMDCVI 840
QY 841 LDGGLFLMANHDDYTNOIGRFFGIDSLMRHLNYSIYAFNKSQVDSQVCEPGAAPKQ 900
Db 841 LDGGLFLMANHDDYTNOIGRFFGIDSLMRHLNYSIYAFNKSQVDSQVCEPGAAPKQ 900
QY 901 GAGHSAYVPSVADILQGWATAAWSLQOFLSLFPRLEAVEMEDDDFTASLSKQ 960
Db 901 GAGHSAYVPSVADILQGWATAAWSLQOFLSLFPRLEAVEMEDDDFTASLSKQ 960
QY 961 SCITEQTYFFDNDKSFSGVLDGNCNRSIFHGEKLMNTNLIFIMVESKGTCPCTRLLI 1020
Db 961 SCITEQTYFFDNDKSFSGVLDGNCNRSIFHGEKLMNTNLIFIMVESKGTCPCTRLLI 1020
QY 1021 QAEQSDGPNPCDMVKQPRYKGPVCDVFNNVLEDTDCGGVS 1063
Db 1021 QAEQSDGPNPCDMVKQPRYKGPVCDVFNNVLEDTDCGGVS 1063

RESULT 3

US-08-223-305C-52
; Sequence 52, Application US/08223305C
; Patent No. 5851824
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-SEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/223,305C
; FILING DATE: April 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,250
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 52516 (P519739)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1091 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-223-305C-52

Query Match 100.0%; Score 5599; DB 2; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1063; Conservative 0; Mismatches 0; Gaps 0;

QY 1 MAAGCLLATLTLFQSLGPGSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
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Db 1 MAAGCLLALTLTLFQSLIGPSEPPSAVTIKSWDKMQEDLVTLAKTAGVGNQLVDI 60
QY 61 YEKYQDLYTVEPNNAOLVIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRREDFASN 120
Db 61 YEKYQDLYTVEPNNAOLVIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRREDFASN 120
QY 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFTEDANFGQISYQAAHVIPTDIYEGSTIVL 180
Db 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFTEDANFGQISYQAAHVIPTDIYEGSTIVL 180
QY 181 NELNWTALDEVEKKNREEDPSLLQVFGSATGLARYYPASPPWVDNSRTPNKIDLYDVR 240
Db 181 NELNWTALDEVEKKNREEDPSLLQVFGSATGLARYYPASPPWVDNSRTPNKIDLYDVR 240
QY 241 RPWYIOGAASPDKMLILVDVSGVSGLTALKIRTSVSEMLETSLDDDFVNVASFNSNAQD 300
Db 241 RPWYIOGAASPDKMLILVDVSGVSGLTALKIRTSVSEMLETSLDDDFVNVASFNSNAQD 300
QY 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNYSRANCNKIIML 360
Db 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNYSRANCNKIIML 360
QY 361 FTGGEERAQEIENKYNKDKKRVFRFVSGQHNYERGIOWMACENKGYIYEIPSGAIR 420
Db 361 FTGGEERAQEIENKYNKDKKRVFRFVSGQHNYERGIOWMACENKGYIYEIPSGAIR 420
QY 421 INTQEYLDVLRPMVLGADKAKOVQWNTVLDALGLVITGLPVENITGQENKTNLK 480
Db 421 INTQEYLDVLRPMVLGADKAKOVQWNTVLDALGLVITGLPVENITGQENKTNLK 480
QY 481 NQLILGVMGVDSLEDIKRLTFTLCPNGYIYFAIDPNGYVLLHPNLQPNKPSQEPVTL 540
Db 481 NQLILGVMGVDSLEDIKRLTFTLCPNGYIYFAIDPNGYVLLHPNLQPNKPSQEPVTL 540
QY 541 DFLDAELENKIVKIRNKMIDGSGEKTFTLVKQSDERYIDKGNRTYITVPVNGTDYSL 600
Db 541 DFLDAELENKIVKIRNKMIDGSGEKTFTLVKQSDERYIDKGNRTYITVPVNGTDYSL 600
QY 601 ALVLPYTSFYIIRAKLETITQARSKKGMKDSITLKPDPNFESGYTFIAPDYCNLDKI 660
Db 601 ALVLPYTSFYIIRAKLETITQARSKKGMKDSITLKPDPNFESGYTFIAPDYCNLDKI 660
QY 661 SDNTEFLNNEFIDRKTNNPNSCNADLNRLVLLDAGFTNQLVQYNSKQNKIKGVKAR 720
Db 661 SDNTEFLNNEFIDRKTNNPNSCNADLNRLVLLDAGFTNQLVQYNSKQNKIKGVKAR 720
QY 721 FVYTDGGITRYVPEAGENMOENPETYEDSFYKRSLDNDNYFTAPYFNKSGPGAYESGI 780
Db 721 FVYTDGGITRYVPEAGENMOENPETYEDSFYKRSLDNDNYFTAPYFNKSGPGAYESGI 780
QY 781 MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPGAGVPCDKRNSDVMDCVI 840
Db 781 MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPGAGVPCDKRNSDVMDCVI 840
QY 841 LDDCGFLMANHDDYTQIGRFFGEIDPILMRHLVNTSVYAFNKSVDYQSVCEPAGAPKQ 900
Db 841 LDDCGFLMANHDDYTQIGRFFGEIDPILMRHLVNTSVYAFNKSVDYQSVCEPAGAPKQ 900
QY 901 GAGHRSAYPSVADILQIGWATAAASIIQQFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960
Db 901 GAGHRSAYPSVADILQIGWATAAASIIQQFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960
QY 961 SCITEQTYQYFFDNDKSFSGVLDCGNCNRSIFHGEKLMNTNLIIFIMVESKGTCTPCDTRLLI 1020
Db 961 SCITEQTYQYFFDNDKSFSGVLDCGNCNRSIFHGEKLMNTNLIIFIMVESKGTCTPCDTRLLI 1020
QY 1021 QAEOTSDGPNPCDMVKOPRYRKGGPDVCFDNNVLEDYTDCCGVS 1063
Db 1021 QAEOTSDGPNPCDMVKOPRYRKGGPDVCFDNNVLEDYTDCCGVS 1063
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RESULT 4

US-08-311-363-25

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; Sequence 25, Application US/08311363
; Patent No. 5876958
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: Human Calcium Channel Compositions and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,363
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-51506
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1091 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-311-363-25
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Query Match 100.0%; Score 5599; DB 2; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MAAGCLLALTLTLFQSLIGPSEPPSAVTIKSWDKMQEDLVTLAKTAGVGNQLVDI 60
Db 1 MAAGCLLALTLTLFQSLIGPSEPPSAVTIKSWDKMQEDLVTLAKTAGVGNQLVDI 60
QY 61 YEKYQDLYTVEPNNAOLVIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRREDFASN 120
Db 61 YEKYQDLYTVEPNNAOLVIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRREDFASN 120
QY 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFTEDANFGQISYQAAHVIPTDIYEGSTIVL 180
Db 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFTEDANFGQISYQAAHVIPTDIYEGSTIVL 180
QY 181 NELNWTALDEVEKKNREEDPSLLQVFGSATGLARYYPASPPWVDNSRTPNKIDLYDVR 240
Db 181 NELNWTALDEVEKKNREEDPSLLQVFGSATGLARYYPASPPWVDNSRTPNKIDLYDVR 240
QY 241 RPWYIOGAASPDKMLILVDVSGVSGLTALKIRTSVSEMLETSLDDDFVNVASFNSNAQD 300
Db 241 RPWYIOGAASPDKMLILVDVSGVSGLTALKIRTSVSEMLETSLDDDFVNVASFNSNAQD 300
QY 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNYSRANCNKIIML 360
Db 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNYSRANCNKIIML 360
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Db 721 FVVTGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNVFTAPYENKSGPGAYESGI 780
QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVPCDCKRNSDVMDCVI 840
Db 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVPCDCKRNSDVMDCVI 840
QY 841 LDDGGFLLMANHDDYTNOIGRFFGIDPSLMRHLVNIISVYAFNKSIDYQSVCEPGAAPKQ 900
Db 841 LDDGGFLLMANHDDYTNOIGRFFGIDPSLMRHLVNIISVYAFNKSIDYQSVCEPGAAPKQ 900
QY 901 GAGHSAYVPSVADILQIGWATAAAWSILOQFLLSLTFPRLLLEAVEMEDDDFTASLSKQ 960
Db 901 GAGHSAYVPSVADILQIGWATAAAWSILOQFLLSLTFPRLLLEAVEMEDDDFTASLSKQ 960
QY 961 SCITEQTOYFFDNDKSKSPGVLDCGNCRIHFHGEKLMNTNLIIFIMVESKGTCPDTRLLI 1020
Db 961 SCITEQTOYFFDNDKSKSPGVLDCGNCRIHFHGEKLMNTNLIIFIMVESKGTCPDTRLLI 1020
QY 1021 QAEQTSQDGNPCDMVKQPRYKRGPDVCFDNNVLEDYTDCCGVS 1063
Db 1021 QAEQTSQDGNPCDMVKQPRYKRGPDVCFDNNVLEDYTDCCGVS 1063

RESULT

US-09-452-007-4
; Sequence 4, Application US/09452007
; Patent No. 6140485
; GENERAL INFORMATION:
; APPLICANT: Franco, Rodrigo
; APPLICANT: Sun Chen, Ai Ru
; APPLICANT: Suey, David J.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL
; TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/452.007
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/713.118
; FILING DATE: 16-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mata, Elizabeth W.
; REGISTRATION NUMBER: 38,236
; REFERENCE/DOCKET NUMBER: ACC96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1091 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-452-007-4

Query Match 99.9%; Score 5595; DB 4; Length 1091;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1062; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAGCLLALTTLTFSLLIGPSSSEPPPSAVTIKSWDKMOEDLVTLAKTAGSVNQLVDI 60
Db 1 MAAGCLLALTTLTFSLLIGPSSSEPPPSAVTIKSWDKMOEDLVTLAKTAGSVNQLVDI 60
QY 61 YEKYQDLYTVEPNNAQLVEIAARDIEKLLSNRSKALYSVLALEAEKVQAAHQRWEDFASN 120
Db 61 YEKYQDLYTVEPNNAQLVEIAARDIEKLLSNRSKALYSVLALEAEKVQAAHQRWEDFASN 120
QY 121 EVVYINAKDDLDPKNDSEPSQRIKPVFIEDANFGROIISQHAHVHIPTDIYEGSTIVL 180
Db 121 EVVYINAKDDLDPKNDSEPSQRIKPVFIEDANFGROIISQHAHVHIPTDIYEGSTIVL 180
QY 181 NELNWTSALEDVFEKKNREEDPSLLWQVFGSATGLARYYPASPWVDNSRTPNKIDLYDVR 240
Db 181 NELNWTSALEDVFEKKNREEDPSLLWQVFGSATGLARYYPASPWVDNSRTPNKIDLYDVR 240
QY 241 RPWYIQGAASPKDMLILVDVSGSVSGLTLKIRTSVSEMLETSLDDDFVNVASFNSNAQD 300
Db 241 RPWYIQGAASPKDMLILVDVSGSVSGLTLKIRTSVSEMLETSLDDDFVNVASFNSNAQD 300
QY 301 VSCFQHLVQANVRNKKVYLKDAVNITAKGITDYKGFSAFEQLLNLYNVRANCNKIIML 360
Db 301 VSCFQHLVQANVRNKKVYLKDAVNITAKGITDYKGFSAFEQLLNLYNVRANCNKIIML 360
QY 361 FTDGGEERAQEIFNKYKDKKVRVFRFSVGOHNTYERGPIONMACENKGYEYIPEISGAIR 420
Db 361 FTDGGEERAQEIFNKYKDKKVRVFRFSVGOHNTYERGPIONMACENKGYEYIPEISGAIR 420
QY 421 INTOEYLDVLGRPMVLADGKAKQVQWNTNVDLDELGLVITGTLPVFNITGOFENKTNLK 480
Db 421 INTOEYLDVLGRPMVLADGKAKQVQWNTNVDLDELGLVITGTLPVFNITGOFENKTNLK 480
QY 481 NQLILGVNGVDVSLIEDIKRLTPRETLCNPGYFAADPNGYVLLHNPLOPKPKSOEPTVL 540
Db 481 NQLILGVNGVDVSLIEDIKRLTPRETLCNPGYFAADPNGYVLLHNPLOPKPKSOEPTVL 540
QY 541 DFLDAELNDIKVEIRNKMIDGESSEKTRFLVKSQDERYIDKGNRTYTWTVPVNGTDSL 600
Db 541 DFLDAELNDIKVEIRNKMIDGESSEKTRFLVKSQDERYIDKGNRTYTWTVPVNGTDSL 600
QY 601 ALVLPTYSFYIKAKLEETITQARSKKGMKMDSETLKPDPNFEESGYTFIAPRDYCNLKI 660
Db 601 ALVLPTYSFYIKAKLEETITQARSKKGMKMDSETLKPDPNFEESGYTFIAPRDYCNLKI 660
QY 661 SDNTEFLLNNEFTDRKTPNNPCNADLINRVLLDAGFTNELVQNYWSKOKNIKGVKAR 720
Db 661 SDNTEFLLNNEFTDRKTPNNPCNADLINRVLLDAGFTNELVQNYWSKOKNIKGVKAR 720
QY 721 FVVTGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNVFTAPYENKSGPGAYESGI 780
Db 721 FVVTGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNVFTAPYENKSGPGAYESGI 780
QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVPCDCKRNSDVMDCVI 840
Db 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVPCDCKRNSDVMDCVI 840
QY 841 LDDGGFLLMANHDDYTNOIGRFFGIDPSLMRHLVNIISVYAFNKSIDYQSVCEPGAAPKQ 900
Db 841 LDDGGFLLMANHDDYTNOIGRFFGIDPSLMRHLVNIISVYAFNKSIDYQSVCEPGAAPKQ 900
QY 901 GAGHSAYVPSVADILQIGWATAAAWSILOQFLLSLTFPRLLLEAVEMEDDDFTASLSKQ 960
Db 901 GAGHSAYVPSVADILQIGWATAAAWSILOQFLLSLTFPRLLLEAVEMEDDDFTASLSKQ 960
QY 961 SCITEQTOYFFDNDKSKSPGVLDCGNCRIHFHGEKLMNTNLIIFIMVESKGTCPDTRLLI 1020
Db 961 SCITEQTOYFFDNDKSKSPGVLDCGNCRIHFHGEKLMNTNLIIFIMVESKGTCPDTRLLI 1020
QY 1021 QAEQTSQDGNPCDMVKQPRYKRGPDVCFDNNVLEDYTDCCGVS 1063
Db 1021 QAEQTSQDGNPCDMVKQPRYKRGPDVCFDNNVLEDYTDCCGVS 1063

Db 1016 QABQTSQGNPCDMVKQPRYKGPVCFDNNVLEDYDCGGVS 1058

RESULT 8
US-08-223-305C-54
; Sequence 54, Application US/08223305C
; Patent No. 5851824
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/223,305C
; FILING DATE: April 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,250
; FILING DATE: April 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 52516 (P519739)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1086 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-223-305C-54

Query Match 99.3%; Score 5559.5; DB 2; Length 1086;
Best Local Similarity 99.5%; Pred. No. 0;

		Matches 1058;	Conservative	0;	Mismatches	0;	Indels	5;	Gaps	1;
QY	1	MAAGCLLALTLT	FOSLLIGPSSEPF	SAVTIKSWDKMQED	LVTAKTASGVNQLVDI	60				
DB	1	MAAGCLLALTLT	FOSLLIGPSSEPF	SAVTIKSWDKMQED	LVTAKTASGVNQLVDI	60				
QY	61	YEKYQDLYTVE	PNNARQLVEIAA	RDIEKLLSNRSK	ALVSLALEAEKVA	AAHQWREDFASN	120			
DB	61	YEKYQDLYTVE	PNNARQLVEIAA	RDIEKLLSNRSK	ALVSLALEAEKVA	AAHQWREDFASN	120			
QY	121	EVVYNKDDLD	PEKNDSEPGSQ	RKPKVPIEDAN	GRQISYQHAHVH	IPDTIYEGSTIVL	180			
DB	121	EVVYNKDDLD	PEKNDSEPGSQ	RKPKVPIEDAN	GRQISYQHAHVH	IPDTIYEGSTIVL	180			
QY	181	NELNWTSD	ALDEVFKKNRE	EDPSLLMQVFG	SAGLARYYPAS	PWVDSNRTPNKID	LDYDVR 240			
DB	181	NELNWTSD	ALDEVFKKNRE	EDPSLLMQVFG	SAGLARYYPAS	PWVDSNRTPNKID	LDYDVR 240			
QY	241	RPWYIQGA	SPKMDLILV	DVSGSVSGLT	LKLIRTSVSE	MLETLSDDDFV	NVASFNSNAQD 300			
DB	241	RPWYIQGA	SPKMDLILV	DVSGSVSGLT	LKLIRTSVSE	MLETLSDDDFV	NVASFNSNAQD 300			
QY	301	VSCFOH	LVQANVRN	KKVLKDAVNN	ITAKITDYK	KGFSFAFOLL	NYNVRANCNKIIML 360			
DB	301	VSCFOH	LVQANVRN	KKVLKDAVNN	ITAKITDYK	KGFSFAFOLL	NYNVRANCNKIIML 360			
QY	361	FTDGGEE	RAQELFNK	YKDKKVR	FRFSYGOH	NYERGP	IQWACENKGYIETPSIGAIR 420			
DB	361	FTDGGEE	RAQELFNK	YKDKKVR	FRFSYGOH	NYERGP	IQWACENKGYIETPSIGAIR 420			
QY	421	INTQEV	LDVLRPM	VLADGKAK	QVQWNTN	VYLDAL	ELGLVITGTPLVFNTITGOFENKTNLK 480			
DB	421	INTQEV	LDVLRPM	VLADGKAK	QVQWNTN	VYLDAL	ELGLVITGTPLVFNTITGOFENKTNLK 480			
QY	481	NOLILG	VMGVDS	LEDIKRL	TPRTLC	PNGYIFA	IDPNGYVLLHPNLQPNKPSQBPVIL 540			
DB	481	NOLILG	VMGVDS	LEDIKRL	TPRTLC	PNGYIFA	IDPNGYVLLHPNLQPNKPSQBPVIL 540			
QY	541	DFLDAE	LENDIK	VEIRNKM	DGESG	EKTRTLVK	SODERYIDKGNRTYTPTVNGDYSL 600			
DB	541	DFLDAE	LENDIK	VEIRNKM	DGESG	EKTRTLVK	SODERYIDKGNRTYTPTVNGDYSL 600			
QY	601	ALVLP	TYSEYI	AKLEET	ITQARS	KKGMKDS	ETLKPDNFESGYTFIAPRDYCNLDKI 660			
DB	601	ALVLP	TYSEYI	AKLEET	ITQARS	KKGMKDS	ETLKPDNFESGYTFIAPRDYCNLDKI 660			
QY	661	SDNTE	FLNFEF	IDRKT	PNPNS	CNADLIN	RVLLDAGFTNELVQNYWSKQNIKGVKAR 720			
DB	661	SDNTE	FLNFEF	IDRKT	PNPNS	CNADLIN	RVLLDAGFTNELVQNYWSKQNIKGVKAR 720			
QY	721	FVYTD	GGITRV	YPKEA	GNQEN	PETED	SFYKRSIDNDNYVETAPYENKSGPGAYESGI 780			
DB	721	FVYTD	GGITRV	YPKEA	GNQEN	PETED	SFYKRSIDNDNYVETAPYENKSGPGAYESGI 780			
QY	781	MVSKA	VEIYIQ	GKLLP	AVVG	IKIDVNS	WIENTFTKSIRDP	CAGPVCDCKRNSDVMDCVI 840		
DB	781	MVSKA	VEIYIQ	GKLLP	AVVG	IKIDVNS	WIENTFTKSIRDP	CAGPVCDCKRNSDVMDCVI 840		
QY	841	LDDG	FLMAN	HDDY	TNQIG	RFFGE	IDPSLMRHLVINSIYAFNKS	YDYQSVCEPGAAPQ 900		
DB	841	LDDG	FLMAN	HDDY	TNQIG	RFFGE	IDPSLMRHLVINSIYAFNKS	YDYQSVCEPGAAPQ 900		
QY	901	GAGH	RSAYV	PSVAD	ILQIG	WATAAA	WSILQQFLLSITPPRL	LEAVEMEDDDFTASLSQ 960		
DB	901	GAGH	RSAYV	PSVAD	ILQIG	WATAAA	WSILQQFLLSITPPRL	LEAVEMEDDDFTASLSQ 960		
QY	961	SCITE	QTYFFD	NDKSF	SGVLD	CGNCS	RIFFHGEKLMNTNLI	FIIMVESKGTCTPCDTRLLI 1020		
DB	961	SCITE	QTYFFD	NDKSF	SGVLD	CGNCS	RIFFHGEKLMNTNLI	FIIMVESKGTCTPCDTRLLI 1020		
QY	1021	QABQ	TSQGNPC	DMVKQPR	YKGPV	CFDNNV	LEDYDCGGVS 1063			
DB	1021	QABQ	TSQGNPC	DMVKQPR	YKGPV	CFDNNV	LEDYDCGGVS 1063			

Mon Jul 23 08:36:36 2001

RESULT 9
 US-08-455-543A-56
 ; Sequence 56, Application US/08455543A
 ; Patent No. 5792846
 ; GENERAL INFORMATION:
 ; APPLICANT: Harpold, Michael
 ; APPLICANT: Ellis, Steven
 ; APPLICANT: Williams, Mark
 ; APPLICANT: Feldman, Daniel
 ; APPLICANT: McCue, Ann
 ; APPLICANT: Brenner, Robert
 ; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 ; TITLE OF INVENTION: METHODS
 ; NUMBER OF SEQUENCES: 57
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Brown, Martin, Haller & McClain
 ; STREET: 1660 Union Street
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 92101-2926
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/455,543A
 ; FILING DATE: May 31, 1995
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 08/223,305
 ; FILING DATE: April 4, 1994
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 07/868,354
 ; FILING DATE: April 10, 1992
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/745,206
 ; FILING DATE: 15-AUG-1991
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/620,250
 ; FILING DATE: 30-NOV-1990
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/482,384
 ; FILING DATE: 20-FEB-1990
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/603,751
 ; FILING DATE: 04-APR-1989
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/US89/01408
 ; FILING DATE: 04-APR-1989
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/176,899
 ; FILING DATE: 04-APR-1988
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seidman, Stephanie L.
 ; REGISTRATION NUMBER: 33,779
 ; REFERENCE/DOCKET NUMBER: 6362-52517
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619)238-0999
 ; TELEFAX: (619)238-0062
 ; INFORMATION FOR SEQ ID NO: 56:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1084 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FRAGMENT TYPE: internal
 ; US-08-455-543A-56

Query Match 99.0%; Score 5542.5; DB 1; Length 1084;
 Best Local Similarity 99.2%; Pred. No. 0;
 Matches 1055; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY	1	MAAGCLLALTTLFQSLIGPSEEPFPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI	60
DB	1	MAAGCLLALTTLFQSLIGPSEEPFPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI	60
QY	61	YEQYQDLYTVEPNNAQOLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDEFSN	120
DB	61	YEQYQDLYTVEPNNAQOLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDEFSN	120
QY	121	EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRIQISYQHAHVHIPTDIYEGSTIVL	180
DB	121	EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRIQISYQHAHVHIPTDIYEGSTIVL	180
QY	181	NELNWTSALEDEVFKKREEDPSLLQVFGSATGLARYYPASPVWDSNTPNKIDLYDVR	240
DB	181	NELNWTSALEDEVFKKREEDPSLLQVFGSATGLARYYPASPVWDSNTPNKIDLYDVR	240
QY	241	RPWYIQGAASPKDMLILVDVSGVSGLTCLKIRTSVSEMLETSLDDEDFNVASFNSAQD	300
DB	241	RPWYIQGAASPKDMLILVDVSGVSGLTCLKIRTSVSEMLETSLDDEDFNVASFNSAQD	300
QY	301	VSCFOHLYQAVNRNKKVLKDAVNNTAKGITDYKGFSAFQQLLNNVSRANCKNIIML	360
DB	301	VSCFOHLYQAVNRNKKVLKDAVNNTAKGITDYKGFSAFQQLLNNVSRANCKNIIML	360
QY	361	FTDGGERAQEIFNKYNDKVRFRSVGQHYERGPIONMACENKGYIYEPSIGAIR	420
DB	361	FTDGGERAQEIFNKYNDKVRFRSVGQHYERGPIONMACENKGYIYEPSIGAIR	420
QY	421	INTQEYLDVLRPMVLGAKQVQWNTNYLDALGLVITGLPVFNITGTFENKTNLK	480
DB	421	INTQEYLDVLRPMVLGAKQVQWNTNYLDALGLVITGLPVFNITGTFENKTNLK	480
QY	481	NQILGVMGVDSLEDIKRLTPRTLCPCNGYFAIDPNGYVLLHPLNLPKNPKSQEPVTL	540
DB	481	NQILGVMGVDSLEDIKRLTPRTLCPCNGYFAIDPNGYVLLHPLNLPKNPKSQEPVTL	540
QY	541	DFLDAELENDIKVEIRNKMIDGESGKFTFLVKSQDERYIDKGNRTYTPVNGTDYSL	600
DB	541	DFLDAELENDIKVEIRNKMIDGESGKFTFLVKSQDERYIDKGNRTYTPVNGTDYSL	600
QY	601	ALVLPYTSFYIIKAKLEETITQARY-----SETLPDNEFSESGYTFIAPRDYCNLDKI	660
DB	601	ALVLPYTSFYIIKAKLEETITQARY-----SETLPDNEFSESGYTFIAPRDYCNLDKI	660
QY	661	SDNTEFLLNFEIDRKTPNNPCNADLINRVLLDAGFTNELVQYVWSKOKNIKGVKAR	720
DB	661	SDNTEFLLNFEIDRKTPNNPCNADLINRVLLDAGFTNELVQYVWSKOKNIKGVKAR	720
QY	721	FVWTDGGITRVYPKEAGENWQENPETYEDSFYKRSNDNDNVFTAPYFNKSGPGAYESGI	780
DB	721	FVWTDGGITRVYPKEAGENWQENPETYEDSFYKRSNDNDNVFTAPYFNKSGPGAYESGI	780
QY	781	MYSKAVEIYIOGKLLKPAVVGKIDVNSWNIENFTTSIRSDPCAGVPCDCKRNSDVMDCVI	840
DB	781	MYSKAVEIYIOGKLLKPAVVGKIDVNSWNIENFTTSIRSDPCAGVPCDCKRNSDVMDCVI	840
QY	841	LDGGFLLMANHDDYTNQIGRFFGEIDPMSLRHLNYSVYAFNKSVDYOSVCEPGAAPKQ	900
DB	841	LDGGFLLMANHDDYTNQIGRFFGEIDPMSLRHLNYSVYAFNKSVDYOSVCEPGAAPKQ	900
QY	901	GAGHSAYVPSVADILQIGWATAAASWILQOFLSLTPRLLLEAVEMEDDDFTASLSKQ	960
DB	901	GAGHSAYVPSVADILQIGWATAAASWILQOFLSLTPRLLLEAVEMEDDDFTASLSKQ	960
QY	961	SCITEQTQYFFDNDKSKFSGLVDCGNCSTRIFHGEKLMNTNLIIFIMVESKGTCPDTRLLI	1020
DB	961	SCITEQTQYFFDNDKSKFSGLVDCGNCSTRIFHGEKLMNTNLIIFIMVESKGTCPDTRLLI	1020
QY	1021	QAEQTSDBGPNPCDMVKQPRYKRGPDVCFDNNVLEDYTDCCGVS 1063	

Db 1014 QAEQTSDEGNPCDMVKQPRYRKGPVCFDNNVLEDTDCGGVS 1056

RESULT 10

US-08-223-305C-56
; Sequence 56, Application US/08223305C
; Patent No. 5851824
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/223.305C
; FILING DATE: April 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,250
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 52516 (P519739)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1084 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-223-305C-56

Query Match 99.0%; Score 5542.5; DB 2; Length 1084;

Best Local Similarity 99.2%; Pred. No. 0;
Matches 1055; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

Qy 1 MAAGCLLALTLTLFQSLIGPSSSEPPPSAVTIKSWDKQEDLVTAKTAGVYNQLYDI 60
Db 1 MAAGCLLALTLTLFQSLIGPSSSEPPPSAVTIKSWDKQEDLVTAKTAGVYNQLYDI 60
Qy 61 YEKYODLYTVEPNNAQOLVEIAARDIEKLLNSRKALVSLALEAEKVQAAHQRDFASN 120
Db 61 YEKYODLYTVEPNNAQOLVEIAARDIEKLLNSRKALVSLALEAEKVQAAHQRDFASN 120
Qy 121 EVVYINAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIYSQHAHVHIPTDIYEGSTIVL 180
Db 121 EVVYINAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIYSQHAHVHIPTDIYEGSTIVL 180
Qy 181 NELNWTSALEDEVFKKNREEDPSLLWQVFGSATGLARYYPASPDVNSRTPNKKIDLYDVR 240
Db 181 NELNWTSALEDEVFKKNREEDPSLLWQVFGSATGLARYYPASPDVNSRTPNKKIDLYDVR 240
Qy 241 RPWYIOGAASPKDMLILVDVSGVSGLTGLKIRTSVSEMLETSLDDDFVNVASFNSNAQD 300
Db 241 RPWYIOGAASPKDMLILVDVSGVSGLTGLKIRTSVSEMLETSLDDDFVNVASFNSNAQD 300
Qy 301 VSCFQHLVQANVRNKKVYLKDAVNNTAKGIDYKKGFSFAFEQLLNNVSRANCKIIML 360
Db 301 VSCFQHLVQANVRNKKVYLKDAVNNTAKGIDYKKGFSFAFEQLLNNVSRANCKIIML 360
Qy 361 FTDGGEERAQEIFNKYNKDKKVRVFRFVSGQHNRYERGIOWMACENKGYEYIPEISGAIR 420
Db 361 FTDGGEERAQEIFNKYNKDKKVRVFRFVSGQHNRYERGIOWMACENKGYEYIPEISGAIR 420
Qy 421 INTOEYLDVLRPMVLADGKAKQVQNTNVYLDALBELGIVITGTLVFNITGOFENKTNLK 480
Db 421 INTOEYLDVLRPMVLADGKAKQVQNTNVYLDALBELGIVITGTLVFNITGOFENKTNLK 480
Qy 481 NQLILGVMGVDVSLIEDIKRLTPRTLCPNGYFFADPNGYVLLHPLNLPKPKSQEPVTL 540
Db 481 NQLILGVMGVDVSLIEDIKRLTPRTLCPNGYFFADPNGYVLLHPLNLPKPKSQEPVTL 540
Qy 541 DFLDAELENDIKVEIRNKMIDGESGEKFTLVKSQDERYIDKGNRTYTWTVPNGTDSL 600
Db 541 DFLDAELENDIKVEIRNKMIDGESGEKFTLVKSQDERYIDKGNRTYTWTVPNGTDSL 600
Qy 601 ALVLPYTFYIKAKLEETITQARSKGKMKDSETLKPDNFEESGYTFIAPRDYCNDLKI 660
Db 601 ALVLPYTFYIKAKLEETITQARSKGKMKDSETLKPDNFEESGYTFIAPRDYCNDLKI 660
Qy 661 SDNTEFLNFEFIDRKTTPNPNPCNADLINRVLDAGFTNELVQNYWSKQKNIKGVKAR 720
Db 661 SDNTEFLNFEFIDRKTTPNPNPCNADLINRVLDAGFTNELVQNYWSKQKNIKGVKAR 720
Qy 721 FVVTGGITRVYPKEAGENWOENPETYEDSFYKRSLDNDNYYFTAPYFNKSGPGAYESGI 780
Db 721 FVVTGGITRVYPKEAGENWOENPETYEDSFYKRSLDNDNYYFTAPYFNKSGPGAYESGI 780
Qy 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSKIENFTKTSIRDPDPCAGPVCDCRNSDYMDCVI 840
Db 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSKIENFTKTSIRDPDPCAGPVCDCRNSDYMDCVI 840
Qy 841 LDDGGFLLMANHDDYTNQIGRFFGIDPSLMRHLVNI SVYAFNKSVDYQSVCPEGAAPKQ 900
Db 841 LDDGGFLLMANHDDYTNQIGRFFGIDPSLMRHLVNI SVYAFNKSVDYQSVCPEGAAPKQ 900
Qy 901 GAGHRSAYVPSVADILQIGWATAAAWSILOQFLSLTFPPRLLEAVEMEDDDFTASLSKQ 960
Db 901 GAGHRSAYVPSVADILQIGWATAAAWSILOQFLSLTFPPRLLEAVEMEDDDFTASLSKQ 960
Qy 961 SCITEQTQYFFDNDKSFSGVLDGCGNCRIFPHGEKLMNTNLIFIMVESKGTCCPTRLLI 1020
Db 961 SCITEQTQYFFDNDKSFSGVLDGCGNCRIFPHGEKLMNTNLIFIMVESKGTCCPTRLLI 1020
Qy 1021 QAEQTSDEGNPCDMVKQPRYRKGPVCFDNNVLEDTDCGGVS 1063
Db 1021 QAEQTSDEGNPCDMVKQPRYRKGPVCFDNNVLEDTDCGGVS 1063

Db 1014 QAEQSDGPNPCDMVKOPRYRKGPVCFDNNVLEDYTDGCGVS 1056

RESULT 11

US-08-455-543A-53

Sequence 53, Application US/08455543A

Patent No. 5792846

GENERAL INFORMATION:

APPLICANT: Harpold, Michael

APPLICANT: Ellis, Steven

APPLICANT: Williams, Mark

APPLICANT: Feldman, Daniel

APPLICANT: McCue, Ann

APPLICANT: Brenner, Robert

TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

TITLE OF INVENTION: METHODS

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESS: Brown, Martin, Haller & McClain

STREET: 1660 Union Street

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/455,543A

FILING DATE: May 31, 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/223,305

FILING DATE: April 4, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/869,354

FILING DATE: April 10, 1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/745,206

FILING DATE: 15-AUG-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/620,250

FILING DATE: 30-NOV-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/482,384

FILING DATE: 20-FEB-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/603,751

FILING DATE: 04-APR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US89/01408

FILING DATE: 04-APR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/176,899

FILING DATE: 04-APR-1988

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L.

REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 6362-52517

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619)238-0082

TELEFAX: (619)238-0082

INFORMATION FOR SEQ ID NO: 53:

SEQUENCE CHARACTERISTICS:

LENGTH: 1103 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

US-08-455-543A-53

Query Match	98.6%	Score 5523;	DB 1;	Length 1103;
Best Local Similarity	97.5%	Pred. No. 0;		
Matches 1055;	Conservative	0;	Mismatches	1;
			Indels	26;
			Gaps	2;
QY	1	MAAGCLLALTLTQSLIGSSSEPPSAVTIKSWDKMOEDLVTLAKTAGVGNQVLVDI	60	
DB	1	MAAGCLLALTLTQSLIGSSSEPPSAVTIKSWDKMOEDLVTLAKTAGVGNQVLVDI	60	
QY	61	YEKYODLYTVPNNARQOLVEITAARDIEKLLSNRSKALYSLEAEKQAAHQRDEFASN	120	
DB	61	YEKYODLYTVPNNARQOLVEITAARDIEKLLSNRSKALYSLEAEKQAAHQRDEFASN	120	
QY	121	EVVYVNAKDDLDPKNDSEPGSQRIKPVIEDANFGRQISYQHAHVHPTDIYEGSTIVL	180	
DB	121	EVVYVNAKDDLDPKNDSEPGSQRIKPVIEDANFGRQISYQHAHVHPTDIYEGSTIVL	180	
QY	181	NELNMTSALDEYFKKNREEDPSLLMQVFGSATGLARYYPASPVWDNRSRTPNKIDLYDVR	240	
DB	181	NELNMTSALDEYFKKNREEDPSLLMQVFGSATGLARYYPASPVWDNRSRTPNKIDLYDVR	240	
QY	241	RMWYIQAASPKDMLILVDVSGVSGITLKLIRTSVSEMLETSLSDDDFVNVSFNSNAQD	300	
DB	241	RMWYIQAASPKDMLILVDVSGVSGITLKLIRTSVSEMLETSLSDDDFVNVSFNSNAQD	300	
QY	301	VSCFQHLVQANVRNKKVLDVANNITAKGITYDKKGFSAFQELLNYSRANCNKIIML	360	
DB	301	VSCFQHLVQANVRNKKVLDVANNITAKGITYDKKGFSAFQELLNYSRANCNKIIML	360	
QY	361	FTDGGERAQEIENKYNKDKKRVFRFVSGOHNYERPIQWMACENKGYIYEIPISGAIR	420	
DB	361	FTDGGERAQEIENKYNKDKKRVFRFVSGOHNYERPIQWMACENKGYIYEIPISGAIR	420	
QY	421	INTQEYLDVLGRPMVLAGDKAKQVQWNTNVLDALEGLVITGLTPVNITGQFENKTNLK	480	
DB	421	INTQEYLDVLGRPMVLAGDKAKQVQWNTNVLDALEGLVITGLTPVNITGQFENKTNLK	480	
QY	481	NQLILGVMGVDVSLIEDIKRLTPRETLCPNGYFAIDPNGYVLLHPNLPQKPIGVGIPIN	540	
DB	481	NQLILGVMGVDVSLIEDIKRLTPRETLCPNGYFAIDPNGYVLLHPNLPQKPIGVGIPIN	540	
QY	531	-----NPKSQEPVTLDFDALENDIKVEIRNKNMIDGESGKTFRTLVKSODERYI	581	
DB	541	LRKRRPNIQNPKSQEPVTLDFDALENDIKVEIRNKNMIDGESGKTFRTLVKSODERYI	600	
QY	581	DGNRTYTWTPVNGDYSLALVLPITYFYIYAKLEETITQARSKKGMKSEILKPNF	641	
DB	601	DGNRTYTWTPVNGDYSLALVLPITYFYIYAKLEETITQARSKKGMKSEILKPNF	653	
QY	642	BESGYTFIAPRDYCNLDKISDNNTTEFLNFEFIDRKTPNPNPCNADLINRVLLDAGFTN	701	
DB	654	BESGYTFIAPRDYCNLDKISDNNTTEFLNFEFIDRKTPNPNPCNADLINRVLLDAGFTN	713	
QY	702	ELVQYWSKQKNIKGVARFVTDGGITRVYPKEAGENWQENPEYEDSFYKRSLDNDNY	761	
DB	714	ELVQYWSKQKNIKGVARFVTDGGITRVYPKEAGENWQENPEYEDSFYKRSLDNDNY	773	
QY	762	VFTAPYFNKSGPGAYESGIMVSKAVEIYIQGLKLPVAVGIIKIDVNSWTENTKTSIRDP	821	
DB	774	VFTAPYFNKSGPGAYESGIMVSKAVEIYIQGLKLPVAVGIIKIDVNSWTENTKTSIRDP	833	
QY	822	CAGPVCDCRNSDVMDCVILDDGGFLLMANHDDYTQIGRFEGEIDPSLMRHLVNI SVYA	881	
DB	834	CAGPVCDCRNSDVMDCVILDDGGFLLMANHDDYTQIGRFEGEIDPSLMRHLVNI SVYA	893	
QY	882	FNKSYDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAAWSILQOQLLSLTFPR	941	
DB	894	FNKSYDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAAWSILQOQLLSLTFPR	953	
QY	942	LLEAVEMEDDDFTASLSKQSCITEQTYQFPDNDKSKFSFSGVLDGCGNCSRIFPHGKLMNTNL	1001	
DB	954	LLEAVEMEDDDFTASLSKQSCITEQTYQFPDNDKSKFSFSGVLDGCGNCSRIFPHGKLMNTNL	1013	

QY 1002 IFIWKESKTCPCDTRLLIQABQTSDBGNPCDMVKOPRYRKGPDYCFDNNVLEDYTDGCG 1061
Db 1014 IFIWKESKTCPCDTRLLIQABQTSDBGNPCDMVKOPRYRKGPDPVCFDNNVLEDYTDGCG 1073
QY 1062 VS 1063
Db 1074 VS 1075

RESULT 12

US-08-223-305C-53
Sequence 53, Application US/08223305C
Patent No. 5851824
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/223,305C
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 52516 (P519739)
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1103 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

FRAGMENT TYPE: internal
US-08-223-305C-53

Query Match 98.6%; Score 5523; DB 2; Length 1103;
Best Local Similarity 97.5%; Pred. No. 0;
Matches 1055; Conservative 0; Mismatches 1; Indels 26; Gaps 2;

QY 1 MAAGCLLALTTLFQSLILGPSSEEPFSAVTIKSWDKMQEDLVTLAKTAGVNLVDI 60
Db 1 MAAGCLLALTTLFQSLILGPSSEEPFSAVTIKSWDKMQEDLVTLAKTAGVNLVDI 60
QY 61 YEKYQDLYTVEPNNAQQLVEIAARDIEKLLSNRSKALVSALAEAEKVQAAHOWREFASN 120
Db 61 YEKYQDLYTVEPNNAQQLVEIAARDIEKLLSNRSKALVSALAEAEKVQAAHOWREFASN 120
QY 121 EYVYNNAKDDLPKNDSEPGSORIKPVFIEDANFORQISYQAAVHIPTDIYEGSTIVL 180
Db 121 EYVYNNAKDDLPKNDSEPGSORIKPVFIEDANFORQISYQAAVHIPTDIYEGSTIVL 180
QY 181 NELNMTSALDEVFKKNREEDPSLLQVFGSATGLARYYPASPMVDNSRTPNKIDLDVRR 240
Db 181 NELNMTSALDEVFKKNREEDPSLLQVFGSATGLARYYPASPMVDNSRTPNKIDLDVRR 240
QY 241 RPWYIQGAASPDKMLILVDVSGSVGLTLKLI RTSYSEMLETLSDDDDFVNVSFNSNAQ 300
Db 241 RPWYIQGAASPDKMLILVDVSGSVGLTLKLI RTSYSEMLETLSDDDDFVNVSFNSNAQ 300
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITYDKGFSFAFEOQLLNNVSRANCKIIML 360
Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITYDKGFSFAFEOQLLNNVSRANCKIIML 360
QY 361 FTDGGEERAQELFNKYNKDKKVRFRFSYGOHNYERGPIQWACENKGYIYEPSIGAIR 420
Db 361 FTDGGEERAQELFNKYNKDKKVRFRFSYGOHNYERGPIQWACENKGYIYEPSIGAIR 420
QY 421 INTQEYLDVLGRPMVLADGKAKOVQNTNVLDALEGLVITGTLPVFNITGQFENKTLK 480
Db 421 INTQEYLDVLGRPMVLADGKAKOVQNTNVLDALEGLVITGTLPVFNITGQFENKTLK 480
QY 481 NQILGVMGVDVSLEDIKRLTPRTLCPNGYIFAIDPNGVLLHPNLQPK----- 530
Db 481 NQILGVMGVDVSLEDIKRLTPRTLCPNGYIFAIDPNGVLLHPNLQPK----- 530
QY 531 -----NPKSQEPVTLDFDAELENDIKVEIRKNMIDGESGEKTFRLVKSQDERYI 581
Db 541 LRKRRPNIONPKSQEPVTLDFDAELENDIKVEIRKNMIDGESGEKTFRLVKSQDERYI 600
QY 582 DKGNTYTTVPVNGTDYSLALVLPYTSFYIKAKLEETITQARSKKGKMDSETLKPDNF 641
Db 601 DKGNTYTTVPVNGTDYSLALVLPYTSFYIKAKLEETITQARY-----SETLKPDNF 653
QY 642 EESGYTFIAPRDYCNLDKISDNNTFELLNFEFIDRKTNNPNSCNADLINRVLLDAGFTN 701
Db 654 EESGYTFIAPRDYCNLDKISDNNTFELLNFEFIDRKTNNPNSCNADLINRVLLDAGFTN 713
QY 702 ELVQNTWSKQKNIKGVKARFVVDGGITRVYPKEAGENQWENPETYEDSYKKSLODNKY 761
Db 714 ELVQNTWSKQKNIKGVKARFVVDGGITRVYPKEAGENQWENPETYEDSYKKSLODNKY 773
QY 762 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRD 821
Db 774 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRD 833
QY 822 CAGPVCDCRNSDVMDCVILDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLNVSIVA 881
Db 834 CAGPVCDCRNSDVMDCVILDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLNVSIVA 893
QY 882 FNKSYDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAANSILOQFLLSLTFPR 941
Db 894 FNKSYDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAANSILOQFLLSLTFPR 953
QY 942 LLEAVEMEDDDFTASLSKQSCITEQTQYFFPDNDSKSFSGVLDCGNC-SRIFPHGEKLMNTNL 1001

QY 901 GAGHSAYVPSVADILQIGWATAAWSILOQFLLSLTTPRLLLEAVEMEDDDFTASLSKO 960
Db 889 GAGHSAYVPSVADILQIGWATAAWSILOQFLLSLTTPRLLLEAVEMEDDDFTASLSKO 948
QY 961 SCITEQTOYFFDNDKSFSGVLDGNCGRIFHGEKLMNTNLIFIMVESKGTCPDTRLLI 1020
Db 949 SCITEQTOYFFDNDKSFSGVLDGNCGRIFHGEKLMNTNLIFIMVESKGTCPDTRLLI 1008
QY 1021 QABQTSQDGNPCDMVKOPRYRGPDVCFDNNVLEDYTDGCGYS 1063
Db 1009 QABQTSQDGNPCDMVKOPRYRGPDVCFDNNVLEDYTDGCGYS 1051

RESULT 14

US-08-223-305C-55
; Sequence 55, Application US/08223305C
; Patent No. 5851824
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/223,305C
; FILING DATE: April 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,250
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 52516 (P519739)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 1079 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-223-305C-55

Query Match 98.3%; Score 5503; DB 2; Length 1079;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1050; Conservative 0; Mismatches 1; Indels 12; Gaps 2;

QY 1 MAAGCILLALTTLFOSLLIGPSSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNOLVDI 60
Db 1 MAAGCILLALTTLFOSLLIGPSSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNOLVDI 60
QY 61 YEKYQDLTYVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALEAEKVAQAQHWREDFASN 120
Db 61 YEKYQDLTYVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALEAEKVAQAQHWREDFASN 120
QY 121 EYVYNKADLDPEKNDSEPGSQRIKPVFIEDANFGRIQISYQHAHVHIPTDIYEGSTIVL 180
Db 121 EYVYNKADLDPEKNDSEPGSQRIKPVFIEDANFGRIQISYQHAHVHIPTDIYEGSTIVL 180
QY 181 NELNWTSAIDVEFKKNREEDPSLLMQVFGSATGLARYYPASPWVDNSRTPNKIDLDVRR 240
Db 181 NELNWTSAIDVEFKKNREEDPSLLMQVFGSATGLARYYPASPWVDNSRTPNKIDLDVRR 240
QY 241 RPWYIQGAASPDKMLILVDVSGVSGLTLLKLTISVSEMLETLSDDDDFVNVASFNSNAOD 300
Db 241 RPWYIQGAASPDKMLILVDVSGVSGLTLLKLTISVSEMLETLSDDDDFVNVASFNSNAOD 300
QY 301 VSCFQHLVOANVRNKKVLDVANNITAKGIDYKKGFSFAFEPQOLLNYSRANCNKIIML 360
Db 301 VSCFQHLVOANVRNKKVLDVANNITAKGIDYKKGFSFAFEPQOLLNYSRANCNKIIML 360
QY 361 FTDGGEERAQEIFNKYKDKKVRFRFSVGQHNRYERGPIQWMACENKGYEYIETPSIGAIR 420
Db 361 FTDGGEERAQEIFNKYKDKKVRFRFSVGQHNRYERGPIQWMACENKGYEYIETPSIGAIR 420
QY 421 INTQEYLDVLRPMVLADGKAKQVQWNTVYLDALGLVITGTPVFNITGQFENKTNLK 480
Db 421 INTQEYLDVLRPMVLADGKAKQVQWNTVYLDALGLVITGTPVFNITGQFENKTNLK 480
QY 481 NQLILGVMGVDSLEDIKRLTPRFTLCNGYIFAIDPNGVYLHPNLPKNPQSQBPTVL 540
Db 481 NQLILGVMGVDSLEDIKRLTPRFTLCNGYIFAIDPNGVYLHPNLPKNPQSQBPTVL 540
QY 541 DFLDAELENDIKVEIRNKMIDGESGKFTTLVKSDERYIDKGNRTYTTWTPVNGTDYSL 600
Db 541 DFLDAELENDIKVEIRNKMIDGESGKFTTLVKSDERYIDKGNRTYTTWTPVNGTDYSL 600
QY 601 ALVLPYISFYIYKAKLEETITQARSKKGMKMSSETLKPONFEESGYTFIAPRDYCNLDKI 660
Db 601 ALVLPYISFYIYKAKLEETITQARSKKGMKMSSETLKPONFEESGYTFIAPRDYCNLDKI 660
QY 661 SONNTEFLNFEFIDRKTPNPNPSCNADLINRVLLDAGFTNELVQYWSKQKIKGVKAR 720
Db 661 SONNTEFLNFEFIDRKTPNPNPSCNADLINRVLLDAGFTNELVQYWSKQKIKGVKAR 720
QY 721 FVYTDGGLTRVYPKEAGENWOENPETEYDSFYKRSLDNDNYVFTAPVFNKSGPGAYESGI 780
Db 721 FVYTDGGLTRVYPKEAGENWOENPETEYDSFYKRSLDNDNYVFTAPVFNKSGPGAYESGI 780
QY 781 MYSKAVEIYIQGLKLPVAVGVIKIDVNSWIENFTKTSIRDPACAGPVCDCRNSDVMDCVI 840
Db 781 MYSKAVEIYIQGLKLPVAVGVIKIDVNSWIENFTKTSIRDPACAGPVCDCRNSDVMDCVI 840
QY 841 LDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNIISVAFNKSITDYOSVCEPGAAPKQ 900
Db 841 LDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNIISVAFNKSITDYOSVCEPGAAPKQ 900
QY 889 LDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNIISVAFNKSITDYOSVCEPGAAPKQ 920
Db 889 LDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNIISVAFNKSITDYOSVCEPGAAPKQ 920

QY 901 GAGHRSAYVPSVADILQIGWATAAAWSILQFLLSLTFFRLLLEAVEMEDDDFTASLSKQ 960
DB 889 GAGHRSAYVPSVADILQIGWATAAAWSILQFLLSLTFFRLLLEAVEMEDDDFTASLSKQ 948
QY 961 SCTEQTYFFDNDKSFSGVLCGNCGRIFHGEKLMNTNLIFTMVESKGTCPDTRLLI 1020
DB 949 SCTEQTYFFDNDKSFSGVLCGNCGRIFHGEKLMNTNLIFTMVESKGTCPDTRLLI 1008
QY 1021 QAEQTSQGNPCDMVKQPRYKRGPDVCFDNNVLEDYDCGVS 1063
DB 1009 QAEQTSQGNPCDMVKQPRYKRGPDVCFDNNVLEDYDCGVS 1051

RESULT 15
US-08-435-675B-5
; Sequence 5, Application US/08435675B
; Patent No. 5710250
; GENERAL INFORMATION:
; APPLICANT: Ellis, Steven Bradley
; APPLICANT: Williams, Mark E.
; APPLICANT: Harpold, Michael Miller
; APPLICANT: Schwartz, Arnold
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,675B
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,083
; FILING DATE: 28-SEP-1994
; APPLICATION NUMBER: US 07/914,231
; FILING DATE: 13-JUL-1992
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 08-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-53193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1106 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-435-675B-5

Query Match 96.2%; Score 5385.5; DB 1; Length 1106;
Best Local Similarity 94.9%; Pred. No. 0;
Matches 1030; Conservative 14; Mismatches 12; Indels 29; Gaps 4;

DB 1 MAAGRPLAWTLTLMQAWLILIGSPSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLV 60
QY 59 DIYEKYODLYTVEPNNAQQLVEIAARDIEKLLSNRSKALVSLAEAEKVQAAHQRWEDFA 118
DB 61 DIYEKYODLYTVEPNNAQQLVEIAARDIEKLLSNRSKALVRLAEAEKVQAAHQRWEDFA 120
QY 119 SNEVYYNAKDDLDPEKNDSEPGSQRIKPFVIEDANFGRQISYQHAHVHPTDIEGSI 178
DB 121 SNEVYYNAKDDLDPEKNDSEPGSQRIKPFVIEDANFGRQISYQHAHVHPTDIEGSI 180
QY 179 VLNELNWTSSALDEYFKKREDEPSLLMQVFGSATGLARYYPASVPWVNSRTPNKIDLYDV 238
DB 181 VLNELNWTSSALDEYFKKREDEPSLLMQVFGSATGLARYYPASVPWVNSRTPNKIDLYDV 240
QY 239 RRPWYIQGAASPKDMLILVDVSGVSGLTLLKLTIRTSVSEMLETLSDDDFVNVASFNSA 298
DB 241 RRPWYIQGAASPKDMLILVDVSGVSGLTLLKLTIRTSVSEMLETLSDDDFVNVASFNSA 300
QY 299 QDVSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFQOLLNRYNVRANCNKII 358
DB 301 QDVSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFQOLLNRYNVRANCNKII 360
QY 359 MLFTDGGEEERAOEILFNKYNDKVKRVFRFVSQGHNYERGPQIOWMACENKGYIYIPISGA 418
DB 361 MLFTDGGEEERAOEILFNKYNDKVKRVFRFVSQGHNYERGPQIOWMACENKGYIYIPISGA 420
QY 419 IRIINTQEYLDVLRPMVLGADKAKOVQWNTVYLDALGLVITGTLPVFNITGTFENKTN 478
DB 421 IRIINTQEYLDVLRPMVLGADKAKOVQWNTVYLDALGLVITGTLPVFNITGTFENKTN 480
QY 479 LKNQILIGVMGVDSLEDIKRLTFRFLCPNGYIFAIDPNGYVLLHPLNLPK - - - - - 530
DB 481 LKNQILIGVMGVDSLEDIKRLTFRFLCPNGYIFAIDPNGYVLLHPLNLPKRGVIGPT 540
QY 531 - - - - - NPKSQEPVTLDAELNDIKYIRNKMIDGSGEGTFTTLVKSQDER 579
DB 541 INLRKRPVONPKSQEPVTLDAELNDIKYIRNKMIDGSGEGTFTTLVKSQDER 600
QY 580 YIDKGNRTYTPVNGTDY - SLALVLPYTFYIYKAKLEETITQARSKKGMKQSETLKP 638
DB 601 YIDKGNRTYTPVNGTDYSSALVLPYTFYIYKAKLEETITQARS - - - - - SETLKP 653
QY 639 DNFESGYTFLAPRDYCNLDKISDNTEFLNFEFIDRKTNNPNSCNADLNRLVLLDAG 698
DB 654 DNFESGYTFLAPRDYCNLDKISDNTEFLNFEFIDRKTNNPNSCNADLNRLVLLDAG 713
QY 699 FTNELVQYWSKQKNIKGVKARFVVTGCGITRVYPKEAGENQWENPETEYDSFYKRSLDN 758
DB 714 FTNELVQYWSKQKNIKGVKARFVVTGCGITRVYPKEAGENQWENPETEYDSFYKRSLDN 773
QY 759 DNYVFTAPYFNKSGPGAYESGIMVSKAVEIYIQGKLLPAPVVGKIDVNSWIENFTKTSI 818
DB 774 DNYVFTAPYFNKSGPGAYESGIMVSKAVEIYIQGKLLPAPVVGKIDVNSWIENFTKTSI 833
QY 819 RDPGAGPYCDCKRNSDVNDVILDDGGFLMANHDDYTNQIGRFFGEIDPDSLMRLHVNIS 878
DB 834 RDPGAGPYCDCKRNSDVNDVILDDGGFLMANHDDYTNQIGRFFGEIDPDSLMRLHVNIS 893
QY 879 VYAFNKSYDYQSVCEPAGAPKQAGHRSAYVPSVADILQIGWATAAAWSILQFLLSLT 938
DB 894 VYAFNKSYDYQSVCEPAGAPKQAGHRSAYVPSVADILQIGWATAAAWSILQFLLSLT 953
QY 939 FPRLEAVEMEDDDFTASLSKQSCITEQTYFFDNDKSFSGVLCGNCGRIFHGEKLMN 998
DB 954 FPRLEAADMEDDDFTASLSKQSCITEQTYFFDNDKSFSGVLCGNCGRIFHGEKLMN 1013
QY 999 TNLIFIMVESKGTCPDTRLLIQAEOQSDGNPCDMVKQPRYKRGPDVCFDNNVLEDYTD 1058
DB 1014 TNLIFIMVESKGTCPDTRLLIQAEOQSDGNPCDMVKQPRYKRGPDVCFDNNVLEDYTD 1073
QY 1059 CGVS 1063
DB 1074 CGVS 1078

Mon Jul 23 08:36:36 2001

Search completed: July 23, 2001, 07:39:25
Job time: 552 sec

359 MLFTDGGERAQEIFNKYNKDKKVRVRESVGQHNHYERGIQWMACENKGYIYPSIGA 418
 361 MLFTDGGERAQEIFNKYNKDKKVRVRESVGQHNHYERGIQWMACENKGYIYPSIGA 420
 419 IRTQYLDVLRPMVLAGDRAKQVQWTVNYLDALGLVITGTLPVFNITQGFENKTN 478
 421 IRTQYLDVLRPMVLAGDRAKQVQWTVNYLDALGLVITGTLPVFNITQGFENKTN 480
 479 LKNQLILGVMGVDSLEDIKRLTPRTLCPCNGYFAIDPNGYVLLHPNLPK ----- 530
 481 LKNQLILGVMGVDSLEDIKRLTPRTLCPCNGYFAIDPNGYVLLHPNLPKPIGVGPT 540
 531 -----NPKSOPVTLDFDALENDIKVEIRKMKIDGESGKTFRTLVKSQDER 579
 541 INLRKRPVONRSPQVTLDFDALENDIKVEIRKMKIDGESGKTFRTLVKSQDER 600
 580 YIDKNGTYTTPVNGTDY-SLALVLTFTYFYIKALEETITQARSKGKMKDSETLKP 638
 601 YIDKNGTYTTPVNGTDYSSALVLTFTYFYIKALEETITQARSKGKMKDSETLKP 653
 639 DNFEESGYTFAPRDYNDLKSNDNTEFFLNFEEDRKTNNPNSCNDLINRVLLDAG 698
 654 DNFEESGYTFAPRDYNDLKSNDNTEFFLNFEEDRKTNNPNSCNDLINRVLLDAG 713
 699 FTNELVQWNSKQNIKGVKARFVVDGIGITRVYPKEAGENWQENPETYEDSFYKRSLDN 758
 714 FTNELVQWNSKQNIKGVKARFVVDGIGITRVYPKEAGENWQENPETYEDSFYKRSLDN 773
 759 DNYVTFAPFNKSGPAYESGIMVSKAVEIYQGLKLPVAVGKIDVNSWIENFTKTSI 818
 774 DNYVTFAPFNKSGPAYESGIMVSKAVEIYQGLKLPVAVGKIDVNSWIENFTKTSI 833
 819 RDPGAGVCDCKRNSVMDCVILDDGGFLMANHDDYTNOIGRFFGEIDPRLMRHLNIS 878
 834 RDPGAGVCDCKRNSVMDCVILDDGGFLMANHDDYTNOIGRFFGEIDPRLMRHLNIS 893
 879 VTAFNKSIDYQSVCEPAAKOGAGHRSAYVPSVADILQIGMWATAAASIIQQFLSLT 938
 894 VTAFNKSIDYQSVCEPAAKOGAGHRSAYVPSVADILQIGMWATAAASIIQQFLSLT 953
 939 FPRLLAEVEMEDDDFTASLSKSCITEQTOYFPDNDKSFSGVLDGNCGRIFHGEKLMN 998
 954 FPRLLAEVEMEDDDFTASLSKSCITEQTOYFPDNDKSFSGVLDGNCGRIFHGEKLMN 1013
 999 TNLIFIMVESKGCPCDTRLLIQAQESDGPDCDMVKQPRYKRGPDVCFDNNVLEDTD 1058
 1014 TNLIFIMVESKGCPCDTRLLIQAQESDGPDCDMVKQPRYKRGPDVCFDNNVLEDTD 1073
 1059 CGGVS 1063
 1074 CGGVS 1078

RESULT 4
 T30256
 calcium channel alpha-2-delta-C chain - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 20-Jun-2000
 R:Klugbauer, N.; Lacinova, L.; Marais, E.; Hobom, M.; Hofmann, F.
 J. Neurosci. 19, 648-691, 1999
 A:Title: Molecular diversity of the calcium channel alpha2delta subunit.
 A:Reference number: 220794
 A:Accession: T30256
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1091 <KLU>
 A:Cross-references: EMBL:AJ010949; PIDN:CAA09423.1
 A:Experimental source: brain
 C:Superfamily: calcium channel alpha-2 chain

Query Match 20.0%; Score 1119.5; DB 2; Length 1091;

1020 IQAETSDGPNPCDMVKQPRYKRGPDVCFDNNVLEDTDCCGVS 1063
 1020 MQAETSDGPNPCDMVKQPRYKRGPDVCFDNNVLEDTDCCGVS 1063

RESULT 3
 CHABA2
 calcium channel protein alpha-2 chain precursor - rabbit
 N:Alternate names: dihydropyridine-binding protein, 140K
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 22-Jun-1999
 C:Accession: S10579; A33409
 R:Ellis, S.B.; Williams, M.E.; Ways, N.R.; Brenner, R.; Sharp, A.H.; Leung, A.T.; Campbell, K.P.
 Science 261, 1661-1664, 1988
 A:Title: Sequence and expression of mRNAs encoding the alpha(1) and alpha(2) subunits of
 A:Reference number: S10579; MUID:88336904
 A:Accession: S10579
 A:Molecule type: mRNA
 A:Residues: 1-1106 <ELL>
 A:Cross-references: EMBL:M21948; NID:g164762; PIDN:AAA81562.1; PID:g164763
 A>Note: This sequence represents the amino end of a glycosylated peptide that appears at
 e at the amino end and identical molecular weights (17K) following deglycosylation
 R:Hamilton, S.L.; Hawkes, M.J.; Brush, K.; Cook, R.
 Biochemistry 28, 7820-7828, 1989
 A:Title: Subunit composition of the purified dihydropyridine binding protein from skeletal
 A:Reference number: A33409; MUID:90122765
 A:Accession: A33409
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 27-44, 'S', 46-47 <HAM>
 C:Superfamily: calcium channel alpha-2 chain
 C:Keywords: calcium, disulfide bond; glycoprotein; ion channel; membrane protein; phosph
 F:1-26/Domain: signal sequence status predicted <SIG>
 F:27-1106/Product: calcium channel alpha-2 chain status predicted <MAT>
 F:94,138,186,326,350,470,477,606,615,678,697,784,827,891,898,988,1001,1081/Binding site:

Query Match 96.1%; Score 5380.5; DB 1; Length 1106;
 Best Local Similarity 94.8%; Pred. No. 0;
 Matches 1029; Conservative 15; Mismatches 12; Indels 29; Gaps 4;

QY 1 MAAGCLLALTLTQFQS--LLIGPSSEPPFPSTVTKSWDKMQEDLVTLAKTAGVGNQLV 58
 DB 1 MAAGRPALWTLTQWMLLIGPSSEPPFPSTVTKSWDKMQEDLVTLAKTAGVGNQLV 60
 QY 59 DIYEKYQDLTYVEPNNAQLVEIARIEKLLSNRSLVSLALEAEKQVAAHQWREDDFA 118
 DB 61 DIYEKYQDLTYVEPNNAQLVEIARIEKLLSNRSLVSLALEAEKQVAAHQWREDDFA 120
 QY 119 SNEVYVNAKDDLPKNDSPGSGRIKPVIEDANFGRIQSYQHAHVHIPTDIYEGSTI 178
 DB 121 SNEVYVNAKDDLPKNDSPGSGRIKPVIEDANFGRIQSYQHAHVHIPTDIYEGSTI 180
 QY 179 VLNELNWT-SALDEVFKKREDDPSLLMQVFGSATGLARYYPASPWVDSRTPNKIDLYDV 238
 DB 181 VLNELNWT-SALDEVFKKREDDPSLLMQVFGSATGLARYYPASPWVDSRTPNKIDLYDV 240
 QY 239 RRRPWTIOGAASPKDMLILVDVSGSGLTLLKRTSVSEMLETISDDDEVNVAFSNSNA 298
 DB 241 RRRPWTIOGAASPKDMLILVDVSGSGLTLLKRTSVSEMLETISDDDEVNVAFSNSNA 300
 QY 299 QDVSCFOHLVQVARNKKVLDVANNITAKGTDYKKGFSFAFEQLLNYNVSRANCKII 358
 DB 301 QDVSCFOHLVQVARNKKVLDVANNITAKGTDYKKGFSFAFEQLLNYNVSRANCKII 360

Best Local Similarity 28.5%; Pred. No. 2.3e-59;		Matches 321; Conservative 230; Mismatches 443; Indels 131; Gaps 41;	
QY	3	AGCLLALTTLFOSLIGSPSEPPFSATVITKSWDKMOEDLVTLAKTASGVNQLVDIYE	62
DB	14	ASALLA-TALLYAALGDVVRSEQQIPLSV-VKLWASAFGEIKSIAKYSGSOLLQKKYK	71
QY	63	KYQDLVTVPEPNNAQVLVEIAARDIEKLLNSRKALVSLALEAKVQAQAHQWRDFASNEV	122
DB	72	EYKQVAIEEDIGLQVLKLAIMEEMFKKSEAVRLVEAABEHLKHEFDADL---QY	128
QY	123	VYNAK---DDLDEKNDSEPGSORIIPVTFEDANFR-QISYQHAHVHPTDIEGSTIV	179
DB	129	EYFNAVILNERDRDGNFLELKGKEFI---LAPNDHFNNLPVNISLSDVQVPTNNYKDPAI	185
QY	180	LNELNLTALDEVEFKKNNREDPSLLWQVFSATGLARIYPASPWVDNSRTPNPKIDLYDVR	239
DB	186	VNGVWSESLINKVFDVDFDRDPSLIWQVFSAGFFRQYPIKKEPDE---NGVIAFDCR	242
QY	240	RRPWYIOGAASPKDMLILVDVSGVSGLTLLKLTSTVSSEMLETISDDDFVNVASFNNAQ	299
DB	243	NRWYIOQAATSPKDVVTLVDVSGMSKGLRTIAKQTVSSILDTLGDGDDFFNIITYNEELH	302
QY	300	DVS-CFO-HLVQANVRNKKVYLKDAVNNTAKGTYDKKGFSEAFQOLLNVNVRAN--CN	355
DB	303	YVEPCLNGTLVQADRTNKEHFRHLDKLFPAGIGMLDIALNEAFNILSDFNHTCGGSICS	362
QY	356	KIIMFLFDGGEEARAQEIFKNYN-KDKKVRVFRFSVGQHNRYERGPIOMACENKGYIYEIP	414
DB	363	QAIMLITDGAVDVDTYTFKYNWPDVKRVITFTYLGREAAAFADNLKWMACANKGFFQIS	422
QY	415	SIGAIRNTQBYLDVGRPMVLADGKAKQVQWTVYLD-----ALEGLVI--TGT	463
DB	423	TLADVQNVMEYHLVLSRPKYI--DOEHVVTWEAYIDSTLPQAQKLADGQGLVMTVA	480
QY	464	LPVFNITQGFENKTNLKNOLLGVMGVDVSLDEIKRTPRFTLCPNGYIYFAIDPNGVLL	523
DB	481	MPVFS---KONETRSKG-ILLGVVGDVDPVKELLKIPYKLGIIHYAFAITNNGVILT	535
QY	524	HPNLQP---KNPKSQEP--VTLDLDALENDIKVEIRNKMIDGESGEKTRTLVKSQDE	578
DB	536	HPELRPLYEECKRRKPNYSVDLSEVEDRDDV-LRNAMVRNKTGK--FSMEVK----	588
QY	579	RYIDKGNRT-----YWPVTVNGTDYSLALVLPY-YSEFYIKAKLEETIQARSKKGMK	631
DB	589	KTVDKGRVLTMTNDYTYTDIKGTFPSLGVALSRGHGKIYF-----RGNVT	634
QY	632	DSETLKPDNFEESGYTFIAPRDYCN-DLKISDNTTEFLNFEFIDRKTNNPNSCNADLI	690
DB	635	IEEGL--HDLHPDVPVSLADEWSYCNLDLHPHRLSLQLEAIKLYLKKEP--LLQCDKELI	691
QY	691	NRVLIDAGFTNELVQNYWS-----KKNIKGVKARFVVTDDGTRVYVP-----	733
DB	692	QEVLFDA-VVSAPTEAYWTSALANKSENSDKGVEVAFGLTGTGLSRINLRFVGAELTNQD	750
QY	734	KEAGENQENPETYEDSFYKRSLDN--DNYVFTAPY-----FNKSGPGAYESGIWVSKAV	786
DB	751	FLKAGDKENIFNADHFLPWLARRAAEQIAGSFVYSIPFSTGTVNSK-----NVVTASTSI	804
QY	787	EYIIOGKLLKPAVGIKIDVNSWNTENFTKTSIRDPACGVPDCKRNSDVMDCVILDDGGF	846
DB	805	QLLDERKSPVVAAGVIOKMLEFFORKEFTWASROCASLDGKCSISCDDETVCNYCLIDNNGF	864
QY	847	LIMAHNDYTNQIGRFGCEIDPSLMRHLVNTSVYAFNKSIDYQSVCEPGAAPKOGAGHRS	906
DB	865	ILVS---EDIT-OTGDFFEVAGVANKLLTWMGSKRITLYIQAMCR---ANKSSDSAH	918
QY	907	AYXPSVADILQIGWATAAASIIQQFLLSTLTPRLLFAVEMEDDDFTASLSK-----QS	961
DB	919	GLLDYPKAPL-----SAKWMTELVLFLVEF-----NLCSWHSHSDMTAKAKLKQTLPEP	968
QY	962	CITEOTQYFFDNDNSKFSGLVDCGNCRIFFHGEKLMNTNLIFFIYVESKGTCPCDTRLIIQ	1021

DB	969	CDTEYPAFVSERTIKETTGNACDCSKSFVIQQIPSSNLFVWVDS--SCLCESVAPIT	1026
QY	1022	ABQTSQDPN---PCDMVKQPRYRKGPDPVCFDNNVLEDYTDGCGVS	1063
DB	1027	MAPIEIRYNESLKERLKAQKRRRPSCHGFHPEENARECGGAS	1071
RESULT 5			
S44617			
C50C3.11 protein - Caenorhabditis elegans			
C:Species: Caenorhabditis elegans			
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001			
C:Accession: S44617			
R:Favell, A.D.			
submitted to the EMBL Data Library, May 1993			
A:Description: Sequence of the C. elegans cosmid C50C3.			
A:Reference number: S44618			
A:Accession: S44617			
A:Status: preliminary			
A:Molecule type: DNA			
A:Residues: 1-734 <PAV>			
A:Cross-references: EMBL:L14433; NID:g289649; PID:g289650			
C:Genetics:			
A:Introns: 24/2; 87/3; 175/1; 259/1; 290/3; 346/3; 460/3; 538/3			
Query Match		10.8%; Score 607; DB 2; Length 734;	
Best Local Similarity		26.8%; Pred. No. 9.6e-29;	
Matches 180; Conservative 127; Mismatches 258; Indels 112; Gaps		20;	
QY	47	LAKTASGNVLVDIYEKYQDLTVPEPNNAQVLVEIAARDIEKLSNRS----	KALVSLAL 102
DB	36	MKETFSKISHETILKQNYEKLVVEEQDPAELKSKHRIEDYLKVSQFAYKAKIS--L	93
QY	103	EAEKVQAAHOREDFASNVVYNAKDDLDPEK--NDSEPGSQRIKP-----VFIEDANP	155
DB	94	EARSVRNDSTVNDPQSKSFIRFMSAKOGNDGTTIYESNHGLKRLKVNRETKSFNTQANF	153
QY	156	-GROISYQHAHVHPTDIYEGSTIVLAEINLWNTSALDEVEFKKNNREDPSLLWQVFGSATGL	214
DB	154	YTLPSTSVSSAVHPTFLYDRNEDLLRKIDW--SDIDAVYRNRETKDLAFQLFCSEAGY	212
QY	215	ARYYPASFPW--DNSRTPNKNIDLYDVRPWPYIOGAASPKDMLILVDVSGVSGYJTLKLIR	273
DB	213	MRYYPASWFDNQ--DEHLDLFCRNTWYINSATNSKNVLIIMLDNSGSMGQRYEVAK	270
QY	274	TSVSEMLETISDDDFVNVASFNSNA---QDVSCFQHLVQANVRNKKVCLKDAVNITAKGI	330
DB	271	QTTEAILETLSHNDYFNIMTFSKNTFLDGCNGTNGLIQATMRNKKALRRKMDTYQSEKG	330
QY	331	TDYKGFSAFEQILLNYN-----VSRANCNIIIMLFTDGGEEARAQEIFKNYKDKKVRVF	385
DB	331	AEYEKALPLAFSVLLDINNNGGDNRRGACENVIMLTDGAPNAYKKIYFDIMNADKKVRVF	390
QY	386	RFSVQGNHYERGPQIOWACENKGYIYEIPSIGAIRNTQEYL---DVLGRPMVLADGKA	441
DB	391	TFVLGDEAIDNEVREMACNRRGYMHWVANMADVDEKTHHVRMSRVVGRHYKESGOLS	450
QY	442	KOVQWTVNYLDALBGL--VITGLPVENITQFENKTN-----	478
DB	451	---NWTGVYRERLYLPREIFAEPVPIINQSFVAVNMKASRRKIRLQKSEARSRMFVTV	507
QY	479	----LKNQLILGVMGVDSLEDIRLTPRFTLCPNGYIYFAIDPNGYVLLHNPQLKPNP--	532
DB	508	SYPVTVNETMGVAANIPLTEVAQKSHPANIGSKSYFFMLDQNGFVMTHPQLRPIDPFT	567
QY	533	--KQEPVTLDFD-----	561
DB	568	KYHKQNYNNMDLLEVEGQGNVRSQKSAQVSDLVCSGGANYACVDDLRKAVKRMID	627
QY	562	GESGEKTRTLVKSODERY----IDK---GNRTYTWTPVNGTDYSLALVLPITYSYPIKA	614
DB	628	CDNSD-----VQQLDVLVYATELLDRVYPOINTYTYAECINHANFVLGLAVAKGDDYRVVK	681

QY 615 KLEETITQARSKKGMK 631
| : : : : :
Db 682 K-----QKKYDFGRVK 692

RESULT 6
T18770
probable calcium channel protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C:Accession: T18770; T25249
R:Sulston, J.
submitted to the EMBL Data Library, June 1995
A:Reference number: Z19019
A:Accession: T18770
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1148 <W1>
A:Cross-references: EMBL:Z49907; PIDN:CAA90091.1; GSPDB:GN000020; CBSP:T24F1.6
A:Experimental source: clone B0491
R:Chui, C.
submitted to the EMBL Data Library, June 1995
A:Reference number: Z20004
A:Accession: T25249
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1148 <W12>
A:Cross-references: EMBL:Z49912; PIDN:CAA90141.1; GSPDB:GN000020; CBSP:T24F1.6
A:Experimental source: clone T24F1
C:Genetics:
A:Map position: 2
A:Introns: 91/2; 131/3; 170/3; 283/1; 322/2; 410/3; 487/1; 563/1; 602/3; 654/3; 683/3; 7

Query Match 10.4%; Score 580.5; DB 2; Length 1148;
Best Local Similarity 21.2%; Pred. No. 7.7e-27;
Matches 244; Conservative 217; Mismatches 437; Indels 251; Gaps 43;

QY 37 VDKMQEDVTLA-----KTASGVNOLVDIYEKYQDLYTVEPNNAQLVEIAARDI 86
| : : : : :
Db 99 VDIIEAPASIAQFSANILRDFQTSRFSLVQEEFKLPDIKSKEDAAEKLVRATEHL 158
| : : : : :
QY 87 EKLNSRKALVSLALEAEKVAQHWRDFAENVEVYVYNAKDDLPKNDSEPGSQ-- 144
| : : : : :
Db 159 DRLVTNRVDALKLASSAESAFAVE-----DEYDDQAVAVPQADKRC 201
| : : : : :
QY 145 --TKPVFIEDANTGROISYQH---AAVHPTDIYEGSTIVLNLNWTSA--LDEVFKNR 197
| : : : : :
Db 202 AYMKKNESDMHFVSNN-VEHNSKSGIHITVESYQCDPRVYRDFWTGTRHLEKTSNDK 260
| : : : : :
QY 198 EEDPSLLQWVGSGATGLARYYPASPVDNSRTENKLDYDVRPRPYIQAASPKDMLIL 257
| : : : : :
Db 261 EKAPEMGHQVIGYISGLTRMYPRRH- KVEPTITIDLPDRFPMPVNAESPDKLVFL 319
| : : : : :
QY 258 VDVSGVSGILTKLRTSVMSEMLTSDDDFVNVSFNSNAQD-VSCFQH-LVQAANYRK 315
| : : : : :
Db 320 LDYSGVGKPTMLIKITMYYILSTLSPNDYFFGVFNHFNPIISCANTEMPTATSNK 379
| : : : : :
QY 316 KVLKDAVNNTAKIYDYKGFSAFEQL---LNVNVS-----RANCKNIMLFTDGGEE 367
| : : : : :
Db 380 KVPFELGMLERKDOAHFATPLAFSLDLVLRGNLDSNQSLFADYRSEGHKLLIIFTGVDE 439
| : : : : :
QY 368 RAOEIEFN---KYNKDKVVRVESVGOHNVGPIQWACENKGYVEIPISGAIRINTO 424
| : : : : :
Db 440 WPHQIDEEFQTRNSLEIRIFGSMGYSGLSLPLQIYMAKCKSHGYSSEIDSIMDKPQSR 499
| : : : : :
QY 425 EYLDVLGRPMVLADGKAK-----QVQWTVNVDLALGLVITGLVPFNITGQFENKT 477
| : : : : :
Db 500 TIONVLSQ---VRGDELKGTNAEKRPSTWLYNEVQGGPIVTLSPILT-----SEQR 551
| : : : : :
QY 478 NLKNQILGVMGVDVSLEDIKRLTPRTLCNPGYFAIDPNPGYVLLHPNLQ-PKNPK--- 533
| : : : : :

Db 552 IWRDQKLAGVVAIDISIKETKHLP--TSSEQMYGYIVDNNGMILYHPQLQIPKTEVHCV 609
| : : : : :
QY 534 -----SQEPV-----TLDFDAELENIDIKVIRN 557
| : : : : :
Db 610 RRSACYDAQVKQKAGSGLRVHYGFSDEYVRLVGLDLSIPTLDMYLEGDSAIRDLRR 669
| : : : : :
QY 558 KMIDGESGKTRFLVKSQDERYIDKGNRTYTPVNGTYSALV--LPTYSFYIYKAK 615
| : : : : :
Db 670 -----RITTKTCYEEAKDMSKEYHCSHIDKSPFTLVIVNNIOLKTVYDDSV 717
| : : : : :
QY 616 LEETITQ-----ARSKKGMKDSKSETLKPDNFEESGYTFIAPRDYC--NDLKISDNNT 665
| : : : : :
Db 718 QELGLTDNKLVTFFPRDVCQMKLDEYAAHDFRV--WSDISEKEICAQDDMKLPRAFT 775
| : : : : :
QY 666 EFLINFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQVNSKQKNIRKVGARFVYTD 725
| : : : : :
Db 776 KGLSMTQSWPKSDIEHTC-----LLAQYPENASVPHYNS-----FVHTR 817
| : : : : :
QY 726 GGTRVYPKEAGENQENPETYEDSFYKRSLDNDNVYFTAPYFNKSGPGAYESGIMVSKA 785
| : : : : :
Db 818 SKLTAFYPTCSSHDMKAVNKKFDEEI--KLTDNDFV---QFSMR-----SESLIYRT 866
| : : : : :
QY 786 VEIYIOGKLLKPAVVGKIDVN---SWIENFTKTSIRDCAGPVCDCRNSD-----VMD 837
| : : : : :
Db 867 IADYDNNRL---AVVGQWKENFDFQYDNFT-----RQPNWKICKRQE 908
| : : : : :
QY 838 CVILDDGGFLIMAHDDYTNQIGRFFGEIDPSLMRHLVNISVAFNKSVDYQSVCEPGAA 897
| : : : : :
Db 909 CSIITRNGHVIASSAHRAHAHLAKF---DPQLFESLVKYNLVYSTNSWTEVQSECK---- 960
| : : : : :
QY 898 PKOGAGHRSAYVPSVADILQIGWATAA--AWSILOQFLSLTFPRLEAVEMEDDDFTA 955
| : : : : :
Db 961 -----AKRVAPWSSAAGSSSILRYFTVTSI-----FKLAKTSFWR 995
| : : : : :
QY 956 SLSKQSCITEQTOYFFDNDSDKSPGVLDGNC-SRIFHGKLMNTNLIFFIWESKGTG-- 1012
| : : : : :
Db 996 NLLESALTLDVADQSPMTGTCTTQKIKPFERCFMKFHYRMTLNITK-OLQLTGMSTCSR 1054
| : : : : :
QY 1013 -----PCDTRLLIOAEQTSQGNP-----CDMVKQPRYRKGPVDCFD--N 1050
| : : : : :
Db 1055 YAKLYPVPHTTLSLIITADRACSYRPRKIFESPRKLEKCDVV-HSHARRRDALNDWKI 1113
| : : : : :
QY 1051 NVLEDYTC 1059
| : : : : :
Db 1114 DLQNKHVDC 1122

RESULT 7
C86880
hypothetical protein yvvc [imported] - Lactococcus lactis subsp. lactis (strain IL140
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
C:Accession: C86880
R:Solotkin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarre, K.; Weissenbach, J.; Eh
Genome Res. in press, 2001
A:Title: The complete genome sequence of the lactic acid bacterium.
A:Reference number: A86625
A:Accession: C86880
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1450 <STO>
A:Cross-references: GB:AE005176; NID:gl2725093; PIDN:AAK06141.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: yvvc

Query Match 3.5%; Score 198; DB 2; Length 1450;
Best Local Similarity 21.0%; Pred. No. 0.0013;
Matches 242; Conservative 149; Mismatches 439; Indels 322; Gaps 56;

QY 37 VDKMQEDVTLAKTASGVNOLVDIYEKYQDLYTVEPNNAQLVEIAARDIEK-----L 89
| : : : : :

Db 69 INKTENKELKLFPSFGNQPPIEE--NESWTKENKT-----IISDFEKENEGKIVL 120
QY 90 LSNRSKALVLALEAEKVOAHQWR---EDFA-----SNEVYYNA 127
Db 121 RANNSISLLNLEIQADAKLIENDQEVISEDILAKKESTIFSLYPENKADSKDKNKNT 180
QY 128 KDDLDPKNDSEPGSORIKP---VFIEDANFGQISVOHAAVH----- 167
Db 181 EEVLNNESSQETVQKQDOSQAFSPNFGIKASFNDAQNYENISPIRYODETGISP 240
QY 168 ---IPTDIIEGSTIVLNELNWTLSALDEVEKKNREEDPSLLQWFGSATGLARYYPASPW 223
Db 241 NWSWIPT---GNTVVNHOHNSF-----SSQWDGVNSWN--GEATNLENSYIEYAG 287
QY 224 VDN-----STPNKIDLY-DVRRPWPYIOGAASPKDMLILVDVSGVSGITLK 270
Db 288 VNNPVPDFALRYAKETETPGDYLVNVRGN--VQNPKPVDIVLVIDMSGMOGAKET 344
QY 271 LIKTSVSEMLETISDD---DFVNV--ASFNSAQDYSCFOHLVQANVRNKKVLKD---A 321
Db 345 AVROGVDFLSITONTAYADYVNVGVISYSPGNYVTGASGYITVPI--DKVSSESHVKS 402
QY 322 VNNITA---KGITDYKKGFSFAFEQLLNYNVSRANCKIIMLFTDGGEEAQAQIFNKYNK 378
Db 403 INQALAPQFSGGTFTQLGRKGTML---EODSSDNQKMMILMTDG-----VPTFSYKVS 455
QY 379 DKVVR--VFRFSVQGHNYERG---PIQ---WMAENKNGYYEII-----PSGAIKRNTOQE 425
Db 456 ASKVDNVIYQSGFAESRDEPGNTSKIQSPYVVDKINGGSIENIRDTWAATLGEAEISKQE 515
QY 426 YLDVLRGPRVLAD-----RAKQVQWTVNVLDALEGLVITGLPVENITQOFE 474
Db 516 ISEIHTLGIQMGDSYLSQSEVKSRTSLIATGLYODANSAN-----DITDYLK 565
QY 475 NKTN-----LKNQILGVMGVDSLEDKRLTPRTFLCPNGYFAIDPNGYVILLHPN 526
Db 566 NQANVLRSFNTITNGILLDPLGAQFEYKTK-----PEINSVG----- 604
QY 527 LQPNKPSQSPVLDFDLDALENDIKVEIRNKMIDGSGEKTFTLVKSODEYIDKGNR 586
Db 605 -----EDSIDNLTPTKINEKGLEISNLNI--GKNQVQIHYQVRLNTETDDFKTNY 653
QY 587 TY-----TTPVNGT--DYSLALVPTYFYIKAKLE-----ETIQARSKK 627
Db 654 WYQMGTEITLP--NGSNPDKNKVFGPSAKSGINTLLEKOWLANSNIPENVELLIGR 712
QY 628 GKMKDSE-----TLKPDNFEESGYFTIAPRDYCNLDKISDNNTTEFLNFEIDRKTNN 682
Db 713 SAQISSDWTKTVILKEDEWRSQLENLPKYSILGEEFYIEIKDEIVLN--SEIYDWITIGE 771
QY 683 PSCHADLINRVLD---AGFTNELVQNYWSKOKNIKGVKARFVVDGTRVYPKEAGE 738
Db 772 DKTTIANIEKFRLOIKTSNHDNEPLSEVEFLKNSOGEEIDKAVTN-----EKGE 822
QY 739 -NQWENETVEDSFYKSLONDVNYVFTAPFNKSGPAGYESGIMVSK-----AVEIYIQ 791
Db 823 ILFDKTRNLGEEYQVLEIKSPHSGLEGPKIKT---EPENGQPIIKVDGEQIALDEHN 879
QY 792 GKLLKPAVVGKIDVNSWIENFTKTSIRDPCAGVPCDKRNSDVMDCVILD-----DG-- 844
Db 880 KFMIS---LNTINDIN--VVEF-----RNSVTIDKRAVDSEKLDGAV 917
QY 845 -GFLLMANHDYTNQIGRFFGEIDPSLMRHLVNIYSYAFNKSVDYQSCVCPGAPKQAG 903
Db 918 FNLQIESVDDELQTKPL--EITNLLPLGL-----YALQESVSPNGYIRDEV 964
QY 904 H--RSAVPSVADILQGWATAAANSILOQFL-----LSITF- 939
Db 965 HFFRVKNGSVIAITGSEG-----IDIPFLDENESKNGLVNBEENGDLHLTLIFY 1015
QY 940 ---PRLEAVEMEDDDFTASLSKQSC--ITEQTYQFPDNDSD---KSFQVLDGCGNCSRI 990

Db 1016 NQAVPPLQLEVDKIDDDFTSPLAGVSFELTRIGRKSTSDSDSKRINSDFRILAKTN--NE 1073
QY 991 FHGEKL-MMNTNL 1001
Db 1074 FTGETIALKSNL 1085
RESULT 8
S54355
inter-alpha-trypsin inhibitor heavy chain 3 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 04-Feb-2000
C:Accession: S54355
R:Chan, P.; Risler, J.L.; Raguenez, G.; Salier, J.P.
Biochem. J. 306, 505-512, 1995
A:Title: The three heavy-chain precursors for the inter-alpha-inhibitor family in mou
A:Reference number: S54353; MUID:95194326
A:Accession: S54355
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-886 <CHA>
A:Cross-references: EMBL:X70993; NID:g695635; PIDN:CAA49843.1; PID:g695636
C:Superfamily: inter-alpha-trypsin inhibitor complex component II
Query Match 3.5%; Score 194.5; DB 2; Length 886;
Best Local Similarity 19.9%; Pred. No. 0.00094;
Matches 185; Conservative 138; Mismatches 347; Indels 261; Gaps 44;
QY 27 FPSAVTIKSNVDKQEDLVLTAKTASGVNQLVDIYKYQDLYTVEPNNAQRLVEIAARDI 86
Db 98 YPGNVKEVQAQYKAVSQGTAG---LVKASGRKLEKFTVSVNVAAGSKVTFELTY 153
QY 87 EKLSSRSKALVSLALEAEKVOAHQWRDFASNEVYVYNAKDDLDPEKNDSEPGSQRIK 146
Db 154 EELL-KRNKGKYEMLKVQPKQLVRHFEID-----AHIFEP-----Q 189
QY 147 PVIEDANFGRLISYQHAHVHPTDIYEGSTIVLNELNWTLSALDEVEKKNREEDPSLLQW 206
Db 190 GISMLDAE-----ASFITNDL-LGSALTQSF----- 214
QY 207 VFGSATGLARYYPASPVWDNSRT-PNKID-----LYDVRRRP-----WYI-- 245
Db 215 -----SGKKGHVSKFSLDQORSCPTCTDSLLNGDFITVDVNRSPGNVQIVNGYEVHF 269
QY 246 ---QG--AASPKDMLILVDVSGVSGITLKLIKRTSVSMLTSLDDEDFVNVASNSNAQDV 301
Db 270 FAPQGLPVVPKNIVFVIDVSGMSGRKIQOTREALLKILDDVKEDDYLNELFEST---DV 326
QY 302 SCFQ-HLVQANVRNKKVLRDAVNITAKGITDYKKGFSFAFEQLLNYNVSRAN-----C 354
Db 327 TTWKDHLVQATPANLKEAKTFVKNIHQDSMTNINDGLLKGIEML---NKAREDHVTPERS 383
QY 355 NKIMLFTDG---GEARQAEIENKYNK--DKKVRFRFSVQGHNYERGPIQWMACENKG 408
Db 384 TSIIMLTGDGANTGESRPEKIQENVRNAIGKPEPLYNLQFG-NLNLNFEILELHNHG 442
QY 409 YYYEIPSIGAIRINTOEYLDVLRGPMVLGADKAKQVQWTVNVLDALEGL--VITGLPV 466
Db 443 LARRIYEDSDANLOQGYEEVANPLL-----TNVEVEYEPENAILDLTRNSYPH 491
QY 467 FNTIGFENKTNLKNQLILGVGVDSLEDIKRLTPRTFLCPNGYFAIDPNGYVILLHPN 526
Db 492 F-----YDG-----SEIVVAGRLVDRNMDN-----FKADVKGHGALN-- 523
QY 527 LQPNKPSQSPVLDFDLDALENDIKVEIRNKMIDGSGEK--TFRTLKVSQBERYIDKG 584
Db 524 -----DLTTFTEVDNEEMDAALK-----EQYIFGDIYERLWAYLTIEQLLEKRNKAG 572
QY 585 NRTYTTVPVNGTDYSLA--DVLPTYFYIYKAKLEETITQARSKKGMKMDSET-----LK 637
Db 573 DEKENIT-AEALDLSLKYHEVTPLTSMVVTKPEDNEQDTSIADNAGEAPAEETMTSFLT 631

QY 638 PDNFESGYFIAPDYCNLDKISDNTEYELLNENEDRKTNPNSCNADLINRVLLDA 697
 Db 632 TQSQSQSPYIVV-----DGPDPHFIQI-----PGKNDSCIFNIDEKP 668
 QY 698 GFTNELVQNTYMSKOKNIKGVKARVVDGGITRVYPKREAGNMOENPETVEDSFYKSLD 757
 Db 669 GTVLRLIQD-----PVT--GIT-VTGOIIGD-----KRS-- 694
 QY 758 NDNVFTAPFNKSGPAYESGIMSKAVIYIIGKLLKPAVVGIKIDVNSWIENFTKTS 817
 Db 695 NASSRTGKTGYFGKLGITNANWDFRVEVTEKIILG-----TGAELSTESWLDIVTVTQ 747
 QY 818 IRDPCAGVCDCKRNSDVMCDVILDDG-GELLMAN-----HDDYTNQIGRFFGEIDP 868
 Db 748 -----TGLSVTIINRKNMV--VSFGDGISFVILHQVKKRHPVHQDFLG-----FYVDS 795
 QY 869 SLMRHLNIVISVYAFNKSVDYQSV-CEPGAAP 898
 Db 796 HRMSAQPHGLLGQFFQFPDFKVFGRGSDP 826

RESULT 9
 S30350
 N; alternate names: HC3; inter-alpha-trypsin inhibitor chain H3; pre-alpha-inhibitor heavy
 C; Species: Homo sapiens (man)
 C; Date: 03-May-1994 #sequence_revision 20-Feb-1995 #text_change 04-Feb-2000
 C; Accession: S30350; S02141; D34245; A39079; B53642; A59167
 R; Bourguignon, J.; Diarra-Mehrpour, M.; Thiberville, L.; Bost, F.; Sesbouee, R.; Martin,
 Eur. J. Biochem. 212, 771-776, 1993
 A; Title: Human pre-alpha-trypsin inhibitor-precursor heavy chain cDNA and deduced amino-
 A; Reference number: S30350; MUID:93215656
 A; Accession: S30350
 A; Molecule type: mRNA
 A; Residues: 1-885 <BOU1>
 R; Bourguignon, J.
 A; Cross-references: EMBL:X67055; NID:g288562
 submitted to the EMBL Data Library, June 1992
 A; Reference number: S34123
 A; Accession: S34123
 A; Molecule type: mRNA
 A; Residues: 1-310, 'K', 312-343, 'R', 345-885 <BOU2>
 A; Cross-references: EMBL:X14690; NID:g35464; PIDN:CAA47439.1; PID:g288563
 R; Diarra-Mehrpour, M.; Bourguignon, J.; Sesbouee, R.; Mattei, M.G.; Passage, E.; Salier,
 Eur. J. Biochem. 179, 147-154, 1989
 A; Title: Human plasma inter-alpha-trypsin inhibitor is encoded by four genes on three ch
 A; Reference number: S02141; MUID:89137072
 A; Accession: S02141
 A; Status: not compared with conceptual translation
 A; Molecule type: mRNA
 A; Residues: 341-356, 'G', 358-845, 'H', 847-885 <DIA1>
 A; Cross-references: EMBL:X14690; NID:g35464; PIDN:CAA32821.1; PID:g35465
 R; Engild, J.J.; Thogersen, I.B.; Pizzo, S.V.; Salvesen, G.
 J. Biol. Chem. 264, 15975-15981, 1989
 A; Title: Analysis of inter-alpha-trypsin inhibitor and a novel trypsin inhibitor, pre-al
 A; Reference number: A92736; MUID:89380192
 A; Accession: D34245
 A; Molecule type: protein
 A; Residues: 30-49 <ENGL>
 R; Engild, J.J.; Salvesen, G.; Hefta, S.A.; Thogersen, I.B.; Rutherford, S.; Pizzo, S.V.
 J. Biol. Chem. 266, 747-751, 1991
 A; Title: Chondroitin 4-sulfate covalently cross-links the chains of the human blood prot
 A; Reference number: A39079; MUID:91093267
 A; Accession: A39079
 A; Molecule type: protein
 A; Residues: 631-647 <ENG2>
 R; Diarra-Mehrpour, M.; Bourguignon, J.; Sarafan, N.; Bost, F.; Sesbouee, R.; Muschio-Bon
 Biochim. Biophys. Acta 1219, 551-554, 1994
 A; Title: Tandem Orientation of the inter-alpha-trypsin inhibitor heavy chain H1 and H3 g
 A; Reference number: S50133; MUID:95002176
 A; Accession: S50133
 A; Status: preliminary
 A; Molecule type: DNA

A; Residues: 1-27 <DIA2>
 A; Cross-references: EMBL:X75318
 R; Wisniewski, H.G.; Burgess, W.H.; Oppenheim, J.D.; Vilcek, J.
 Biochemistry 33, 7423-7429, 1994
 A; Title: TSG-6, an arthritis-associated hyaluronan binding protein, forms a stable co
 A; Reference number: A53642; MUID:94217199
 A; Accession: B53642
 A; Molecule type: protein
 A; Residues: 30-34, 'X' <WIS>
 R; Jessen, T.E.; Faarvang, K.L.; Ploug, M.
 FEBS Lett. 230, 195-200, 1988
 A; Title: Carbohydrate as covalent crosslink in human inter-alpha-trypsin inhibitor: a
 A; Reference number: S02431; MUID:88167187
 A; Accession: A59167
 A; Molecule type: protein
 A; Residues: 30-32, 'GEKQAVDT' <JES>
 C; Comment: As pre-alpha-inhibitor, this protein is covalently cross-linked by chondro
 C; Genetics:
 A; Gene: GDB:ITIH3
 A; Cross-references: GDB:120109; OMIM:146650
 A; Map position: 3p13-3p12
 C; Superfamily: Inter-alpha-trypsin inhibitor complex component II
 C; Keywords: chondroitin sulfate proteoglycan; glycoprotein; heterodimer; proteinase I
 F; 1-19/Domain: signal sequence #status predicted <SIG>
 F; 20-647/Domain: propeptide #status predicted <PRO>
 F; 648-885/Domain: inter-alpha-trypsin inhibitor heavy chain 3 #status experimental <M
 F; 87-576/Binding site: carboxyl-terminal propeptide #status predicted <CTP>
 F; 647/Modified site: chondroitin sulfate ester carboxyl end (Asp) (in mature form) #s

Query Match 3.3%; Score 185; DB 2; Length 885;
 Best Local Similarity 20.9%; Pred. No. 0.0035;
 Matches 137; Conservative 101; Mismatches 239; Indels 180; Gaps 34;

QY 27 FPSAVTIKSWDKQEDLVTLAKTAGSNQVLVDIYKYQDLYTVEPNNAQLVEIAARDI 86
 Db 97 YPGNVKEVAKQYKAVSQGTAG-----LVKASGRKL 131
 QY 87 EKLLSNRSKAL---VSLALEAEKVAQAAHQWREDFASNEVYVYNAKDDLDPEKNDSEPGSQ 143
 Db 132 EKRTSVNVAAAGSKVTFELTYEELLKRHKGK-----YEMLYKVQPK-----Q 173
 QY 144 RIKPVTEDANFGQISYQAAHVHPTDIYEGSTIVLNELNWTSALDEVEFKKNREEDPSL 203
 Db 174 LVKHFIE-----VDIFEPOGI-----SMLD-----AEASFI 200
 QY 204 LMQVFGSA-----TGLARYYPASPWVDNSRT-PNKID-----LYDYRRRP----- 242
 Db 201 TNDLLGSALT KSFSGKKGHVSFKPSLDQORSCPTCTDLSLNGDFTTYDYNRESPGNVQI 260
 QY 243 ---WYI-----QG-AASPRDMLLVDSVSGVSGITLKLITSYSEMLETSDDDFVNVA 293
 Db 261 VNGFYVHFPAQGLPVVPKNAFVIDISGSMAGRKLEQTKAALLRIELEDQEDYLNFI 320
 QY 294 FNSNAQDVSCF-GHLVQAVNRNKKVLKDAVNNTAKGIDYKGFSAFQQLNLYNSR- 351
 Db 321 FSG---DVSTWKEHLVQAPENLQEAFTVKSMEDKGMTINDGLRGISML---NKARE 374
 QY 352 -----ANCKNIIMFLTDG-----GEERAQEIFNKYNK--DKKVVFRFVSQGHYERGIQ 400
 Db 375 EHRIPERSTSVIMLTLDGANVANVSPEKIQENVRNAIGKFFLYNLGFG--NNLNYNFLE 433
 QY 401 WMAENKGYIYEPSIGAIRINQVEYLDVLRPWLVLGADKAKQOVNTNYVLDALD----- 455
 Db 434 NMALENHGFAIRIYEDSDADLQGFYEAVANPL-LTGVEMEYPE--NAILDLTQNTYQH 490
 QY 456 ----LGLVITGTLPVFNITQGFEKNKNLK-----NOLILGVMGVDYSLDIKRLTPRFTL 506
 Db 491 FVDGSEIVVAGRL-VDEDNNSF--KADVKGHGATNDL---TFTEFVDMKEMEK-----AL 539
 QY 507 CPNGYYFAIDPN-----GYVLLHPNLQPK---NPKSQEPVTLDFDAELENDIKVEIRN 557

Db 540 QERDYIFG---NYIERLWAYLTIEQLLEKRNNAHGEERENLTARALDLSLKYHFVTPPLTS 596
QY 558 KMIDGESGKTRTLVKSDERYI--DKGNRIYTTWTPVN-GTDYSALVLPLPSFYI 612
Db 597 MVTKPE-----DNEDEIRAIAKPGCEADAEATPVSPAMSYLTSYQPPQNPYYIV 644

RESULT 10
JC5576
Inter-alpha-trypsin inhibitor heavy chain 3 - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 17-Mar-1999
C:Accession: JC5576; PC4486
R:Nakatani, T.; Suzuki, Y.; Yamamoto, T.; Sinochara, H.
J. Biochem. 122, 71-82, 1997
A:Title: Molecular cloning and sequencing of cDNAs encoding three heavy-chain precursors
sin inhibitor heavy chain family.
A:Reference number: JC5574; MUID:97420688
A:Accession: JC5576
A:Molecule type: mRNA
A:Residues: 1-869 <NA>
A:Cross-references: DDBJ:D89287
A:Experimental source: liver
A:Accession: PC4486
A:Molecule type: protein
A:Residues: 34-53,449-475;509-526 <NA2>
C:Comment: In the plasma three inter-alpha-trypsin inhibitor heavy chains 1, 2 and 3 were
that the complexes play important role for pancreatic cancer.
C:Superfamily: inter-alpha-trypsin inhibitor complex component II
F:236-239,664-865/Disulfide bonds: #status predicted

Query Match 2.9%; Score 164.5; DB 2; Length 889;
Best Local Similarity 23.2%; Pred. No. 0.061;
Matches 66; Conservative 56; Mismatches 112; Indels 51; Gaps 11;

QY 202 SLLWVFGSATGLARYIPASPVDSRT--PNKID-----LYDVRRL-PWYIOGA-- 248
Db 211 SALTFSFGKKGHVSEKPS--LDQRSCTCTDLSLLNGDFIVDVNRSPGVQVYNG 267
QY 249 -----ASPKDMILVDVSGVSGSLTKLRTSVSEMLETSLDSDDFVNVASFNS 296
Db 268 YFVHFAPQGLPWPKNIVFVVDISGMAGRIQOTRVALLKILDDMKQDDYLNFLFST 327
QY 297 NQDVSCFQHLVQANVRNKKVLKDVANNITAKITDYKGFSAFEQLLN-----YNSRA 352
Db 328 GV--TTWKDSLQVATPANLEEARFVRSISDQGMNTINDGLLRGINMLTDAREQHTVPER 385
QY 353 NCNKIIMLFTDG---GEERAQEIFNKNKRVFRFSVG-QHNYERGPQWMAACENK 407
Db 386 STSIIML-TDGDANTGESRPEKIQENVRKAIEGRPLYNLNGFNMLNFTLEWALENH 444
QY 408 GYVEIPSIGAIRINTEYLDVIGRPWVLGDKAKOVQNTVYLD 452
Db 445 GVARRIYSDANLQIGFVEEVANELL-----TNVEVE 478

RESULT 11
T28155
variant-specific surface protein 1 - malaria parasite (Plasmodium falciparum) (fragments
N:Alternate names: erythrocyte membrane binding protein 1 (EMPI)
C:Species: Plasmodium falciparum
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C:Accession: T28155
R:Rowe, J.A.; Moulds, J.M.; Newbold, C.I.; Miller, L.H.
Nature 388, 292-295, 1997
A:Title: Plasmodium falciparum rosetting is mediated by PfEMP1 and requires complement
A:Reference number: Z20477; MUID:97373957
A:Accession: T28155
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-2706 <ROW>
A:Cross-references: EMBL:Y13402; PIDN:CAA73831.1

A:Experimental source: strain IT 4/25/5
C:Genetics:
A:Introns: 2493/3
A:Note: R29R+var1

Query Match 2.9%; Score 161; DB 2; Length 2706;
Best Local Similarity 18.2%; Pred. No. 0.57;
Matches 183; Conservative 137; Mismatches 345; Indels 338; Gaps 46;

QY 36 WDKMQEDLVTLAKTASGVNLVDIYKQDLYTVEPNNA-----RQL 78
Db 308 WFDEWAEFCRIRKI-----KLENVKKECRD-----EPNNKYCSGDGDCRKYTLKDNITF 358
QY 79 VEIARDEKLLSNRSKALVSLAEAKVQAAHOREDFASNEVYVYNAKDDLDPEKNS 138
Db 359 IDLNCPCRCNACSNYTK-----WIEQRKQFDKQRK--YMEI---KIKTWNINNDK 408
QY 139 E-----PGSORIKPVFIEDANFGRQISYQAAVHIPTDIYEGSTIVLNLNMTSALDE 191
Db 409 EYENLDKKGYSTIN-TFLESLNHGKQCQ-----DN 438
QY 192 VFKNREEDPSLLWQVFGSATGLARYIPASP-----WDNSRTPNKI 233
Db 439 IDKKNKTNFKNL-ETFGP-----SGYCEACPIYGVKCSNEKCTPVTEWNSNNRLPTDT 493
QY 234 DLYDVRPWPYIOGAASPKDMILLDVSGVSGSLTKLRTSVSEMLETSLDSDDFVNVAS 293
Db 494 STKNLN-----ATNIDMLVNDGIGNAI----- 515
QY 294 FNSNAQDVSCFQHLVQANVRNKK-----VLKDVANNITAKITDYKGFSAFEQLL 345
Db 516 --DNELEKCTKYGLKKGKQKQWCOYLNNIDQCKINNVMNSGYFDNKIAFNVLFRWL 573
QY 346 NYNVRANCKNIIMLTGDEERAQEIFNKNKDKKRVFRFSVGOHNTYERGPQWMAE 405
Db 574 RYFVRDHRNLK-----EKIDVCIKKENINENICIKCKTN-----CE 610
QY 406 NKGYVEIPSIGAIRI---NTQEVLDVIGRPWVLGDKAKOVQNTVYLDALGLVIT 461
Db 611 CVGKLEKEAEWDKINQHYNOKNHNIFLIPIWYNGFYEK-ITFPNDFKALE-----DV 665
QY 462 GLPVENITGPFENKTLNKLQILGVMGVDVSLDEDIKRLTPRTLCPNGYIFAIDPNGVY 521
Db 666 DFINVLDLTKECQD-THCKIEKIRSI-DVDLIKEIISLWQNKIEVCKS--HHDEKHEYC 721
QY 522 LHPLNLQPNKPSQEPVTLDFLDAELENDIKVEIRKNKMDIGESGEXT-----FRT 571
Db 722 C---DILPKSVDDDEDD--EYDDEKEESSQTTKRN--ISQKGTKSASCVKGACAIVKG 775
QY 572 LVKSQDERVID---KGNRTYTW---TPVNGTD-----YSLALVLPYFS 609
Db 776 VLOQKNGSIDNCNAKRNKNNEWQCDKNTFVDGNEGVCMPPRKSKICINHLTLEEQTKK 835
QY 610 Y-----YIKAKLEET-ITOQSRKKGKMKDSETLK-----PDNFEE-SGYTFIAPRDYC--N 656
Db 836 YQIREAFIKCAAKETNLWDKYKNDKNEAEELLKKGKIPEDFMRINFTYFGDFRDCLEN 895
QY 657 DL-----KTSNNTEPLNFNEFIDRK-----TPNPFSC-NADLINRVLLDAGTNNEL 703
Db 896 DMGKDVKDKVKNKINLVFNNSKRGPKKIDPNWNNWNGPQIWNGLCALIHADTKDSIKN 955
QY 704 VQNY-----W-----SKOKNIKGVKARFVV 723
Db 956 KONYKYEKVTILAKRDGSGNGMTLSEFAKPKFLRWVEMTDDYCKERQKRVTEVASTCKS 1015
QY 724 TDGGITRV-----YKPEAGENWQENPETEYDSFYKRSLDN-----DNVYV- 762
Db 1016 IDGGQLKCDRCGCKNCKDEYKKNRKKKEEWNLDQKYKDKRENKIDKGPIGIIVKDYVL 1075
QY 763 -----FTAPYKNSGPGAYESGIMVSKAVETIYOGKLLKPAVGIKIDVNSWI-- 810
Db 1076 ANAKYELKKKFTASCVTSSGKAQNSATEEVYKKNIELLEEYQ-----YDADQYCGC 1126

Qy	71	EPNNAROLVIAIARDIEKLLSNRSKALVSLAEAEKVQAAHWRDEFASNEVVYVYNAKD	130
Db	22	OPENKESQOQPSTPTTEQVLAQAQAIAK---EAEQSAAA---AKALAQEQVOYSDDKQA	75
Qy	131	LDPEKND-----SEPSQRKPKVFIEDANFGROISVQHAA---VHIPTDOI	172
Db	76	LOGRLQEAPTFARAAKAKATHIANPGTARYQQF---DDNPVKQVQACNPATFSLDVTGJS	132
Qy	173	YEGSTIVLNE-----LNNWTSALDEVFVKKNEEDPSLLWQVFGSATGLARY	218
Db	133	YANVRRLNGGLPPDPAVNRVEIVYFSPDWDI---KDKQSIAPSKPIPFAMRYELA---	187
Qy	219	PASPVWDNSRTPNKIDLYDVRRRPWTIQGAASPKMDLILVDVSGS-VSGLTKLIRTSVS	277
Db	188	PA-PW-NEQRTLKVLDILAKDRKSEELPAS-----NLVFLIDTSGSMISDERPLQISSUK	241
Qy	278	EMLETISDDDFVNVASFNSNAQDVSCFOHLVQAVNRNKKVLDKANVNIIPAKGITYDKKG	337
Db	242	LLYKVELREQDNIAIVYAGDSRTA-----LPSISGSHKAEIINADISLDAEGSTNGGAGL	296
Qy	338	SFAFEQLLNNVSRANCKIIMLFTDQ-----GEBRAQOEIPFNKYNKKKVRVFRFSVQG	391
Db	297	ELAYOATK-GFTKGGINR-ILLATQGDENVGIDDPKSTESVMKKORSGVTLSTFGVGN	354

QY 278 EMLTSLDDDFVNVASFNSAQDVSCFQHLVQANVRNKKVLKDAVNNITAK---GITDYK 334
Db 1366 ELIENI-----LSKLNIEDNKII---LNNHTINEYGDINESN 1399
QY 335 KGFSAFAEQLLNKN-----VSR-----NCKNIIMLETD-----GGEERAQ 370
Db 1400 RFLSLTFFSILEDINIIEIDLVSKYKILLSCNMKLIENSDDIOQKIDHIGFNGEHQKY 1459
QY 371 E1FN-----KYN-----KDKYVFRFVSQOHNYERGPQIWMACENKGYEIPISGAIR 420
Db 1460 IPYSYIDNETKNGFTDYSKRGLTABESNEIIRN--IYMPDSNNLFIYSSKDLKDIR 1517
QY 421 INTQEVLDVLRPMVLGAKAQ-----VQWTVYVLDALGLGLVITGTLP 465
Db 1518 IINK-----GDVKLLIGNFKDDMKVLSFTIEDNTIKLNGVYLDE-----NGVAQ 1564
QY 466 VENITQFENKTNLKNQILGVMGVDVSLEDIKRLTPRETLCPNGCYFFAIDPNGYVLLHP 525
Db 1565 ILKFMNNAKSALNTSNLMFLESINIK-----NIFYNNLOPNIETILT 1609
QY 526 NLOPKNPKSQEPVTLDFDLAELENDIKVEIRNKMIDGSEGEKTFRTLVKSOQDERVIDKGN 585
Db 1610 NF-----IISGNSISQOFE-LICDKDN-----1631
QY 586 RYTWTPVNGTDSIALVLPYTSFYIYKAKLEETITQARSKKGMKMDSETLKPDPNFESG 645
Db 1632 -----IQP-----YFINFKIKET-----SYTLVGNRQN--1655
QY 646 YTEIAPRDCYNDLKISDNTEFLNFNE---FIDR---KTPNPNPCNADLIN-----691
Db 1656 -LIVEPSYHLDD---SGNISVTINFSOKLYGIDRYVKNVYIAPNLTYDEINITPVYKP 1711
QY 692 -----RVLLDAGTNE-----LYQNTW-----SKOKNIGVKARFVVT 724
Db 1712 NYICEVILLDANYINEKINYNINDLSIRYVNDNGSDLIILIANSEEDNQPVKIRFV--1769
QY 725 DGGITRYVPKEAGE-----NWOENPE-----TYEDSFYKR-----SLDNDNY 761
Db 1770 -----NVFKSDTAADKLSFNSDRQDVSVSKIIISTFSLAAYSDGFFDYEFGLVSLDND--1822
QY 762 VFTAPYFNKSGPGAYESGIMYSKAVEIYIOGKL--LKPAVVGKIDVNSWIENFTKTSIR 819
Db 1823 -----YFINSFGNNVSGL-----IYINDSLYFKP-----PKNNLITGFTTI---1860
QY 820 DPCAGPVCCKRNSDVMDCVILDDGFFLMAHDDYTNOIGRFFGEIDPCLMRHLVNISV 879
Db 1861 -----DGN-----KYFDPKSGAASIGET-----TIDGKD 1886
QY 880 YAFNKSVDYQSVCEPAGPQAGHRSAVPSVADIIQIGWATAAAWSILQQFLLSLTF 939
Db 1887 YIFN-----RQG-----ILQVGVINSDG---LKYFAPAGTL 1915
QY 940 PRLEAVEEME-----DDFTASLSKQSCITEQTQYFFFDNDSKFSGVLDG 985
Db 1916 DENLEGESVNFIGNKINDGKIYFEDNYRAAV-EWKLLDDDETYFNFKGTGALKGLHQIG 1974
QY 986 NCSRIHFHGEKLMNTNLIFI 1004
Db 1975 DNKYFDDNGIMQTGFITI 1993

Search completed: July 23, 2001, 07:38:34
Job time: 531 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 23, 2001, 07:48:25 ; Search time 66.28 seconds
(without alignments)

549.390 Million cell updates/sec

Title: US-09-397-548-17

Perfect score: 5599

Sequence: 1

MAAGCLLALTLTFLFSLIG.....PDVCFDNNVLEDTDCGGVS 1063

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5599	100.0	1091	1	CIC2_HUMAN
2	5390	96.3	1091	2	CIC2_RAT
3	5380.5	96.1	1106	1	CIC2_RABIT
4	607	10.8	734	1	UN36_CAEEL
5	194.5	3.5	886	1	ITH3_MOUSE
6	182	3.3	885	1	ITH3_HUMAN
7	180.5	3.2	887	1	ITH3_RAT
8	164.5	2.9	886	1	ITH3_MESAU
9	161	2.9	1829	1	DPOL_THEST
10	159	2.8	1956	1	ATX1_PLAFA
11	157.5	2.8	575	1	YFBK_ECOLI
12	154.5	2.8	946	1	ITH2_HUMAN
13	152	2.7	1290	1	BXC1_CLOBO
14	151.5	2.7	420	1	Y103_SNY3
15	150.5	2.7	921	1	ITH4_PIG
16	150	2.7	854	1	MCPC_BACSU
17	149	2.7	930	1	ITH4_HUMAN
18	148	2.6	964	1	DPOL_CBEV
19	144	2.6	1087	1	YXN3_CLOTM
20	143	2.6	946	1	ITH2_MESAU
21	142.5	2.5	382	1	YLJ0_CAEEL
22	141	2.5	1251	1	RBP2_PLAAB
23	140.5	2.5	935	1	ITH2_PIG
24	140	2.5	2710	1	TOXA_CLODI
25	140	2.5	3305	1	APLP_MANSE
26	139.5	2.5	764	1	PAG_BACAN
27	139	2.5	1513	1	STUL_YEAST
28	138	2.5	1180	1	C4AA_BACTI
29	137	2.4	984	1	HYSA_STRAG
30	136.5	2.4	3063	1	CAIC_HUMAN
31	135.5	2.4	946	1	ITH2_MOUSE
32	134.5	2.4	2077	1	TEGU_HSV6U
33	133	2.4	862	1	MUTS_BORBU

34	133	2.4	1323	1	ADRI_YEAST	P07248	saccharomyc
35	132.5	2.4	547	1	SYM_BUCAI	P57210	buchnera ap
36	132.5	2.4	929	1	CA1C_NOTVI	O91145	notophthalm
37	132.5	2.4	1679	1	YIO9_YEAST	P40457	saccharomyc
38	132	2.4	697	1	YE9C_SCHPO	O13773	schizosacch
39	131.5	2.3	1018	1	YC14_METJA	Q38611	methanococc
40	131	2.3	1634	1	DPOL_METJA	Q58295	methanococc
41	131	2.3	1658	1	YM67_YEAST	Q03661	saccharomyc
42	130.5	2.3	987	1	YD94_METJA	Q38789	methanococc
43	129	2.3	1244	1	X307_MYCPN	P75342	mycoplasma
44	128.5	2.3	1254	1	UBPC_YEAST	P39538	saccharomyc
45	128	2.3	1113	1	Y140_MYCPN	P75033	mycoplasma

ALIGNMENTS

RESULT 1							
CIC2_HUMAN							
ID	CIC2_HUMAN	STANDARD;	PRT;	1091 AA.			
AC	P54289;						
DT	01-OCT-1996 (Rel. 34, Created)						
DT	01-OCT-1996 (Rel. 34, Last sequence update)						
DT	01-OCT-2000 (Rel. 40, Last annotation update)						
DE	DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-2/DELTA SUBUNIT PRECURSOR.						
GN	CACNA2D1 OR CACNL2A OR CCHL2A.						
OS	Homo sapiens (Human).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.						
OX	NCBI_TaxID=9606;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RX	MEDLINE=92110010; Pubmed=1309651;						
RA	Williams M.E., Feldman D.H., McCue A.F., Brenner R.,						
RA	Valicielebi G., Ellis S.B., Harpold M.M.;						
RT	"Structure and functional expression of alpha 1, alpha 2, and beta subunits of a novel human neuronal calcium channel subtype.";						
RL	Neuron 8:71-84(1992).						
CC	-1- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN EXCITATION-CONTRACTION COUPLING.						
CC	-1- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS: ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS HETERODIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).						
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.						
CC	-1- TISSUE SPECIFICITY: CENTRAL NERVOUS SYSTEM, SKELETAL MUSCLE AND AORTA TISSUES.						
CC	-1- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM A PRECURSOR FORM (BY SIMILARITY).						
CC	-1- SIMILARITY: TO OTHER SPECIES ALPHA-2 SUBUNIT.						
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).						
CC	EMBL: M76559; AAA51903.1; -						
DR	MTM; 114204; -						
DR	InterPro; IPR002035; -						
DR	Pfam; PF00092; vwa; 1.						
DR	PROSITE; PS0234; VWFA DOMAIN; 1.						
KW	Ionic channel; Transmembrane; Ion transport; Voltage-gated channel; Calcium channel; Glycoprotein; Phosphorylation; Signal.						
FT	SIGNAL 1 24 POTENTIAL.						
FT	CHAIN 25 944 L-TYPE CALCIUM CHANNEL ALPHA-2 SUBUNIT (BY SIMILARITY).						
FT	CHAIN 945 1091 L-TYPE CALCIUM CHANNEL DELTA SUBUNIT (BY SIMILARITY).						
FT	TRANSMEM 446 469 POTENTIAL.						
FT	TRANSMEM 906 930 POTENTIAL.						


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FT TRANSMEM 1067 1086 POTENTIAL.
FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 324 324 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 348 348 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 475 475 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 585 585 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 594 594 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 663 663 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 769 769 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 876 876 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 883 883 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 973 973 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 986 986 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 501 501 PHOSPHORYLATION (BY CAPK)
FT FT (BY SIMILARITY).
FT MOD_RES 833 833 PHOSPHORYLATION (BY CAPK)
FT FT (BY SIMILARITY).
FT SEQUENCE 1091 AA; 123183 MW; 284E13EE29A47837 CRC64;

Query Match 100.0%; Score 5599; DB 1; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLTFLQSLIGSPSEPPSAVTKSWVDKMQEDLVTLAKTASGVNQLVDI 60
DB 1 MAAGCLLALTLTFLQSLIGSPSEPPSAVTKSWVDKMQEDLVTLAKTASGVNQLVDI 60
QY 61 YEKQDLYTVEPNARQLVEAARDIEKLSNRKALVSLALEAEKVQAAHQWREDFASN 120
DB 61 YEKQDLYTVEPNARQLVEAARDIEKLSNRKALVSLALEAEKVQAAHQWREDFASN 120
QY 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRQISVQHAHVHPDIDYEGSTIVL 180
DB 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRQISVQHAHVHPDIDYEGSTIVL 180
QY 181 NELNWTGALDVFKNKREDDPSLWQVFGSATGLARYYPASPWVDNSRTPNKIDLYDVR 240
DB 181 NELNWTGALDVFKNKREDDPSLWQVFGSATGLARYYPASPWVDNSRTPNKIDLYDVR 240
QY 241 RPWYIQAASPKMLILVDVSGVSGTGLKIRTSVSEMLETLSDDDFVNVASFNSNAQD 300
DB 241 RPWYIQAASPKMLILVDVSGVSGTGLKIRTSVSEMLETLSDDDFVNVASFNSNAQD 300
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIIDYKKGFSFAFEQLLNYSRANCKIIML 360
DB 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIIDYKKGFSFAFEQLLNYSRANCKIIML 360
QY 361 FTDGEERAQEIFNKYNDKVKRVFRFSVGOHNYERGPQIWMACENKGYEIPSGAIR 420
DB 361 FTDGEERAQEIFNKYNDKVKRVFRFSVGOHNYERGPQIWMACENKGYEIPSGAIR 420
QY 421 INTOEYLDVLRPMVLGDKAKQVQWNVYLDLELGLVITGLTPVNTGQFENKTNLK 480
DB 421 INTOEYLDVLRPMVLGDKAKQVQWNVYLDLELGLVITGLTPVNTGQFENKTNLK 480
QY 481 NQLILGVMGVDSLEIDKRLPRTFLCPNGYFFAIDPNGYVLLHPNLQPNKPSQEPVTL 540
DB 481 NQLILGVMGVDSLEIDKRLPRTFLCPNGYFFAIDPNGYVLLHPNLQPNKPSQEPVTL 540
QY 541 DFLDALENDIKVEIRNMIDGSEKTFRLVKSQDERYIDKGNRYTWTVPVNGTDYSL 600
DB 541 DFLDALENDIKVEIRNMIDGSEKTFRLVKSQDERYIDKGNRYTWTVPVNGTDYSL 600
QY 601 ALVLPYTFYIKAKLETITQAKSKGKMDSETLPKDPNFEESGYTFIAPRDCNDLKI 660
DB 601 ALVLPYTFYIKAKLETITQAKSKGKMDSETLPKDPNFEESGYTFIAPRDCNDLKI 660
QY 661 SDNNTFLLNFEIDRKTNNPCNADLINRVLLDAGFTNELVQNYWSKQNKIKGYKAR 720
DB 661 SDNNTFLLNFEIDRKTNNPCNADLINRVLLDAGFTNELVQNYWSKQNKIKGYKAR 720
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DB 661 SDNNTFLLNFEIDRKTNNPCNADLINRVLLDAGFTNELVQNYWSKQNKIKGYKAR 720
QY 721 FVYTDGGITRVYPKEAGENQENPETVEDSFYKRSNDNDNVFTAPYFNKSGPGAYESGI 780
DB 721 FVYTDGGITRVYPKEAGENQENPETVEDSFYKRSNDNDNVFTAPYFNKSGPGAYESGI 780
QY 781 MVSKAIVEIYIQQKLLPAVVGIKIDVNSWIENFTKTSIRDPCAGPVCDCRNSDVMDCVI 840
DB 781 MVSKAIVEIYIQQKLLPAVVGIKIDVNSWIENFTKTSIRDPCAGPVCDCRNSDVMDCVI 840
QY 841 LDGGGFLMANHDDYTNQIGRFGEDIDPSLMRHLVNLVSVAFNKSYDYSVCEPGAAPKQ 900
DB 841 LDGGGFLMANHDDYTNQIGRFGEDIDPSLMRHLVNLVSVAFNKSYDYSVCEPGAAPKQ 900
QY 901 GAGHSRAYSVSADILQIGWATAAASILQOFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960
DB 901 GAGHSRAYSVSADILQIGWATAAASILQOFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960
QY 961 SCITEQTYFFDNDKDSFSGVLDGCGNSRIFHGKLMNTNLIIFIMVESKGTGCPDTRLI 1020
DB 961 SCITEQTYFFDNDKDSFSGVLDGCGNSRIFHGKLMNTNLIIFIMVESKGTGCPDTRLI 1020
QY 1021 QAGQTSQGNPCDMVKQPRYRKGPVDFCNVLEDDYTDGCGVS 1063
DB 1021 QAGQTSQGNPCDMVKQPRYRKGPVDFCNVLEDDYTDGCGVS 1063

RESULT 2
CIC2_RAT
ID CIC2_RAT STANDARD; PRT; 1091 AA.
AC P54290;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-2/DELTA
DE SUBUNITS PRECURSOR.
GN CACNA2D1 OR CACNL2A OR CCHL2A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=9228762; PubMed=1314383;
RX Kim H. L., Kim H., Lee P., King R. G., Chin H.;
RT "Rat brain expresses an alternatively spliced form of the
RL dihydropyridine-sensitive L-type calcium channel alpha 2 subunit.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:3251-3255(1992).
CC -1- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN
CC EXCITATION-CONTRACTION COUPLING.
CC -1- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:
CC ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS
CC HETERODIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM
CC A PRECURSOR FORM (BY SIMILARITY).
CC -1- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.
CC -----
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CC -----
CC ENBL: M85621; AAA41088.1;
CC InterPro: IPR002035;
CC Pfam: PF00092; vwa; 1.
CC PROSITE: PS50234; VWFA_DOMAIN; 1.
CC Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW
```

KW Calcium channel; Glycoprotein; Phosphorylation; Signal;
KW Alternative splicing.

FT SIGNAL 1 24
FT CHAIN 25 944
FT
FT
FT CHAIN 945 1091
FT
FT
FT TRANSMEM 445 468
FT TRANSMEM 906 930
FT TRANSMEM 1067 1086
FT CARBOHYD 92 92
FT CARBOHYD 136 136
FT CARBOHYD 184 184
FT CARBOHYD 323 323
FT CARBOHYD 347 347
FT CARBOHYD 474 474
FT CARBOHYD 584 584
FT CARBOHYD 593 593
FT CARBOHYD 663 663
FT CARBOHYD 769 769
FT CARBOHYD 812 812
FT CARBOHYD 876 876
FT CARBOHYD 883 883
FT CARBOHYD 973 973
FT CARBOHYD 986 986
FT MOD_RES 500 500
FT
FT MOD_RES 833 833
FT
FT SEQUENCE 1091 AA; 123822 MW; 70549079D343B34 CRC64;

Query Match 96.3%; Score 5390; DB 1; Length 1091;
Best Local Similarity 95.8%; Pred. No. 1.7e-302;
Matches 1019; Conservative 24; Mismatches 19; Indels 2; Gaps 2;

QY 1 MAAGCLLALTLTQSLIGPSEEPSPSAVTKSWDKMQEDLVTLAKTASGVNQLVDI 60
DB 1 MAAGCLLALTLTQSLIGPSEEPSPSAVTKSWDKMQEDLVTLAKTASGVNQLVDI 60
QY 61 YEKYQDLYTVEPNNAQVLEIARDTEKLSNRSKALYSALAEAKVQAQAHQREDFASN 120
DB 61 YEKYQDLYTVEPNNAQVLEIARDTEKLSNRSKALYSALAEAKVQAQAHQREDFASN 120
QY 121 EVVYNAKDDLPDEKNDSEPGSQRIKPVFTEDANFGQISOYQAAVHIPDIDEGSTIVL 180
DB 121 EVVYNAKDDLPDEKNDSEPGSQRIKPVFTEDANFGQISOYQAAVHIPDIDEGSTIVL 180
QY 181 NELNWTSALEVEPKKNEEDPSLLQVFGSATGLARYYPASPWWNSRTPNKIDLYDVR 240
DB 181 NELNWTSALEVEPKKNEEDPSLLQVFGSATGLARYYPASPWWNSRTPNKIDLYDVR 240
QY 241 RPNYIOGAASPKDMLILVDYSGVSGTLKLIKTSVSEMLETISDDDFVNVASFNSNAQD 300
DB 240 RPNYIOGAASPKDMLILVDYSGVSGTLKLIKTSVSEMLETISDDDFVNVASFNSNAQD 300
QY 301 VSCFQHLVQANVKNKVLDAVNNITAKGITYDKKGFSAFQELLNYSRANCNKIIML 360
DB 300 VSCFQHLVQANVKNKVLDAVNNITAKGITYDKKGFSAFQELLNYSRANCNKIIML 360
QY 361 FTGGEERAQEIFKNYKOKKVRFRFSVGQHNRYERGPIQWMAACENKGYIYIPSGAIR 420
DB 360 FTGGEERAQEIFKNYKOKKVRFRFSVGQHNRYERGPIQWMAACENKGYIYIPSGAIR 420
QY 421 INTQEYLDVLRPMVLGADKAKQVQNTNLYDLAELGLVITGLPVENITGQFENKTNLK 480
DB 420 INTQEYLDVLRPMVLGADKAKQVQNTNLYDLAELGLVITGLPVENITGQFENKTNLK 480
QY 481 NQILGVMGVDSLEIDIKRLTPFTLCPCNGYIFAIDPQNGVLLHPNLPKNPKSOEPVTL 540
DB 480 NQILGVMGVDSLEIDIKRLTPFTLCPCNGYIFAIDPQNGVLLHPNLPKNPKSOEPVTL 540
QY 541 DFLDAELENDIKVEIRNKMIDGESGKFTFLVKSQDERYIDKGNRTYTWTPVNGTDYS- 599

DB 540 DFLDAELENDIKVEIRNKMIDGESGKFTFLVKSQDERYIDKGNRTYTWTPVNGTDYR 599
QY 600 LALVLPYSYIYKAKLEETITQARSKKGMKDSKSETLKPONFESGYTFTAPRYCNDLK 659
DB 600 LALVLPYSYIYKAKLEETITQARSKKGMKDSKSETLKPONFESGYTFTAPRYCNDLK 659
QY 660 ISDNTEFLNFEFIDRKTPNNPSCNADLINRVLLDAGFTNVLQVWSKQKNKGVKA 719
DB 660 PSNTEFLNFEFIDRKTPNNPSCNADLINRVLLDAGFTNVLQVWSKQKNKGVKA 719
QY 720 RFVVTGDIIRVYPKEAGENQENPETEYDSFYKRSLDNDNVPYTFAPYFNKSGPAYESG 779
DB 720 RFVVTGDIIRVYPKEAGENQENPETEYDSFYKRSLDNDNVPYTFAPYFNKSGPAYESG 779
QY 780 IMYSKAVEIYIQGLKLPVAVGKIDVNSWENFTKTSIRDPACAGPVCDCKRNSDVMDCV 839
DB 780 IMYSKAVEIYIQGLKLPVAVGKIDVNSWENFTKTSIRDPACAGPVCDCKRNSDVMDCV 839
QY 840 ILDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNSIYAFNKSIDYQSVCEPGAAPK 899
DB 840 ILDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNSIYAFNKSIDYQSVCEPGAAPK 899
QY 900 QGAGHRSAYVPSVADILQIGWATAAAWSILQFLLSLTTPRLLAEVMEDEDDFTASLSK 959
DB 900 QGAGHRSAYVPSITDILQIGWATAAAWSILQFLLSLTTPRLLAEVMEDEDDFTASLSK 959
QY 960 QSCITEQTVFFDNDSKSFVLDGNCGRIFHGCKLMNTNLFIMVESKGTCPDTRLL 1019
DB 960 QSCITEQTVFFDNDSKSFVLDGNCGRIFHGCKLMNTNLFIMVESKGTCPDTRLL 1019
QY 1020 IQAEQTSDEGNPCDMVKQPRYKGPVDFCNVLEDTDCGGVS 1063
DB 1020 MQAEQTSDEGNPCDMVKQPRYKGPVDFCNVLEDTDCGGVS 1063
RESULT 3
CIC2_RABIT STANDARD; PRT; 1106 AA.
AC P13806;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-2/DELTA
DE SUBUNITS PRECURSOR.
GN CACNA2D1 OR CACNL2A OR CCHL2A.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88336904; PubMed=2458626;
RA Ellis S.B., Williams M.E., Ways N.R., Brenner R., Sharp A.H.,
RA Leung A.T., Campbell K.P., McKenna E., Koch W.J., Rui A.,
RA Schwartz A., Harpold M.M.;
RT "Sequence and expression of mRNAs encoding the alpha 1 and alpha 2
RT subunits of a DHP-sensitive calcium channel.";
RL Science 241:1661-1664 (1988).
RN [2]
RP SEQUENCE OF 961-973.
RX MEDLINE=91131638; PubMed=1847144;
RA Jay S.D., Sharp A.H., Kahl S.D., Vedvick T.S., Harpold M.M.,
RA Campbell K.P.;
RT "Structural characterization of the dihydropyridine-sensitive calcium
RT channel alpha 2-subunit and the associated delta peptides.";
RL J. Biol. Chem. 266:3287-3293 (1991).
RN [3]
RP SEQUENCE OF 961-975; 992-1000 AND 1033-1050.
RX MEDLINE=90368635; PubMed=2168391;
RA de Jongh K.S., Warner C., Catterall W.A.;
RT "Subunits of purified calcium channels. Alpha 2 and delta are encoded
RT by the same gene.";

J. Biol. Chem. 265:14738-14741(1990).
 CC - FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN
 CC EXCITATION-CONTRACTION COUPLING.
 CC - SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:
 CC ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS
 CC HETERODIMERS THAT ARE DISULFIDE-LINKED.
 CC - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC - ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE
 CC SPLICING.
 CC - TISSUE SPECIFICITY: SKELETAL MUSCLE.
 CC - PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM
 CC A PRECURSOR FORM.
 CC - SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.
 CC
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 CC EMBL; M21948; AAA81562.1; -;
 DR PIR; S10579; CHRA2.
 DR InterPro; IPR002035; -;
 DR Pfam; PF00092; vwa; 1.
 DR PROSITE; PS0234; VWFA_DOMAIN; 1.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Calcium channel; Glycoprotein; Phosphorylation; Signal;
 KW Alternative splicing.
 FT SIGNAL 1 26
 FT CHAIN 27 960 L-TYPE CALCIUM CHANNEL ALPHA-2 SUBUNIT.
 FT CHAIN 961 1106 L-TYPE CALCIUM CHANNEL DELTA SUBUNIT.
 FT TRANSMEM 448 471 POTENTIAL.
 FT TRANSMEM 921 945 POTENTIAL.
 FT TRANSMEM 1082 1101 POTENTIAL.
 FT CARBOHYD 94 94 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 138 138 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 326 326 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 350 350 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 477 477 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 606 606 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 615 615 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 678 678 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 784 784 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 827 827 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 891 891 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 898 898 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 988 988 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1001 1001 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT MOD_RES 503 503 PHOSPHORYLATION (BY CAPK)
 FT MOD_RES 503 503 (POTENTIAL).
 FT MOD_RES 848 848 PHOSPHORYLATION (BY CAPK)
 FT MOD_RES 848 848 (POTENTIAL).
 FT SEQUENCE 1106 AA; 125042 MW; B00DE7F3C877B618 CRC64;
 Query Match 96.1%; Score 5380.5; DB 1; Length 1106;
 Best Local Similarity 94.8%; Pred. No. 6.2e-302;
 Matches 1029; Conservative 15; Mismatches 12; Indels 29; Gaps 4;
 QY 1 MAAGCULATLTLFQS--LLIGPSSEPPFSAVTTKSWVDKMQEDLVTLAKTASGVNQLV 58
 DB 1 MAAGRPRAWTLTQAWLLIGPSSEPPFSAVTTKSWVDKMQEDLVTLAKTASGVHQLV 60
 QY 59 DIYEKYDLYTVEPNNAQQLVETAAEDIEKLLSNRSKALVSLALEAEKVAQAAHQWREDA 118
 DB 61 DIYEKYDLYTVEPNNAQQLVETAAEDIEKLLSNRSKALVSLALEAEKVAQAAHQWREDA 120
 QY 119 SNEWVYNAKDDLDPEKNDSEPGSQRIKVFIEDANFRGQISQVHAHVHPTDIYEGSTI 178
 DB 121 SNEWVYNAKDDLDPEKNDSEPGSQRIKVFIEDANFRGQISQVHAHVHPTDIYEGSTI 180

QY 179 VLNELNMTSALDEVEFKKNEEDPSLLMQVFGSATGLARYYPASPMVDNSRTPNKIDLDYV 238
 DB 181 VLNELNMTSALDDVFKKNEEDPSLLMQVFGSATGLARYYPASPMVDNSRTPNKIDLDYV 240
 QY 239 RRRPWYIOGAASPKDMLILVDVSGSVSGTLTKLIRTSYSEMLETSSDDDFVNVASFNSA 298
 DB 241 RRRPWYIOGAASPKDMLILVDVSGSVSGTLTKLIRTSYSEMLETSSDDDFVNVASFNSA 300
 QY 299 QDVSCFQHLVQANVRNKKVLDANNITAKGTTDYKKKGFSAFECOLLNYSRANCNKII 358
 DB 301 QDVSCFQHLVQANVRNKKVLDANNITAKGTTDYKKKGFSAFECOLLNYSRANCNKII 360
 QY 359 MLFTDGGERAQEIFKNKDKKRVFRFSVQGHNYERGIQWACENKGYEYIPIPSIGA 418
 DB 361 MLFTDGGERAQEIFKNKDKKRVFRFSVQGHNYERGIQWACENKGYEYIPIPSIGA 420
 QY 419 IRTNQEYLDVLGRPMVLGAKQVQNTNVLDALEGLVITGLPVFNITGQFENKTN 478
 DB 421 IRTNQEYLDVLGRPMVLGAKQVQNTNVLDALEGLVITGLPVFNITGQFENKTN 480
 QY 479 LKNQLILGVMGVDVSLIEDIKRLTPRTLCPNGYEYFAIDPNGYVLLHPNLOPK----- 530
 DB 481 LKNQLILGVMGVDVSLIEDIKRLTPRTLCPNGYEYFAIDPNGYVLLHPNLOPKIGVPT 540
 QY 531 -----NPKSQEPVTLDFDAELENDIKVIRKNMIDGESGEKTFRLVKSQDER 579
 DB 541 INLRKRRNVQNPKSQEPVTLDFDAELENDIKVIRKNMIDGESGEKTFRLVKSQDER 600
 QY 580 YIDKGNRTYTTVPNGTDY-SLALVLPYTFYIYKAKLEETITQARSKGKMKDSETLKP 638
 DB 601 YIDKGNRTYTTVPNGTDYSSALVLPYTFYIYKAKLEETITQARY-----SETLKP 653
 QY 639 DNFEESGTTFTAPROYCNDLKISDNTEFLNFNEFIDRKTNNPNSCNADLINRVLLDAG 698
 DB 654 DNFEESGTTFTAPROYCNDLKISDNTEFLNFNEFIDRKTNNPNSCNADLINRVLLDAG 713
 QY 699 FTNELVQNVWSKQKNIKGVKARFVVDGGITRVYPKEAGENQENPETVEDSFYKRSLDN 758
 DB 714 FTNELVQNVWSKQKNIKGVKARFVVDGGITRVYPKEAGENQENPETVEDSFYKRSLDN 773
 QY 759 DNYVFTAPYFNKSGPAYESGIMVSKAVEIYIQGLKLPVAVGIIKIDVNSWIENFTKTSI 818
 DB 774 DNYVFTAPYFNKSGPAYESGIMVSKAVEIYIQGLKLPVAVGIIKIDVNSWIENFTKTSI 833
 QY 819 RDPGAGPVCDCRNSDVMDCVILDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI 878
 DB 834 RDPGAGPVCDCRNSDVMDCVILDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI 893
 QY 879 VYAFNKSVDYQSVCEPGAAPKOGAGHRSAYVPSVADILQIGWATAAAMSIIQQFLLSUT 938
 DB 894 VYAFNKSVDYQSVCEPGAAPKOGAGHRSAYVPSVADILQIGWATAAAMSIIQQFLLSUT 953
 QY 939 FPRLEAVEMEDDDFTASLSKQSCITEQTYFFDNDKSKFSGLVDCGNCGRIFHGEKLN 998
 DB 954 FPRLEAVEMEDDDFTASLSKQSCITEQTYFFDNDKSKFSGLVDCGNCGRIFHGEKLN 1013
 QY 999 TNLIFIMVESKTCPCDTRLLIQAQOTSDGPNPCDMVKOPRYRKGPVCFDNNVLDYTD 1058
 DB 1014 TNLIFIMVESKTCPCDTRLLIQAQOTSDGPNPCDMVKOPRYRKGPVCFDNNVLDYTD 1073
 QY 1059 CGGV 1063
 DB 1074 CGGV 1078
 RESULT 4
 UN36_CAEEL STANDARD; PRT; 734 AA.
 AC UN36_CAEEL
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)

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DR EMBL: X70393; CAA49843.1; -
DR MGD; MGI:96620; Ith3.
DR InterPro: IPR002035; -
DR Pfam: PF00092; wva; 1.
DR PROSITE: PS0234; WFA_DOMAIN; 1.
KW Serine protease inhibitor; Repeat; Signal; Multigene family;
KW Glycoprotein.
FT SIGNAL 1 18 POTENTIAL.
FT PROPEP 19 30 BY SIMILARITY.
FT CHAIN 31 646 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN
H3.
FT PROPEP 647 886 BY SIMILARITY.
FT DOMAIN 279 439 WFA.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 577 577 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT BINDING 646 646 CHONDROITIN 4-SULFATE, CROSS-LINK SITE
(BY SIMILARITY).
SQ SEQUENCE 886 AA; 98977 MW; 15955308C7F5030A CRC64;

Query Match 3.5%; Score 194.5; DB 1; Length 886;
Best Local Similarity 19.9%; Pred. No. 0.00089;
Matches 185; Conservative 138; Mismatches 347; Indels 261; Gaps 44;

QY 27 FPSAVTKSWDKMOEDVTLAKTAGSNQVLDVIEKYQDLYTYVEPNARQLVEIAARDI 86
DB 98 YGNVKEVAQKQYKAVSGKTG----LVKASGRKLEKFTVSVNVAAGSKVTFELTY 153
QY 87 EKLNSRSKALVSLALEAKYQAAHQWREDFASNEVYVYNAKDLDPEKNDSEPGSRIK 146
DB 154 EELL-KRNKGYEYLVKQPKQVLRHFEID-----AHIFEP-----Q 189
QY 147 PVFIEDANFGRIQSYQHAHVHPTDIYEGSTIVNELNWTSDALDEVFKKNEEDPSLLMQ 206
DB 130 GISMLDAE-----ASFITNDL-LGSALATKSF----- 214
QY 207 VEGSATGLARYPASPWNDSRT-PNKTD-----LYDVRREP-----WYI-- 245
DB 215 -----SGKKGHVSFKPSLDQQRSCPTCDLSLLNGDFTIVDVNRESPOVINGYFVHF 269
QY 246 ---QG-AASPDMILTVDSGVSGLTLKLTSTVSEMLETSLDSDDFNVASFNSAQDV 301
DB 270 FAPQGLPVVPANIVFIDVSGSMGRKIQOTREALKLLDQVKKEDDYLNFLFST---DV 326
QY 302 SCFQ-HLYQANVRNKKVLKDAVNNITAKGITDYKKGFSFAFEQLLNYSVRAN-----C 354
DB 327 TTKDKHLVQATPANLKEAKTEKFNHDSQSMNTINDGLLKGTEML---NKAREDHVTPERS 383
QY 355 NKIIMLFTDG-----GEERAQEIFKNYK--DKKVRVFFSVFSGHNYERGPQWNAENKG 408
DB 384 TSIIIMLTGDGANTGESPEKIQENVRNAIGKFFLYNLGFG--NNLNFNLETALENHG 442
QY 409 YYPEIPSGAIRINTQEVLDVLRGPMVLGAKAKQVQNTVYLDALGLL--VIITGLPV 466
DB 443 LARIYEDSANLQOGVEEVANPL-----TNEVEPEPNAIDLTRNSYPH 491
QY 467 FNITQFQENKLNKILGNGVGVDSLEDKRLTPFTCLPNGYFFAIDPNGYVLLHPN 526
DB 492 F-----YDG-----SEIVVAGRLVDRNMDN-----FKADVKGHGALN-- 523
QY 527 LQPKNPKSOEPTVDFLDAELENKIVKRNKMDGESGEK--FTRLVKQSDERYIDKG 584
DB 524 ----DLTETEEDVMEEMAALK-----EOGYIFGDYIERLWALYLTIEQLLEKRNKAG 572
QY 585 NRTYTWTPVNGVDYSLA--LVLPYTSFYIYAKLEETITQARSKGKMKDSET-----LK 637

DB 573 DEKENIT-AEALDLSLKYHFVPLTSMVTKPEDNEQTSIADNAGEFAFAETMTMSFLT 631
QY 638 PDNEESGYFIAPRDYCNLDKISDNNTELLNFEIDRKTNNPSCNADLINRVLLDA 697
DB 632 TQOSSQSPYIYV-----DGPFIHQI-----PGKNSICNIDEKP 668
QY 698 GFTNELQNTYWSKQKNIKVKAREVVDGTTIRYVPKEAGENWQENPETYBDSFYKRSLD 757
DB 669 GTVLRLIQD-----PVT--GIT-VTGQIIGD-----KRS-- 694
QY 758 NDNVFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVGKIKIDVNSWIENFTKTS 817
DB 695 NASRRTGKTIFYGKLGITNAWMDRFEVETTEKIILG-----TGAELSTFSLDVTVTQ 747
QY 818 IRDPCAGPVCDCKENSDVMDCVILDDG--GFLLMAN-----HDDVTNQIGRFFGEIDP 868
DB 748 -----TGLSVTINKKNNV--VSGDGLISFVIIHQVKKHPVHQDFLG-----FYVDS 795
QY 869 SLMRHLVNIISVYAFNKSYDQSV-CEFGAAP 898
DB 796 HRMSAQTHGLLGQFFQDFKVFGRFGSDP 826
RESULT 6
ITH3_HUMAN STANDARD; PRT; 885 AA.
AC Q06033; Q99085;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY
CHAIN H3) (SERUM-DERIVED HYALURONAN-ASSOCIATED PROTEIN) (SHAP).
GN ITH3
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93215656; PubMed=7681778;
RA Bourguignon J., Diarra-Mehrpour M., Thiberville L., Bost F.,
RA Sesboue R., Martin J.P.;
RT "Human pre-alpha-trypsin inhibitor-precursor heavy chain. cDNA and
RT deduced amino-acid sequence".
RL Eur. J. Biochem. 212:771-776(1993).
RN [2]
RP SEQUENCE OF 341-885 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89137072; PubMed=2465147;
RA Diarra-Mehrpour M., Bourguignon J., Sesboue R., Mattei M.-G.,
RA Passage E., Sallier J.P., Martin J.P.;
RT "Human plasma inter-alpha-trypsin inhibitor is encoded by four genes
RT on three chromosomes".
RL Eur. J. Biochem. 179:147-154(1989).
RN [3]
RP SEQUENCE OF 30-49; 463-477 AND 497-515.
RX MEDLINE=89380192; PubMed=2476436;
RA Enghild J.J., Thøgersen I.B., Pizzo S.V., Salvesen G.;
RT "Analysis of inter-alpha-trypsin inhibitor and a novel trypsin
RT inhibitor, pre-alpha-trypsin inhibitor, from human plasma".
RL J. Biol. Chem. 264:15975-15981(1989).
RN [4]
RP SEQUENCE OF 631-647, AND CROSS-LINKAGE SITE TO BIKUNIN.
RX MEDLINE=91093267; PubMed=1898736;
RA Enghild J.J., Salvesen G., Hefta S.A., Thøgersen I.B.,
RA Rutherford S., Pizzo S.V.;
RT "Chondroitin 4-sulfate covalently cross-links the chains of the
RT human blood protein pre-alpha-inhibitor".
RL J. Biol. Chem. 266:747-751(1991).
CC -!- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE

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CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES.
CC -1- SUBUNIT: I-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN.
CC BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2
CC AND BIKUNIN. INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND
CC BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.
CC -1- P-TM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
CC 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE.
CC -1- SIMILARITY: BELONGS TO THE ITH FAMILY.
CC -1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X67055; CAA47439.1; -
CC EMBL; X14690; CAA32821.1; -
CC MIN; 146650; -
CC InterPro: IPR002035; -
CC Pfam: PF00092; vwa; 1.
CC PROSITE; PS50234; VWFA_DOMAIN; 1.
CC Serine protease inhibitor; Repeat; Signal; Multigene family;
CC Glycoprotein.
CC SIGNAL 1 ? POTENTIAL.
CC PROPEP ? 30 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN
CC CHAIN 31 647 H3.
CC
CC PROPEP 648 885
CC DOMAIN 278 438 VWFA.
CC CARBOVD 87 87 N-LINKED (GLCNAC...) (POTENTIAL).
CC CARBOVD 576 576 N-LINKED (GLCNAC...) (POTENTIAL).
CC BINDING 647 647 CHONDROITIN 4-SULFATE, CROSS-LINK SITE.
CC CONFLICT 344 344 R -> K (IN REF. 2).
CC CONFLICT 357 357 N -> G (IN REF. 2).
CC CONFLICT 846 846 Q -> H (IN REF. 2).
CC SEQUENCE 885 AA; 99121 MW; BC63856F9F5E4A1B CRC64;
CC
CC Query Match 3.3%; Score 102; DB 1; Length 885;
CC Best Local Similarity 20.7%; Pred. No. 0.0046;
CC Matches 136; Conservative 102; Mismatches 239; Indels 180; Gaps 34;
CC
CC QY 27 FPSATIKSWDKMEDLTAKTASGVNQLVDIYEKYQDLTYVEPNARQLVEITAARDI 86
CC DB 97 YPGNYKEVAKKQYKAVSQGTAG-----LVKASGRKL 131
CC
CC QY 87 EXLLNSRKAL---YSLAEAEKQVAAHQRREDFASNEVVYVYNAKDDLDPEKNDSEPGSQ 143
CC DB 132 EKFTSVNVAAGSKVTFELTYEELLRKHGK-----YEMLYKQPK-----Q 173
CC
CC QY 144 RIKPFVIDANFGRIQSYOHAHVHIPTDIYEGSTIVLNELWTSALDEVFKNRDEPDL 203
CC DB 174 LVKHEFE-----VDIFEQGI-----SMLD-----AEASFI 200
CC
CC QY 204 LMQVFGSA-----TGLARYYPASPVWDSRT-PNKID-----LYDVRRP----- 242
CC DB 201 TNDLLGSALTFSFGKGVHFKPSLDQQRSCPTCTDSLLNGDFTITYDVNRESFGNVQI 260
CC
CC QY 243 ---WYI-----QG-AASPKDMLLDVDSGVSGLTLKLRTSVSEMLETLSDDDFVNVA 293
CC DB 261 VNGIFYVHFPAQGLPVVPKNAFAVIDISGMAGKLEQTKALLRLEDMKEEDYINFLI 320
CC
CC QY 294 FNSNAQDVSCF-OHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSAFEQLINNVSR- 351
CC DB 321 FSG---DVTWEHLVQAPENLQEARTFVKSMDKGMNINDGLRLGISM---NKARE 374
CC
CC QY 352 -----ANCNKIIMLFTDG-----GEERAQEIFNKYNK--DKKVRVFRFSVQGHNYERGPIQ 400
CC DB 1000
```

Mon Jul 23 08:36:42 2001

FT	PROPEP	648	887	BY SIMILARITY.	
FT	DOMAIN	282	442	WFVA.	
FT	CARBOHYD	91	91	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	580	580	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	BINDING	647	647	CHONDROITIN 4-SULFATE, CROSS-LINK SITE (BY SIMILARITY).	
FT	SEQUENCE	887 AA;	99097 MW;	3B9FOFF96D514096 CRC64;	
Query Match 3.2%; Score 180.5; DB 1; Length 887;					
Best Local Similarity 18.5%; Pred. No. 0.0056;					
Matches 173; Conservative 139; Mismatches 350; Indels 275; Gaps 39;					
QY	27	FTSAVTKISWDMQDLVTLAKTAGSVNQLVDIYEKYQDLYTVEPNNAQVLEIAARDI	86		
Db	101	YPGSVKEVAQKYEKAVSQGKTAG---LVKASGRKLEKFTSVNVAAAGSKVIFELTY	156		
QY	87	EKLLSNRSKALVSLALEAEKVAQAQWRED---FASNEVYVYNAKDDLDPEKNDEPGSQ	143		
Db	157	EELL-KRNRKGYEMYLKQPKQLVRHFEIDAHIPEQGISMLDA-----	199		
QY	144	RKPFVIEDANFGQISYCHAAVHIPTDIYEGSTIVLNELNMTSALDEVEFKKNREDDPSL	203		
Db	200	-----DASF-----ITNDL-LGSALTKEF-----	217		
QY	204	LMOVFGSATGLARYYPASPVDNSRT-PNKID-----LYDVRRRP-----WY	244		
Db	218	-----SGKKHVSFKPSLDOORSCPTCTDSLLNGDEFTIVDVNRESPGNVQIYNGYF	269		
QY	245	I-----QG-AASFMDLILVDVSGSVGLTKLIRYSVSEMLETLSDDDPFNVVASFNSNA	298		
Db	270	VHFAPQGLVPVFNIAFVIVDSGSGRKIQOTRALUKILDDMKEDLYNLFISTGV	329		
QY	299	QDVSCFQHLVQANRKNKVLKDAVNNTAKGIDYKKGFSFAFEQLNLYNVRAN----	353		
Db	330	--TWKDLVKAIPANLEEARAFVKNIORSMTNINDGLLRIEML--NKAREDLVPE	384		
QY	354	-CNKIIMLFTD---GEERAQEIFKNYKDKVYFRFSVG-OHNVERGPIOWMACENK	407		
Db	385	RSTSILVMTDGAQNTGESRPEKIQENVRNAIRGKFPYLNLFNGNUNYNFLESALENH	444		
QY	408	GYEIEPSGAIRINTEYLDVLRPMVLADGAKAQVQWNTNVLDALEGL--VITGTLF	465		
Db	445	GFARIYEDSDASLOLQGFVEEVANPLL-----TNVELEYENALDLTRNSYP	493		
QY	466	VENITGFENKTNLKNOLILGVMGVDSLEDIKRLTPFTLCPNGYFYFAIDPNGYVLLHP	525		
Db	494	HF-----YDG-----SEIVVAGRLVDRVDN-----FKADVKGHGALN-	526		
QY	526	NLOPKNPKSQBPVYLDLDALENDIKVEIRNKMIDGESKEKT-----RTLKVSODER	579		
Db	527	-----DLTFTTEEDMKEMDAALK-----EQGYIFGDYIERLWAYLTIEQLLEKRNAR	574		
QY	590	YIDKGNRTYTWTPNGTDYSLA--LVLPYTSFYIKAKLEETIQARSKKMKDSET--	635		
Db	575	GDEKENIT-----AAELSLSLKHYFVPLTSMWYTKPEDNEDQTAIAADKPGEEAISATA	629		
QY	636	-LKPDPNEESGYFTIAPRDYCNLDKISDNNTFFLLNF---NEFIDRKTTPNNPSCNADLIN	691		
Db	630	YLTQSQSHSPYVY-----DGDPHFIQVPGKNDTICFNIDKPKGVLSLIQ	677		
QY	692	RYLLDAGFTNELVQVNSKQNKIKGVKARFVVTGDTITRVYKPEAGENWQENPETYEDSF	751		
Db	678	DPVTGIATVGQII-----GEKGNNASSRTGKT-----	704		
QY	752	YKRLSDNDNVFTAPYFNKSGPGAYESIMVSKAVEIYIQGLLKPAVVGIKIDVNSWIE	811		
Db	705	-----YFKGLGTANAMDMFRIEVTTEKILGN-----GDALSTFSLWD	742		
QY	812	NFTKTSIRDPCAGPVCDCKRNSVDVMDVILDDG-GFLMAN-----HDDYTNQIGRF	862		
Db	743	TVTVTQ-----TGLSVTINRKNMV--VSFEDGISFVILVHQVKKHPVHQDFLG-----	790		

QY	863	FGEIDPSLMRLHVNISVYAFNKSVDYQSV-CEPGAAP	898		
Db	791	FYVDVSHRMSAQTHGLLQGFQFPDEFKVDYRPGSDP	827		
RESULT 8					
ITH3_MESAU		STANDARD;	PRT;	886 AA.	
ID	ITH3_MESAU				
AC	P97280;				
DT	15-JUL-1998 (Rel. 36, Created)				
DT	15-JUL-1998 (Rel. 36, Last sequence update)				
DT	01-OCT-2000 (Rel. 40, Last annotation update)				
DE	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3) (HC3).				
GN	ITIH3.				
OS	Mesocricetus auratus (Golden hamster).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;				
OC	Mesocricetus.				
OX	NCBI_TaxID=10036;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Liver;				
RX	MEDLINE=97420688; PubMed=9276673;				
RA	Nakatani T., Suzuki Y., Yamamoto T., Sinohara H.;				
RT	"Molecular cloning and sequencing of cDNAs encoding three heavy-chain precursors of the inter-alpha-trypsin inhibitor in Syrian hamster: implications for the evolution of the inter-alpha-trypsin inhibitor heavy chain family."				
RT	J. Biochem. 122:71-82(1997).				
RL	FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY SIMILARITY).				
CC	-!- SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN, BIKUNIN INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2 AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.				
CC	-!- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY SIMILARITY).				
CC	-!- SIMILARITY: BELONGS TO THE ITIH FAMILY.				
CC	-!- SIMILARITY: CONTAINS 1 WFVA DOMAIN				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
CC	EMBL: D89287; BAA13940.1; ..				
DR	InterPro: IPR002035; ..				
DR	Protein: PF00092; WVA; 1.				
DR	PROSITE: PS0234; WFVA_DOMAIN; 1.				
KW	Serine protease inhibitor; Repeat; Signal; Multigene family; Glycoprotein.				
FT	SIGNAL	1	18	POTENTIAL.	
FT	PROPEP	19	30	BY SIMILARITY.	
FT	CHAIN	31	646	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3.	
FT	PROPEP	647	886	BY SIMILARITY.	
FT	DOMAIN	279	439	WFVA.	
FT	CARBOHYD	88	88	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	577	577	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	BINDING	646	646	CHONDROITIN 4-SULFATE, CROSS-LINK SITE (BY SIMILARITY).	
FT	SEQUENCE	886 AA;	99018 MW;	AC0594C685257688 CRC64;	

Query Match 2.9%; Score 164.5; DB 1; Length 886;
Best Local Similarity 23.2%; Pred. No. 0.047;
Matches 66; Conservative 56; Mismatches 112; Indels 51; Gaps 11;

QY 202 SLLWVFGSATGARYYPASPDWNSRT-PNKID-----LYDVRP-PWYIQA-- 248
DB 208 SALTSGFGKKGHSFKS---LDQRSCPTCTDSSLNGDFTIVYDVNRSPGNVQVYNG 264
QY 249 -----ASPKDMLILVDVSGVSGTLKLRISVSSEMLETSLDDDFVNVASFNS 296
DB 265 YVHFFAFOGLPVVPEKIVFVIDISSMAGRKIQOTRVALLKILDDMKQDDYLNILFST 324
QY 297 NAQDVSCFQHLVQANVRKVLKDAVNITAKITDYKKGSAFAEQLN-----YVNSRA 352
DB 325 GV--TTWKDSILVQATPANLEEARTEVRSISQGMNTINDLGIRMLTDAREQHTVPER 382
QY 353 NCKNIMLFTDG-----GEARQEIFNKYKDKKVFVRSVG-QHNYERGPIOWMACENK 407
DB 363 STSIIML-TGDANTGESREKIQENVRKALEGRFPYINLGFNGNMLNINFLTMALENH 441
QY 408 GYVEIPSIGAIRINTQBYDLVGRPMVLADGKAKQVQVNTNYLD 452
DB 442 GVARRIEDSDANLQLOQFYEVANPLL-----TNVEVE 475

RESULT 9
DPOL_THEST STANDARD; PRT; 1829 AA.
AC O33845;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE DNA POLYMERASE (EC 2.7.7.7).
GN POL.
OS Thermococcus sp. (strain TV).
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Thermococcus.
OX NCBI_TaxID=86030;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98094267; PubMed=9434178;
RA Niehaus F., Frey B., Antranikian G.
RT "Cloning and characterisation of a thermostable alpha-DNA polymerase
from the hyperthermophilic archaeon Thermococcus sp. TY.";
RL Gene 204:153-158(1997).
CC -1- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE -
N PYROPHOSPHATE + DNA(N).
CC -1- PTM: THIS PROTEIN UNDERGOES A PROTEIN SELF SPLICING THAT INVOLVES
A POST-TRANSLATIONAL EXCISION OF THE THREE INTERVENING REGION
(INTINS) FOLLOWED BY PEPTIDE LIGATION.
CC -1- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL: Y13030; CAA73475.1;
CC InterPro: IPR002064;
CC InterPro: IPR002203;
CC Pfam: PF00136; DNA_pol_B; 4.
CC PRINTS: PR00379; INTEIN.
CC PROSITE: PS00116; DNA_POLYMERASE_B; FALSE_NEG.
CC PROSITE: PS00881; PROTEIN_SPLICING; 3.
CC Transferrase; DNA-directed DNA polymerase; DNA replication;
KW DNA-binding; Hydrolase; Endonuclease; Autocatalytic cleavage;
KW Protein splicing.
FT CHAIN 1 409 DNA POLYMERASE, 1ST PART (POTENTIAL).
FT CHAIN 410 769 INTEIN 1.
FT CHAIN 770 855 DNA POLYMERASE, 2ND PART (POTENTIAL).
FT

FT CHAIN 856 1392 INTEIN II.
FT CHAIN 1393 1441 DNA POLYMERASE, 3RD PART (POTENTIAL).
FT CHAIN 1442 1598 INTEIN III.
FT CHAIN 1599 1829 DNA POLYMERASE, 4TH PART (POTENTIAL).
SQ SEQUENCE 1829 AA; 211875 MW; A113A8BC57EB9CB3 CRC64;

Query Match 2.9%; Score 161; DB 1; Length 1829;
Best Local Similarity 20.1%; Pred. No. 0.21;
Matches 172; Conservative 101; Mismatches 301; Indels 282; Gaps 39;

QY 16 SLLIGPSEEPSPS-----AVTIKSW-----DKMQEDLVTLA 48
DB 229 TLLGRDREHPKPIHRMGDSFAVEIKGRHFDLFPVVRTINLPYTTLEAVEAVLGKT 288
QY 49 KTASGVNOLVDIYKQDL-----YTVENNARQLVEIAARDIEKLLSNRSLALSLALE 103
DB 289 KSKLGAEEAIAIWEETESMKLAQYSME--DARATYEL-----GKEFFPMEAE 334
QY 104 AEKQAAHQWREDFAS--NEVVYV-----NAKDDLDPEKNDSEPGSQRIKPVFI----- 150
DB 335 LAKLIGQSWDVSRSTGNLVEWYLLRVAYERNELAPNKPDEEYRRRLRTTYLGGYKE 394
QY 151 EDANFGROISTQHAHVHPTD---IYEGSTIV-----LNELNWTSALDEVFKKNREEDPSL 203
DB 395 PERGLWENIAYLDFRCH-PADTKVIVKGGIYVNSDVKEGDIYLGIDG----- 441
QY 204 LMQVFGSATGLARYYPASPDWNSR---TPN-KIDLYDVRPWPYIQAASPKDMLILVD 259
DB 442 -WQ-----RVKWKYHYEGKLINGLKCTPNHKVPVVTENDRQTRI-----RDSLAKSF 491
QY 260 VSGSVSGTLKLRISVSSEMLETSLDDDFVNVASFNSN-----FEKTAEEKNKPSEELKGLSGIILAEGTL 537
DB 492 LSGKVKG--KIITKL-----OHLVQVNV-RNKKVLKDAV-----NNTAKG---- 329
QY 298 -AQDVSCF-----OHLVQVNV-RNKKVLKDAV-----NNTAKG---- 329
DB 538 LRKDIEYFDSRRGKRKRISHOYRVEITIGENEKELLERILYIFDKLFGIRPSVKKKGDTNA 597
QY 330 -ITDYKKGFSFAPBOLLNPNVNSRANCKIIMLFTDGGEEARQAEIFNKYKDKKVFVRF 387
DB 598 LKITTAKAVYLQIEELLK-NIESLYAPAVLRGF-----FERDATYKNKIRS 642
QY 388 SV-----GQHYNERGPIQWACENKGY---YVEIPSIGAIRINTQBYDLVGRPMVLADGK 440
DB 643 TIVTQGTNNKKIDIVAKLLDSLGLIPYSRYEYKYIENGKELTKHILITGRD----- 695
QY 441 AKQVQWTVNYLDALGLVITGTLPVFNITQGF-----NKTNLKNOLILGVMGVD 491
DB 696 -----GLILFQTLVGFISSEKNEALEKAIQVRENNRNLKNNSFYNLSTFE 739
QY 492 VSLIEDIKRLTPRETLCPNGYFAIDPNCYVLLHPNLOPKNSQEPVTLDFDLAELENDI 551
DB 740 VSSEYKGEVYDLLEGPNYIFA---NG-ILTHNSLYPSIIVTN-VSPDILERE----- 789
QY 552 KVEIRNKMGIDGSEKTRTLVKQSODERYIDKGNRTYTPVNGTDTYSLALVLTYSFY 611
DB 790 -----GCKNYDVAIPV--YKCFKDFPG----F 811
QY 612 IKAKLEETITQARSKGKMKDSETLKPDNFEESGY-----TFTAPROYNDLKTSD 662
DB 812 IPSILGELITMRQETIKKKMK--ATIDPIEKKMLDYRQRAVKLLANSILNPNE---LPIT 866
QY 663 NNTFLLNFEFIDRKTNPNSCNADLINRVLLDAGFTNELVQNVWSKQKIKGVKAREV 722
DB 867 NGEYKFKIGEFDIRYMEEQDKVTVTDNTEVLEVDNIFAFSLNKSSEKSEIKVKAL-- 924
QY 723 VTDCGITRVYPKEAGE 738
DB 925 -----IRHKYKGEAYE 935

RESULT 10

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ATX1_PLAFA STANDARD; PRT; 1956 AA.

AC Q04956;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE PROBABLE CATION-TRANSPORTING ATPASE 1 (EC 3.6.1.-).

OS Plasmodium falciparum.

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

OX NCBI_TaxID=5833;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=79/96;

RX MEDLINE=93132070; PubMed=8421054;

RA Krishna S., Cowan G., Meade J.C., Wells R.A., Stringer J.R.,

RA Robson K.J.; cation ATPase-like molecules from Plasmodium

RT "A family of cation ATPase-like molecules from Plasmodium

RT falciparum."

RL J. Cell Biol. 120:385-398(1993).

CC -|- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + ORTHOPHOSPHATE.

CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

CC -|- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2

CC ATPASES). SUBFAMILY V.

CC

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CC or send an email to license@isb-sib.ch).

CC

DR EMBL: X65738; CAA46646.1; -

DR InterPro: IPR001757; -

DR Pfam: PF00122; E1-E2_ATPase; 4. 1.

DR PROSITE: PS00154; ATPASE_E1_E2; 1.

KW Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding.

FT DOMAIN 1 35

FT TRANSMEM 36 58

FT DOMAIN 59 61

FT TRANSMEM 62 80

FT DOMAIN 81 407

FT TRANSMEM 408 427

FT DOMAIN 428 440

FT TRANSMEM 441 462

FT DOMAIN 463 1818

FT TRANSMEM 1819 1837

FT DOMAIN 1838 1845

FT TRANSMEM 1846 1863

FT DOMAIN 1864 1881

FT TRANSMEM 1882 1905

FT DOMAIN 1906 1928

FT TRANSMEM 1929 1952

FT DOMAIN 1953 1956

FT MOD_RES 496 496

FT METAL 1760 1760

FT METAL 1764 1764

FT DOMAIN 246 251

FT DOMAIN 252 256

FT DOMAIN 937 941

FT DOMAIN 1344 1347

FT DOMAIN 1363 1372

FT DOMAIN 1680 1684

FT SEQUENCE 1956 AA; 230285 MW; AE708AAE99009335 CRC64;

Query Match 2.8%; Score 159; DB 1; Length 1956;

Best Local Similarity 17.1%; Pred. No. 0.3;

Matches 179; Conservative 144; Mismatches 359; Indels 366; Gaps 45;

QY 58 VDIEYKQDIYVEPNRNOLVFIARDIEKLLSNR-----SKALVSLALEAEK 106

Db 100 INVY-RYNTSYLISS-----ELVPGDIYEIKNNMTIPCDTILSGSVTMSHMLTGES 152

QY 107 VOAAHQWREDFASNEVYVYNAKODLDPEKND-----SEPGSORIKPVFIEDANFGROIS 160

Db 153 V-PIHKERLPFEGNAIINKNNKYDSNDERDDYLRVYNNHASINMIKRNHLIETLGKKDR 211

QY 161 YQHAAVHIPTDIYEGSTIVLNLNW-TSALDEVYFKKNEEDPSLLMQVFGSATGLARYTP 219

Db 212 EYKSNTH-----DLCSMKLCYINNTYDVHMKNNKM----- 244

QY 220 ASPWDNSRTPNPKIDLYVRRRPWYTOGA-ASPKDMLILVDVSGSYGLTKLIRTSVSE 278

Db 245 ---YNNNNNNKKKKINLN-----FVKGYINSNDLL----- 275

QY 279 MLETLSDDDFVNVASFNADQVSCQHLVQVAVNRKVKLDAVNNTAKGIDYKKGFS 338

Db 276 -----DKIGVNIPE---DDVNNMKH--KFNORNIYNNKDTNML-----EYNNKHR 317

QY 339 FAFEQLLNVNVRANCKIIMLFDTGGEERAQEIFNKNNKDKKVRVFRFVSGVGHNERGP 398

Db 318 IYDCLLKVEAISQNKIIY-----SNEDINKY----- 346

QY 399 IOWMACENKGYEYIPEISGAIRINTQYLDVLRPMVLG-----DKAKOV 444

Db 347 ---MLYGGTYVLSLYNINKIKYNNKEENRILGL-VIKTGFITTKGRKIVNNILYHKKEL 401

QY 445 QWTNVYLDALGLGIVITGTLPVFNITQGFENKTNLKNQLILG-----V 487

Db 402 NLINDSYKFLII-LIIVALFSVFIILYTLISNNETHIILIKCLDIITDAIPALPTILT 460

QY 488 MGVDSVLEDKRLTPRTPLTPNGVYFA-----IDPNGYVLLHPNLQ-----PKNPKSQ 535

Db 461 VGISIISRLKKKFSISCLCPHKINIAGIQTWVFDKGT-TLTENNLFQIGITQNNKK 519

QY 536 EPVTLDFDLAELNDIKVEIRNNKIDGESGEKTRTLVKSQDERYIDKGNRTYTWTPVNG 595

Db 520 NMLS-DFIHK-----EMNTESYTHSKDDNNHKN----- 549

QY 596 TDYSLALVLPYFYIYAKLEETITQARSKKMKD-----SETLKPONFEBSG 645

Db 550 -----STISEYIYKDNMKNLHTSSK-KKSTIKERSNLFVQTIKSCLLKDHVKEKK 599

QY 646 YTFIAPRDYCNLDKISDN--TEFLIN-----FNEF--IDRKTNNPSCNADLINRVLLD 696

Db 600 KEYTYNTYCNLDLHNDSTCSSYLLNSETKDAYCEYNIWH-----LCD---INKRND 650

QY 697 AGFTNELQNTWSKQKNIKGVKARFVVDGIGITRYVPREAGENQENETVEDSYKRS 756

Db 651 INSKNELMGYSKKNELMGKTIKNELM-----GKYSKNEL 684

QY 757 DNDNVYFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVG-----IKIDVNSWI 810

Db 685 -----MGYSKKNELMGYSKKNELMGYSKKNELMGYSKKNELMGYSKKNELMGYSKKNEL 737

QY 811 ENFTKTSIRD-PCAGPVCDCKRNSDVMDCV-----ILDDGGFLLMANHDDYTNQIGRF--- 862

Db 738 MNCNDYNDYFPCD---YNCNNDYTHRLEYHNINKNSFNIPPEKNKSYNNISEHIKI 794

QY 863 -----FGEIDPSLMRHLVNIYSVAF-----NESYDQ 889

Db 795 NYPLLFELACCHTLKSNKKNKIMGVLEILMENFNCMDMLNNNSFIKEKKKNCYSIDQ 854

QY 890 SVCEPGAAPKQAGHRSVAVPSVADILQIGWATAAASILQOFLSLTTPRLEAVE 949

Db 855 KI---DGKNIGANDERCHLNN-----NLVSYNILARF----- 884

QY 950 DDDFTASLSKQSCITEQTQYFFDNDNDSK 977

Db 885 --EFQSRLOPMSVIVKST-YGNNDNDNN 909

RESULT 11

YFBK_ECOLI STANDARD; PRT; 575 AA.

ID YFBK_ECOLI

[illegible]

sequencing. Differential reactivity with concanavalin A.";
 Biol. Chem. Hoppe-Seyler 373:1009-1018(1992).
 [7]
 SEQUENCE OF 55-64 AND 681-702, AND CROSS-LINK STRUCTURE.
 MEDLINE-9332026; PubMed-7682553;
 Englund J.J., Salvesen G., Thøgersen I.B., Valnickova Z.,
 Pizzo S.V., Hefta S.A.;
 RA "Presence of the protein-glycosaminoglycan-protein covalent cross-link
 in the inter-alpha-inhibitor-related proteinase inhibitor heavy chain
 2/bikunin.";
 J. Biol. Chem. 268:8711-8716(1993).
 [8]
 SEQUENCE OF 67-101, AND HYALURONAN BINDING.
 TISSUE-Serum;
 RX MEDLINE-94075371; PubMed-7504674;
 Huang L., Yoneda M., Kimata K.;
 RA "A serum-derived hyaluronan-associated protein (SHAP) is the heavy
 chain of the inter-alpha-trypsin inhibitor.";
 J. Biol. Chem. 268:26725-26730(1993).
 [9]
 SEQUENCE OF 699-702, AND COVALENT LINKAGE WITH CHONDROITIN SULFATE.
 TISSUE-Plasma;
 RX MEDLINE-94229087; PubMed-7513643;
 Morelle W., Capon C., Balduyck M., Sautiere P., Kouach M.,
 RA Michalski C., Fournet B., Mizon J.;
 RT "Chondroitin sulphate covalently cross-links the three polypeptide
 chains of inter-alpha-trypsin inhibitor.";
 Eur. J. Biochem. 221:881-888(1994).
 CC -!- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
 BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
 INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
 LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
 ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES.
 CC -!- SUBUNIT: I-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
 ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,
 BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2
 AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND
 BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.
 CC -!- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
 4-SULFATE BRIDGE TO THEIR C-TERMINAL ASPARTATE.
 CC -!- SIMILARITY: BELONGS TO THE ITIH FAMILY.
 CC -!- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X07173; CAA30160.1; ALT_SEQ.
 DR EMBL; M18193; AAA60558.1; .
 DR EMBL; M33033; AAA59195.1; .
 DR PIR; S00346; IYHU2.
 DR PIR; B34245; B34245.
 DR GlycoSuiteDB; P19823; .
 DR MIM; 146640; .
 DR InterPro; IPR002035; .
 DR Pfam; PF00092; vwa; 1.
 DR PROSITE; PS0234; VWFA_DOMAIN; 1.
 KW Serine protease inhibitor; Repeat; Signal; Multigene family;
 KW Glycoprotein.
 FT SIGNAL 1 18
 FT PROPEP 19 54
 FT CHAIN 55 702
 FT INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN
 FT H2.
 FT 703 946
 FT PROPEP 308 468
 FT DOMAIN 118
 FT CARBOHYD 118
 FT CARBOHYD 445 445
 FT CARBOHYD 671 671
 FT MOD_RES 282 282
 FT N-LINKED (GLCNAC. . .)
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOXYLATION.

FT	MOD_RES	283	283	CARBOXYLATION.
FT	BINDING	702	702	CHONDROITIN-4-SULFATE, CROSS-LINK SITE.
FT	CONFLICT	674	674	P -> A (IN REF. 2 AND 3).
FT	CONFLICT	705	705	F -> S (IN REF. 2 AND 3).
FT	CONFLICT	729	729	N -> D (IN REF. 2 AND 3).
FT	CONFLICT	731	731	V -> A (IN REF. 2 AND 3).
FT	CONFLICT	374	374	K -> L (IN REF. 5).
SQ	SEQUENCE	946 AA;	106436 MW;	1478CF3B8F3BA776 CRC64;

Query Match 2.8%; Score 154.5; DB 1; Length 946;
 Best Local Similarity 19.9%; Pred. No. 0.19;
 Matches 133; Conservative 106; Mismatches 259; Indels 171; Gaps 29;

QY	33	IKSWDKKQEDLVTLAKTAGSGVNLVDIYKQDLYTVEPNARQLVETAAARDIEKLLSN	92
DB	26	LSEFVD--YEDIVEL---APGRFQLVAENRRYORSLPGESEEMEEVDQVTLISYKQST	80
QY	93	RSKALSVSLALEAEKVQAAHORE-----DFASN-----	122
DB	81	ITSRMATTMIQSKVNNSPQNVFVQIPKATISNFSMTVDGKTFRSSIKEKTVGRA	140
QY	123	VYNAK-----DDLPEKNDSE----PGSQRKPVFIEDANFGQISYQH-----	163
DB	141	LYAQAARAGKTAGLVRSALDMENFTEVNLPGAKVQELHYQVKKWKLGSYEHRIYL	200
QY	164	-----AAVHIPTDIYEGSTIVLNELNWTSLD-----EYFKKNREB-----	208
DB	201	QFRLAKHLEVDVWVIEPQGLRFLHVPDTFEGHFGVPIVSKGQOKAHVSFRPTVAQO--	258
QY	209	GSATGLARYYPASPVDNSRTNPKIDLYDVRRP-----WYIOGAAS-----	252
DB	259	-----RICPSCR--ETAVDGLVVLVDVKKREKAGELEVNGFVHFPAFDNLDPIPK	309
QY	253	DMLILDVSGVSGLTSLKIRTSVSEMLETSLDDDFVNVASFNNAQDVSCFQHLVQANV	312
DB	310	NILFVIDVSGSMGWKMKQTVKAMTKILDDLAEDHFSVIDFNQIR--TWRNOLISATK	367
QY	313	RKKVKLDAVNNITAKGITYDKKGP---SFAFEQLNLYNVSRANCKIIMLTG-----	365
DB	368	TQVADAKRYIEKIQPSGGTINEALLRAIFILNEANNLGLDLPNSVSLILVSDGDPTVG	427
QY	366	ERAGEIEFNKYNKDKVRVERFSGV-----HNYERGPIQWM-----ACENK	407
DB	428	EKLKSKIOKNVKNENIQDNISLSLGMGDFVDYDFLKLRSNENHGAQRIYGNQDTSSQLK	487
QY	408	GYIEI--PSIGAIRIN--TQYLDVL-----GRPMVLG--DKAKQVQWNTNVIYD	452
DB	488	KFYNQVSTPLLRNVQFNYPHTSVTDVTQNNFHNFGSGSEIVVAGKFDPAK-----	539
QY	453	ALELGLVITGLVPENITGQFENKLNKQLILGVLGVGVDSLEDI-----KRLTPRTICP	508
DB	540	QIE--SVITA-----TSANTQLVLETLAQMDLQDFLSKDKHADPDFTF-R-K	582
QY	509	NGYFAIDPNGVLLHPNLQPKNPQSPEVTLDFLDAELENDIKVEIRKNKMGIDSGEKT	568
DB	583	LWAYLTIN---QLLAERSLAP-TAAAKRRITRSILOMSLDHHIVTPTLSLVINEAGDGR	638
QY	569	FRTLKVSQD 577	
DB	639	MLADAPPQD 647	

RESULT 13
 BXC1_CLOBO
 ID BXC1_CLOBO STANDARD; PRT; 1290 AA.
 AC P18640;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE BOTULINUM NEUROTOXIN TYPE C1 PRECURSOR (EC 3.4.24.69) (BONT/C1)
 DE (BONTOKILYSIN C1).
 OS Clostridium botulinum.

Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
Clostridium.
NCBI_TaxID=1491;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90370487; PubMed=2204031;
RA Hauser D., Eklund M.W., Kurazono H., Binz T., Niemann H., Gill D.M.,
RA Boquet P., Popoff M.R.;
RT "Nucleotide sequence of Clostridium botulinum C1 neurotoxin.";
RL Nucleic Acids Res. 18:4924-4924(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-TYPE C STOCKHOLM / C-ST;
RX MEDLINE=91024998; PubMed=2222445;
RA Kimura K., Fujii N., Tsuzuki K., Murakami T., Indoh T.,
RA Yokosawa N., Takeshi K., Syuto B., Oguma K.;
RT "The complete nucleotide sequence of the gene coding for botulinum
RT type C1 toxin in the C-ST phase genome.";
RL Biochem. Biophys. Res. Commun. 171:1304-1311(1990).
RN [3]
RP SEQUENCE OF 2-25.
RC STRAIN-TYPE C STOCKHOLM / C-ST;
RX MEDLINE=88153072; PubMed=2450068;
RA Tsuzuki K., Yokosawa N., Syuto B., Ohishi I., Fujii N., Kimura K.,
RA Oguma K.;
RT "Establishment of a monoclonal antibody recognizing an antigenic site
RT common to Clostridium botulinum type B, C1, D, and E toxins and
RL tetanus toxin.";
RN Infect. Immun. 56:898-902(1988).
RN [4]
RP IDENTIFICATION OF SUBSTRATE.
RX MEDLINE=94038966; PubMed=7901002;
RA Blasí J., Chapman E.R., Yamasaki S., Binz T., Niemann H., Jahn R.;
RT "Botulinum neurotoxin C1 blocks neurotransmitter release by means of
RT cleaving HPC-1/syntaxin.";
RL EMO J. 12:4821-4828(1993).
CC -1- FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER
CC RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED
CC AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD
CC WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT
CC INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
CC ENDOPEPTIDASE THAT CLEAVES SYNTAXIN.
CC -1- SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAIN (L) AND A
CC HEAVY CHAIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL ACTIVITY,
CC WHILE THE N- AND C-TERMINAL OF THE HEAVY CHAIN MEDIAL CHANNEL
CC FORMATION AND TOXIN BINDING, RESPECTIVELY.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- MISCELLANEOUS: THERE ARE SEVEN ANTIGENICALLY DISTINCT FORMS OF
CC BOTULINUM NEUROTOXIN: TYPES A, B, C1, D, E, F, AND G.
CC -1- MISCELLANEOUS: BOTULINUM TYPE C1 NEUROTOXIN IS SYNTHESIZED BY C
CC SPRAIN OF CLOSTRIDIUM BOTULINUM WHICH CARRY THE APPROPRIATE
CC BACTERIOPHAGE.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27 (ZINC
CC METALLOPROTEASE); ALSO KNOWN AS THE TETANUS/BOTULINUM NEUROTOXIN
CC SUBFAMILY.

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CC or send an email to license@isb-sib.ch).

CC EMBL: X56433; CAA47060.1; -
CC DR EMBL: X72793; CAA51313.1; -
CC DR EMBL: X53751; CAA37780.1; -
CC DR EMBL: D90210; BAA14235.1; -
CC DR EMBL: X62389; CAA44263.1; -
CC DR PIR: S11291; S11291.
CC DR PIR: X53396; A35396.
CC DR PIR: A43503; A43503.
CC DR MEROPS: M27_002; -

DR	InterPro; IPR000130;	-
DR	InterPro; IPR000395;	-
DR	Pfam; PF01742; Peptidase_M27; 1.	
DR	PRINTS; PR00760; BONTOXILYSIN.	
DR	PROSITE; PS00142; ZINC_PROTEASE; 1.	
KW	Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc.	
FT	INT_MET	0
FT	CHAIN	1 448
FT	CHAIN	449 1290
FT	METAL	228 228
FT	ACT_SITE	229 229
FT	METAL	232 232
FT	DISULFID	436 452
FT	CONFLICT	84 84
SQ	SEQUENCE	1290 AA; 1487/34 MW; 71PBE379F97129E8 CRC64;
Query Match		
Best Local Similarity 2.7%; Score 152; DB 1; Length 1290;		
Matches 205; Conservative 125; Mismatches 346; Indels 334; Gaps		
Qy	106 KVQAHHQWRDEFASNEVYVNAKDDLPKNDSEPGSORIK--- <td>157</td>	157
Dd	138 KTRGNWNVKTGSINPSVIITG-----PRENIDPETISFKLNNTFAAQEGFALSITS	192
Qy	158 -----QTSYQHAAVHIPTDIYES-----TIVLNMWTLSALDEVFK---KNRE	198
Dd	193 ISPFMLITYSNAT----NDVGEGRFSKSEFCMDPIITLMHELN--HAMHNLGIAPNDQ	246
Qy	199 EDPSELLMQVSGTAGLARYYP-----ASPVDNSRTPNKIDLYDVRRRPWYTQGAASPKD	253
Dd	247 TISSVTNIIYSQYNVKLEVAEYAFGGPPID--LIPKSARKYFEKADLYRSTAKRLN	304
Qy	254 MLILVDVSG---SVSGLTCLKLR-----TSVSEMLETISDDDFNVASFNSNAQDVSCF	304
Dd	305 SITTANPSFNKYIGEKYLKRIRFYVESGEV--TVNRNKFVEL--YNELTQLIFTFE	360
Qy	305 QHLVQAVNRNKKV-LKDANNITAK-----GITDYKKGFSFAEQI---LNTNVSR----	351
Dd	361 NYAKTYNQVRKTYLGSNVYTPVTANTLDNNVYDIQNGFNIPKSLNVLPMGONLSRNPA	420
Qy	352 --ANCNKIIMFLT-----DGEEERAQEFNKK-----YNDK-----KKRVYFR	386
Dd	421 RKNVPENMLYTKFKCHKAIDG-----RSLYNKTLDCRELLLVKNTDLPFGIDISOVKTDI	475
Qy	387 FSVGQNHYERGPIOWMACENKGYIIPSIGAIRI--NTQEY--LDVL-----	430
Dd	476 FLRKDINEETEVI-----YYPDNSVDQVILSKNTSEHQDLDLLYPSIDSEILP	526
Qy	431 GRPMVLAGDKAKQVQWTN--VVLDALGLGYTGILPVENITQGENTKN-----	478
Dd	527 GENQVFYDNRTQNVYLSNYYLESOKL-----SDNVEDFTFTRSTIEEALDNSAKVYTYFP	582
Qy	479 -LKNOLILVMG-----VDVSLEDIKRLTPRFLTCPNYYFAIDPNQGVYLLHPNLQPK	530
Dd	583 TLANKYNAGVQGGFLFWANDVVEFTTNILRKDYLDKIDSVALIP---YIGPALNIS	638
Qy	531 NPKSQEPVILDF-----LDAELENDI-----KVEIRKNMTGDSEGKEKFTRTL	572
Dd	639 NSVRNGNFTEAFVGTVILLLEAFPFEFTIPALGAIFYISKVOERNEIT-----KTDICN	692
Qy	573 VKSQDERYTDKGNRTWTW-----TPVNGTDYLSALVLPTYSFYFIYKAKLEEITIQ	622
Dd	693 LEQRIRKWD---SYEWAMGTWLSRITQTGFNNISQYMDSL-NYQAGAIRAKAID-----	742
Qy	623 ARSKKGKMKDSSTLKP--DNFEESGYTIAPRDYCNDLKISDNNTEFFLLNFEFI-----	675
Dd	743 LEYKKGYS GDKENIKISOVENLKNS-----LDVKIS-----EAMNNINKIFIRECSV	787
Qy	676 -----DRKTPNPNSCADLINRVLLDA-----	697
Dd	788 TYLFKNMPLKPIDELNEFDRT-----KAKLIN--LTDSHNIILYGEVDKLRKAKVNSF	839

QY 698 -----GFTN-----ELVQYVW-----SKQNIKGVKARFVVTDDGGITRVYKPEAGE 738
Db 840 QNTIPFNISYNNLLKDIINEYFNNDKILSLQNRKNTLDTSG-----YNAEVSE 894
QY 739 --NQENPETVEDSFYKRSNDNDNYTAPYFNKSGPGAYESGIMVSKAVEIYIQGKLLK 796
Db 895 EGDVQLNP-----IF--PFDFKLSSGEGEDRGKVIYTONENIVYNSMVE 935
QY 797 PAVYGIKIDVNSWENTFKYSIRPCAGVCDCKRNSDVMDVLDGDFLLMANHD--- 853
Db 936 SFSISFWIRINKWVSNLPVGTIID-----SVKNNSGWSIGIISNLFVTLTKQNESEQ 988
QY 854 -----DYNQIGR-----FGEIDPSLMRHLNLSVAFNKSVDYQSVCE 893
Db 989 SINFSDISNAPGYNKWFVVTNNMGM---NMKIYNGKLIDTIKVE 1035

RESULT 14
Y103_SYNY3
ID Y103_SYNY3 STANDARD; PRT; 420 AA.
AC Q55874;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL 45.8 KDA PROTEIN SLL0103.
GN SLL0103.
OS Synchocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synchocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96127529; PubMed=8590279;
RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA Sugita M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synchocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT region from map positions 64% to 92% of the genome.;
RL DNA Res. 2:153-166(1995).
CC -1- SIMILARITY: TO E.COLI YF8K.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL; D64004; BAA10635.1; -
DR InterPro; IPR002035; -
DR Pfam; PF00092; vwa; 1.
DR PROSITE; PS0234; VWFA_DOMAIN; 1.
KW Hypothetical protein.
SQ SEQUENCE 420 AA; 45849 MW; E711B51478E74F3 CRC64;
Query Match 2.7%; Score 151.5; DB 1; Length 420;
Best Local Similarity 20.8%; Pred. No. 0.089;
Matches 85; Conservative 85; Mismatches 183; Indels 55; Gaps 16;
QY 251 PADMILVDVSGVSGSLIKLIRTSVEMLETLSDDDVNVVAFNSNAQDSCQHLVQA 310
Db 41 PLNLGLVDHSGSDMDGQPLETVKSAALGLDRLEDDRLSVIAFDHRAKIV-----IENQ 95
QY 311 NVYRNKVLKDVANNITAKGIDYKGFSAFEOLLNLYNVSRANCKIIMLTDDGGEAAQ 370
Db 96 QVRNGAAKATERUKAGGGTAIDBGLKLGQEAAGKEDRV-----HIFLTDGENEHD 152
QY 371 E-----IFNKNKDKKRVFRFSVGQHNTERGPIQWACENKG-----YYYEIPSGAIRINTQ 424
Db 153 NDRCLKLTGVASDYKLTHTLFGDGH--NQDVLKLEIAAQAQSLSYIENPS-EALHTFRQ 210
QY 425 EYLDVIGRPWLKAGKAKQVQVNTVYLDALGLG-----LVITGTLPVFNITQGFENKTNLK 480

Db 211 LF-----QMSNVGLINNAHL--LLELAQAHAI--VKPVAQVSPETMDLT-VQ 254
QY 481 NQILGVMGVDVSLIEDIKRLTPFTLCPNGYFYFAIDPNGVYLLHPNLOPKPKSQE----- 536
Db 255 NOGAIEEVRGLDMLTDQERV-----LLNLNLYLDQLPQGHVIGQVIRYDDDPASGQTNLL 309
QY 537 ----PVTLDFLDAELENDIKVEIRKNMIDGESGKT--FRTLKVSQDERYIDKNNRYTW 590
Db 310 SDPLPLFIQ--VQYQSPSTDVQVESILTTLAKYRQTQIAETKLAAGRQGAATMLQTAAK 368
QY 591 TPVNGTYSALVLTPTYSFYIKAKLEETITQARSKKGMKDSLTKP 638
Db 369 TALQMGDKNGATILQTN-----TRLQSGEDLSEGRDKKTRMVKTTLOP 413

RESULT 15
ITH4_PIG
ID ITH4_PIG STANDARD; PRT; 921 AA.
AC P79263;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H4 PRECURSOR (ITI HEAVY
DE CHAIN H4) (INTER-ALPHA-TRYPsin INHIBITOR FAMILY HEAVY CHAIN-RELATED
DE PROTEIN) (IHRP) (MAJOR ACUTE PHASE PROTEIN) (MAP).
GN ITH4 OR IHRP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-36; 695-703 AND 710-722.
RX TISSUE=Liver;
RA Hashimoto K., Tobe T., Sumiya J.-I., Sano Y., Choi-Miura N.-H.,
RA Ozawa A., Yasue H., Tomita M.;
RT "Primary structure of the pig homologue of human IHRP: inter-alpha-
RT trypsin inhibitor family heavy chain-related protein.;
RL J. Biochem. 119:577-584(1996).
RN [2]
RP PRELIMINARY SEQUENCE OF 267-556 FROM N.A.
RX TISSUE=Liver;
RA MEDLINE=90371455; PubMed=1697703;
RA Buchman T.G., Cabin D.E., Vickers S., Deutschman C.S., Delgado E.,
RA Sussman M.M., Bulkley G.B.;
RT "Molecular biology of circulatory shock. Part II. Expression of four
RT groups of hepatic genes is enhanced after resuscitation from
RT cardiogenic shock.;
RL Surgery 108:559-566(1990).
RN [3]
RP SEQUENCE OF 28-54 AND 223-240.
RX TISSUE=Serum;
RA MEDLINE=96013138; PubMed=7556597;
RA Gonzalez-Ramon N., Alava M.A., Sarsa J.A., Pineiro M., Escartin A.,
RA Garcia-Gil A., Lampreave F., Pineiro A.;
RT "The major acute phase serum protein in pigs is homologous to human
RT plasma kallikrein sensitive PK-120.;
RL FEBS Lett. 371:227-230(1995).
CC -1- FUNCTION: MAY BE INVOLVED IN ACUTE PHASE REACTIONS.
CC -1- TISSUE SPECIFICITY: LIVER-SPECIFIC.
CC -1- INDUCTION: LEVELS INCREASE SIGNIFICANTLY AFTER CARDIOGENIC
CC SHOCK.
CC -1- PTM: APPEARS TO BE BOTH N- AND O-GLYCOSYLATED (BY SIMILARITY).
CC -1- PTM: CLEAVED BY PLASMA KALLIKREIN TO YIELD 55- AND 25-KDA
CC FRAGMENTS.
CC -1- SIMILARITY: BELONGS TO THE ITH4 FAMILY.
CC -1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
CC -1- CAUTION: REF.2 SEQUENCE IS INCORRECT DUE TO FRAMESHIFTS AND OTHER
CC SEQUENCING ERRORS.
CC -----
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DR EMBL; D43164; AAD00024.1; --
DR EMBL; S28800; AAB46821.1; --
DR EMBL; M29507; --; NOT_ANNOTATED_CDS.
DR InterPro; IPR002035; --
DR Pfam; PF00092; vwa; 1.
DR PROSITE; P850234; VWFA_DOMAIN; 1.
KW Serine protease inhibitor; Repeat; Signal; Multigene family;
KW Glycoprotein.
FT SIGNAL 1 27
FT CHAIN 28 921
FT FT
FT FT
FT DOMAIN 270 428
FT CARBOHYD 80 80
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 242 242
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 513 513
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 577 577
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 49 50
FT CONFLICT 703 703
FT CONFLICT 921 921
FT SEQUENCE 921 AA; 102146 MW; E2BF95925DE8D07C CRC64;

Query Match 2.7%; Score 150.5; DB 1; Length 921;
Best Local Similarity 19.9%; Pred. No 0.31;
Matches 156; Conservative 100; Mismatches 264; Indels 265; Gaps 36;

QY 4 GCLLATLT-----FQSLIGPSSEPPFPFSAVIKSWDX---MQED--- 43
DB 10 GLLLVPLLLAVLQSTAHKNDINISLTVDSKVSRAHTVTVSRVNGSAVQEAFTQ 69
QY 44 -----LVTLAKASGVNQLVDIYEK--YQDLYT-VEPNNAQQLVETAAIDIEKL--- 89
DB 70 MELPKAFITNFSMIDGVTYPGNIEKAAQEQYSAVARGESAGLVRAIGRTEQFQVA 129
QY 90 LNSRKALVSLALEAKVQAAHQWREDFASNEVYVYNAKDDLPKNDSEPGSQRKPKVF 149
DB 130 VSVAPAAKVTFFELVYELLARH-----LGVYELLKIQPO-----QLVKHLQ 171
QY 150 IEDANFGQ-ISKY-QHAAVHIPDIYEGSTVLNE---LNWTSALDEVFKKNEEDPSL 203
DB 172 MDIHFEPQGISPLETFMTNELAEALTISQNTKAHIREKPTLSQQ-QKSPEQOETV 230
QY 204 L-----WQVFGSATG-----LARYYPASPVVDNSRTNPKIDLYDVRPRPVIQ 247
DB 231 LDGNFIVRYDVNRTVTGSGTIENGTFVHYFAPEW----- 266
QY 248 AASPDKMLILVDVSGSVSGGLTLKLTISYSEMLETSDDDVNVVASFNSNAQDVSCFOHL 307
DB 267 SAIPKNVIFVIDTSGMRGKIQOTREALIKILGDLGSRDQFNLVFSGEAPR-----RA 322
QY 308 VQANVRKKVLDVANNITAKGTFYKGFSAFEQLLNNVSRANCKI-----IM 359
DB 323 VAASAENVEAKSYAAEIIHAQGTNINDAMLMAVQLL-----ERANRELLPARSVTFII 377
QY 360 LFTDG-----GEERAQEIFNKKDKVRV-----FRFSVGQHNHYERGPIQWMA 403
DB 378 LFTDGDPTVGETNPSKI-----QKNVREAIQGHSLFCLGFGFDVPYAFLEK-----NA 426
QY 404 CENKG-----YY-----YEIPSIGAIRINTOEYLDVL--GR 432
DB 427 LENGGLARIYEDSDSALQLEDFYQEVANPLRLKLVAFEYPS-NAVEEVTQDNPRFLFKGS 485
QY 433 PMVLG---DKAKQVQWNVNLDALGLVITGTLPVFNITQGFENKTNLKNOLILG--- 486
DB 486 ELVAVGKLRDQSPDV-----LSAKVRGQLHWNVTVMESRVAEQAEFLSPKY 534
QY 487 -----VMGVDVSLEDI--KRITPRFTLCPNGYGYFAIDPNGYVLLHPNL 527

DB 535 IFHSEMERLWAYLTIOQLLAQTVYSASDAEKKALEARALSLSLNSYFVYPLTSMVITPEG 594
QY 528 QPKNPKSQEPVTLDFDLDAELENDIKVEIRKNKMDIGESGKTFRTLKVSQDERYIDKGNRT 587
DB 595 QEQSQAQKVP-----VENGNRQGNTHSGHSF-----QFHSVGDRT 630
QY 588 YTWTPVNGTDYSLALVLTPTYSFYIYKAKLEETITQARSKKGMKMDSETLAKPDNFEESGYT 647
DB 631 SRLTGGSSVD-----PVFS-----HRRGWKGQAQ-----GFEKMSY- 661
QY 648 FIAPR 652
DB 662 -LPPR 665

Search completed: July 23, 2001, 07:48:39
Job time: 600 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 23, 2001, 07:47:28 ; Search time 125.88 Seconds
(without alignments)
1117.256 Million cell updates/sec

Title: US-09-397-548-17
Sequence: 1 MAAGCLLALTFLFOSLLIG.....PDVCFDNNVLEDTDCGGVS 1063

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL16:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_unclassified:*
13: sp_vertebrate:*
14: sp_virus:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5565.5	99.4	1110	4 Q9UIU0	Q9ui0 homo sapien
2	5332	98.8	1091	6 O77773	O77773 sus scrofa
3	5447	97.3	1091	11 Q9ERS3	Q9ers3 rattus norv
4	5379	96.1	1103	11 O08532	O08532 mus musculu
5	3823	68.3	745	4 Q9UDQ3	Q9udq3 homo sapien
6	3045	54.4	1150	4 Q9NY47	Q9ny47 homo sapien
7	3017.5	53.9	1143	4 Q9NY48	Q9ny48 homo sapien
8	3015.5	53.9	1156	11 Q9EQG2	Q9eqg2 mus musculu
9	3004.5	53.7	1145	4 Q9Y268	Q9y268 homo sapien
10	2983.5	53.3	1076	4 Q9UEW0	Q9uew0 homo sapien
11	2814	50.3	975	4 Q9NSA6	Q9nsa6 homo sapien
12	1119.5	20.0	1091	11 Q9Z1L5	Q9z1l5 mus musculu
13	1045.5	18.7	997	4 Q9NY16	Q9ny16 homo sapien
14	937	16.7	2190	5 Q9NK64	Q9nk64 drosophila
15	920	16.4	2172	5 Q9VJW0	Q9vjw0 drosophila
16	896.5	16.0	1191	5 Q9VJN7	Q9vjn7 drosophila
17	891.5	15.9	1255	5 Q9NK83	Q9nk83 drosophila
18	875	15.6	170	4 Q9UDL7	Q9udl7 homo sapien
19	841	15.0	1022	5 Q9V6T7	Q9v6t7 drosophila

20	738.5	13.2	519	4 Q9NY18	Q9ny18 homo sapien
21	580.5	10.4	1148	5 Q17517	Q17517 caenorhabdi
22	514.5	9.2	104	4 Q9UD81	Q9ud81 homo sapien
23	506	9.0	100	6 Q9GLH1	Q9glh1 bos taurus
24	498.5	8.9	121	4 Q9UD82	Q9ud82 homo sapien
25	482	8.6	98	4 Q9UDU5	Q9udu5 homo sapien
26	465	8.3	97	4 Q9UD80	Q9ud80 homo sapien
27	452.5	8.3	223	11 Q9RI42	Q9ri42 mus musculu
28	402	7.2	77	4 Q95026	Q95026 homo sapien
29	344	6.1	1185	4 Q9HCJ9	Q9hcj9 homo sapien
30	223	4.0	1449	5 Q9V917	Q9v917 drosophila
31	170.5	3.0	494	5 Q9U7P4	Q9u7p4 eufolliculi
32	167	3.0	796	1 Q9HJF0	Q9hjr0 thermoplasm
33	161	2.9	2708	5 Q15870	Q15870 plasmodium
34	156.5	2.8	903	6 Q9GLY3	Q9gly3 oryctolagus
35	155	2.8	1516	5 Q96154	Q96154 plasmodium
36	155	2.8	2364	2 Q46342	Q46342 clostridium
37	154.5	2.8	1315	2 Q86488	Q86488 staphylococ
38	153	2.7	932	11 Q35802	Q35802 rattus norv
39	152.5	2.7	789	2 Q45793	Q45793 bacillus th
40	152	2.7	1105	14 Q9EMZ8	Q9emz8 ansacta moo
41	151.5	2.7	2867	5 Q9N2M3	Q9n2m3 plasmodium
42	150.5	2.7	2771	5 Q26216	Q26216 plasmodium
43	150	2.7	946	6 Q9GLY6	Q9gly6 oryctolagus
44	149	2.7	459	2 Q25905	Q25905 helicobacte
45	149	2.7	930	4 Q9UQ54	Q9uq54 homo sapien

ALIGNMENTS

RESULT 1

Q9UIU0 Q9UIU0 PRELIMINARY; PRT; 1110 AA.
ID Q9UIU0;
AC Q9UIU0;
DT 01-MAY-2000 (TREMREL. 13, Created)
DT 01-MAY-2000 (TREMREL. 13, Last sequence update)
DT 01-MAR-2001 (TREMREL. 16, Last annotation update)
DE DIHYDROPYRIDINE RECEPTOR ALPHA 2.SUBUNIT.
GN CACNA2D1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20005942; PubMed=10534405;
RA Schleithoff L., Mehrke G., Reutlinger B., Lehmann-Horn F.;
RT "Genomic structure and functional expression of a human alpha(2)/delta
RT calcium channel subunit gene (CACNA2).";
RL Genomics 61:201-209(1999).
DR EMBL; AF083854; AAF03259.1; JOINED.
DR EMBL; AF083817; AAF03259.1; JOINED.
DR EMBL; AF083818; AAF03259.1; JOINED.
DR EMBL; AF083819; AAF03259.1; JOINED.
DR EMBL; AF083820; AAF03259.1; JOINED.
DR EMBL; AF083821; AAF03259.1; JOINED.
DR EMBL; AF083822; AAF03259.1; JOINED.
DR EMBL; AF083823; AAF03259.1; JOINED.
DR EMBL; AF083824; AAF03259.1; JOINED.
DR EMBL; AF083825; AAF03259.1; JOINED.
DR EMBL; AF083826; AAF03259.1; JOINED.
DR EMBL; AF083827; AAF03259.1; JOINED.
DR EMBL; AF083828; AAF03259.1; JOINED.
DR EMBL; AF083829; AAF03259.1; JOINED.
DR EMBL; AF083830; AAF03259.1; JOINED.
DR EMBL; AF083831; AAF03259.1; JOINED.
DR EMBL; AF083832; AAF03259.1; JOINED.
DR EMBL; AF083833; AAF03259.1; JOINED.
DR EMBL; AF083834; AAF03259.1; JOINED.
DR EMBL; AF083835; AAF03259.1; JOINED.
DR EMBL; AF083836; AAF03259.1; JOINED.
DR EMBL; AF083837; AAF03259.1; JOINED.

DR EMBL; AF083838; AAF03259.1; JOINED.
DR EMBL; AF083839; AAF03259.1; JOINED.
DR EMBL; AF083840; AAF03259.1; JOINED.
DR EMBL; AF083841; AAF03259.1; JOINED.
DR EMBL; AF083842; AAF03259.1; JOINED.
DR EMBL; AF083843; AAF03259.1; JOINED.
DR EMBL; AF083844; AAF03259.1; JOINED.
DR EMBL; AF083845; AAF03259.1; JOINED.
DR EMBL; AF083846; AAF03259.1; JOINED.
DR EMBL; AF083847; AAF03259.1; JOINED.
DR EMBL; AF083848; AAF03259.1; JOINED.
DR EMBL; AF083849; AAF03259.1; JOINED.
DR EMBL; AF083850; AAF03259.1; JOINED.
DR EMBL; AF083851; AAF03259.1; JOINED.
DR EMBL; AF083852; AAF03259.1; JOINED.
DR EMBL; AF083853; AAF03259.1; JOINED.
DR InterPro; IPR000885; -
DR InterPro; IPR002035; -
DR Pfam; PF00092; vwa; 1.
DR ProDom; PD02078; -; 1.
KW Receptor.
SQ SEQUENCE 1110 AA; 125307 MW; 8358DC6AD489C074 CRC64;

Query Match 99.4%; Score 5565.5; DB 4; Length 1110;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 1060; Conservative 1; Mismatches 2; Indels 19; Gaps 1;

Qy 1 MAAGCLLATLTLSQSLIGPSSEPPPSAVTIKSWDKMQEDLVTLAKTAGSVNQLVDI 60
Db 1 MAAGCLLATLTLSQSLIGPSSEPPPSAVTIKSWDKMQEDLVTLAKTAGSVNQLVDI 60

Qy 61 YEKYQDLYTVPNNARQLVEIAARDIEKLLNSRKALVSLALEAEKVQAAHQWREDFASN 120
Db 61 YEKYQDLYTVPNNARQLVEIAARDIEKLLNSRKALVSLALEAEKVQAAHQWREDFASN 120

Qy 121 EVVYNKADLLDPEKNDSEPSQRIKPFIEDANFGROISYQHAHVHTPTDIYEGSTIVL 180
Db 121 EVVYNKADLLDPEKNDSEPSQRIKPFIEDANFGROISYQHAHVHTPTDIYEGSTIVL 180

Qy 181 NELNWTSSALDEVFKKREEDPSLQWFGSATGLARYYPASPWVDNSRTPNKIDLYDVR 240
Db 181 NELNWTSSALDEVFKKREEDPSLQWFGSATGLARYYPASPWVDNSRTPNKIDLYDVR 240

Qy 241 RPWYIQGAASPKDMLILVDVSGVSGLTGLKIRTSVSEMLETSLDDDFVNVASNSNAQD 300
Db 241 RPWYIQGAASPKDMLILVDVSGVSGLTGLKIRTSVSEMLETSLDDDFVNVASNSNAQD 300

Qy 301 VSCFOHLVQANVRNKKVLKDAVNNTAKGITDYKKGFSFAFEQLLNNVSRANCKIIML 360
Db 301 VSCFOHLVQANVRNKKVLKDAVNNTAKGITDYKKGFSFAFEQLLNNVSRANCKIIML 360

Qy 361 FTDGGEERAQEIFNKNYKDKKVRFRFSVQGHNYERGPIONMACENKGYIYEIPSIGAIR 420
Db 361 FTDGGEERAQEIFNKNYKDKKVRFTESVQGHNYDRGPIONMACENKGYIYEIPSIGAIR 420

Qy 421 INTQEYLDVLRPMVLAGDKAKQVQWTVNYLDALGLVITGTLVPFNITQGFENKTNLK 480
Db 421 INTQEYLDVLRPMVLAGDKAKQVQWTVNYLDALGLVITGTLVPFNITQGFENKTNLK 480

Qy 481 NQLILGVNGVDVSLIEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHPNLOPK----- 530
Db 481 NQLILGVNGVDVSLIEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHPNLOPKIGVIGIPTIN 540

Qy 531 -----NPKSQBPVTLDFDALENDIKVEIRNKNMIDGESKEPTTLVKQSDERYI 581
Db 541 LKRKRPNIONPKSQBPVTLDFDALENDIKVEIRNKNMIDGESKEPTTLVKQSDERYI 600

Qy 582 DRGNRTYTWTPVNGTDYSLALVLPYSYIYAKLEETITQARSKKGMKQSETLKPONF 641
Db 601 DRGNRTYTWTPVNGTDYSLALVLPYSYIYAKLEETITQARSKKGMKQSETLKPONF 660

Qy 642 EESGYTFIAPRDYCNLKIISDNTEFLNFEFIDRKTTPNNPCNADLINRVLLDAGFTN 701

Db 661 EESGYTFIAPRDYCNLKIISDNTEFLNFEFIDRKTTPNNPCNADLINRVLLDAGFTN 720
Qy 702 ELVQNYWSKQNIKGVKARFVVDGGITRVYPKAGENQWQENPETYEDSFYKRSIDNDNY 761
Db 721 ELVQNYWSKQNIKGVKARFVVDGGITRVYPKAGENQWQENPETYEDSFYKRSIDNDNY 780
Qy 762 VFTAPYENKSGPGAYESGIMYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTKTSIRDP 821
Db 781 VFTAPYENKSGPGAYESGIMYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTKTSIRDP 840
Qy 822 CAGPVCCKRNSDVMDCVILDDGGFLLMANHDDYTNOIGREFGEIDPSLMRHLNYSIYA 881
Db 841 CAGPVCCKRNSDVMDCVILDDGGFLLMANHDDYTNOIGREFGEIDPSLMRHLNYSIYA 900
Qy 882 FNKSYDQSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAAWSILOQFLLSLTPPR 941
Db 901 FNKSYDQSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAAWSILOQFLLSLTPPR 960
Qy 942 LLEAVEMEDDDFTASLSKQSCITQOTQYFFONDSPSGVLDGCGNSRIFHGEKLMNTNL 1001
Db 961 LLEAVEMEDDDFTASLSKQSCITQOTQYFFONDSPSGVLDGCGNSRIFHGEKLMNTNL 1020
Qy 1002 IFINVESKGTCPCTRLLIQAQESDGPNCMDVMKQPRYKRGPDVCFDNNVLEDTDCGG 1061
Db 1021 IFINVESKGTCPCTRLLIQAQESDGPNCMDVMKQPRYKRGPDVCFDNNVLEDTDCGG 1080
Qy 1062 VS 1063
Db 1081 VS 1082

RESULT 2
O77773 PRELIMINARY; PRT; 1091 AA.
AC O77773;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE VOLTAGE-DEPENDENT CALCIUM CHANNEL ALPHA-2 DELTA SUBUNIT PRECURSOR.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=CEREBRAL CORTEX;
RX MEDLINE=98411353; PubMed=9738015;
RA Brown J.P., Gee N.S.;
RT "Cloning and deletion mutagenesis of the alpha2 delta calcium channel
subunit from porcine cerebral cortex. Expression of a soluble form of
the protein that retains [3H]gabapentin binding activity.";
RL J. Biol. Chem. 273:25458-25465(1998).
DR EMBL; AF077665; AAC36289.1; -
DR InterPro; IPR002035; -
DR Pfam; PF00092; vwa; 1.
KW Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 1091 VOLTAGE-DEPENDENT CALCIUM CHANNEL
ALPHA-2 DELTA SUBUNIT.
FT SEQUENCE 1091 AA; 123150 MW; 293DDC7EBE9E60E CRC64;

Query Match 98.8%; Score 5532; DB 6; Length 1091;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1049; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MAAGCLLATLTLSQSLIGPSSEPPPSAVTIKSWDKMQEDLVTLAKTAGSVNQLVDI 60
Db 1 MAAGCLLATLTLSQSLIGPSSEPPPSAVTIKSWDKMQEDLVTLAKTAGSVNQLVDI 60

Qy 61 YEKYQDLYTVPNNARQLVEIAARDIEKLLNSRKALVSLALEAEKVQAAHQWREDFASN 120

```
Db 61 YEKYQDLYTVEPNNAQRLVEIAARDIEKLLSNRSKALVRLALEAEKVAQAHHQWREDFASN 120
QY 121 EYVYNNAKDDLPENKNDSPGSGRIKPVIEDANFGRQISYOHAAVHIPTDIYEGSTIVL 180
Db 121 EYVYNNAKDDLPENKNDSPGSGRIKPVIEDANFGRQISYOHAAVHIPTDIYEGSTIVL 180
QY 181 NELNWTSALEDFVFNKREDDPSLLQWVGSATGLARYYPASPWVDSNRPNNKIDLYDVR 240
Db 181 NELNWTSALEDFVFNKREDDPSLLQWVGSATGLARYYPASPWVDSNRPNNKIDLYDVR 240
QY 241 RPYWYIQAASPKDMLILVDVSGVSLTLKLRISVSEMLETSLDDDFVNVASFNSNAQD 300
Db 241 RPYWYIQAASPKDMLILVDVSGVSLTLKLRISVSEMLETSLDDDFVNVASFNSNAQD 300
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKITDYKKGFSFAFQOLLNYSRANCNKIIML 360
Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKITDYKKGFSFAFQOLLNYSRANCNKIIML 360
QY 361 FTDGGEERAQEIFNKNKDKKVRVFRFSVGOHNYERGPQIOWMACENKGYIYEPSIGAIR 420
Db 361 FTDGGEERAQEIFNKNKDKKVRVFRFSVGOHNYERGPQIOWMACENKGYIYEPSIGAIR 420
QY 421 INTQEYLDVLRPMVLGADKAKQVQNTNYLDALGLVITGTLPVFNITGQFENKTNLK 480
Db 421 INTQEYLDVLRPMVLGADKAKQVQNTNYLDALGLVITGTLPVFNITGQFENKTNLK 480
QY 481 NQILGVMGVDSLEDIKRLTPRFTLCPNGYIFAIDPNGYVLLHLPNLPKNPKSQBPVTL 540
Db 481 NQILGVMGVDSLEDIKRLTPRFTLCPNGYIFAIDPNGYVLLHLPNLPKNPKSQBPVTL 540
QY 541 DFLDALENDIKVEIRNKNMIDGESGKTRTLVKSDERYIDKGNRTYTPTVNGTDYSL 600
Db 541 DFLDALENDIKVEIRNKNMIDGESGKTRTLVKSDERYIDKGNRTYTPTVNGTDYSL 600
QY 601 ALVLPYSFYIYKAKLEETITQARSKKGMKDSITLKPNDNFESGYTFTIAPDYCNDLKI 660
Db 601 ALVLPYSFYIYKAKLEETITQARSKKGMKDSITLKPNDNFESGYTFTIAPDYCNDLKI 660
QY 721 FVYTDGGITRVPYKEAGENQWNPETYEDSFYKRSLDNDNYFTAPYFNKSGPGAYESGI 780
Db 721 FVYTDGGITRVPYKEAGENQWNPETYEDSFYKRSLDNDNYFTAPYFNKSGPGAYESGI 780
QY 781 MYSKAVEIYIQGLKLPVAVGKIDVNSNIENFTKTSIRDPACGVPVCDCKRNSDVMDCVI 840
Db 781 MYSKAVEIYIQGLKLPVAVGKIDVNSNIENFTKTSIRDPACGVPVCDCKRNSDVMDCVI 840
QY 841 LDDGGFLMANHDDYTNQIGRFFGEIDPSLMRLHVNISYVAFNKSVDYOSVCEPGAAPQ 900
Db 841 LDDGGFLMANHDDYTNQIGRFFGEIDPSLMRLHVNISYVAFNKSVDYOSVCEPGAAPQ 900
QY 901 GAGHRSAYVPSVADIQIGWATAAASIIQOFLSLTTPRLLLEAVEMEDDDFTASLSQ 960
Db 901 GAGHRSAYVPSVADIQIGWATAAASIIQOFLSLTTPRLLLEAVEMEDDDFTASLSQ 960
QY 961 SCITEGTOYFFNDKSFSGVLDGNCRSIFHGEKLMNTNLIPIVYESKGTCPDTRLLI 1020
Db 961 SCITEGTOYFFNDKSFSGVLDGNCRSIFHGEKLMNTNLIPIVYESKGTCPDTRLLI 1020
QY 1021 QABQTSIDGPNPCDMVQKPYRKGPDVCFNNVLEDYTDGCGVS 1063
Db 1021 QABQTSIDGPNPCDMVQKPYRKGPDVCFNNVLEDYTDGCGVS 1063
```

RESULT 3

Q9ERS3

ID Q9ERS3 PRELIMINARY; PRT; 1091 AA.

AC Q9ERS3;

DT 01-MAR-2001 (Tremblrel. 16, Created)

DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)

```
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE VOLTAGE-GATED CALCIUM CHANNEL ALPHA2/DELTA-1 SUBUNIT.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=SUPERIOR CERVICAL GANGLIA;
RL Lin Y., Lipscombe D.;
RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF286488; AAG28164.1;
FT VARIANT 209 212 GSAT -> AADR.
FT VARIANT 338 338 S -> T.
FT VARIANT 599 600 SL -> RY.
FT VARIANT 869 869 S -> R.
SQ SEQUENCE 1091 AA; 123467 MW; C155088971628E19 CRC64;
```

Query Match 97.3%; Score 5447; DB 11; Length 1091;
Best Local Similarity 96.5%; Pred. No. 0;
Matches 1026; Conservative 22; Mismatches 15; Indels 0; Gaps 0;

QY 1 MAAGCLLALTILFQSLIGPSSEEPFSAVITKSWDKQEDLVTLAKTASGNOLVDI 60

Db 1 MAAGCLLALTILFQSLIGPSSEEPFSAVITKSWDKQEDLVTLAKTASGNOLVDI 60

QY 61 YEKYQDLYTVEPNNAQRLVEIAARDIEKLLSNRSKALVRLALEAEKVAQAHHQWREDFASN 120

Db 61 YEKYQDLYTVEPNNAQRLVEIAARDIEKLLSNRSKALVRLALEAEKVAQAHHQWREDFASN 120

QY 121 EYVYNNAKDDLPENKNDSPGSGRIKPVIEDANFGRQISYOHAAVHIPTDIYEGSTIVL 180

Db 121 EYVYNNAKDDLPENKNDSPGSGRIKPVIEDANFGRQISYOHAAVHIPTDIYEGSTIVL 180

QY 181 NELNWTSALEDFVFNKREDDPSLLQWVGSATGLARYYPASPWVDSNRPNNKIDLYDVR 240

Db 181 NELNWTSALEDFVFNKREDDPSLLQWVGSATGLARYYPASPWVDSNRPNNKIDLYDVR 240

QY 241 RPYWYIQAASPKDMLILVDVSGVSLTLKLRISVSEMLETSLDDDFVNVASFNSNAQD 300

Db 241 RPYWYIQAASPKDMLILVDVSGVSLTLKLRISVSEMLETSLDDDFVNVASFNSNAQD 300

QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKITDYKKGFSFAFQOLLNYSRANCNKIIML 360

Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKITDYKKGFSFAFQOLLNYSRANCNKIIML 360

QY 361 FTDGGEERAQEIFNKNKDKKVRVFRFSVGOHNYERGPQIOWMACENKGYIYEPSIGAIR 420

Db 361 FTDGGEERAQEIFNKNKDKKVRVFRFSVGOHNYERGPQIOWMACENKGYIYEPSIGAIR 420

QY 421 INTQEYLDVLRPMVLGADKAKQVQNTNYLDALGLVITGTLPVFNITGQFENKTNLK 480

Db 421 INTQEYLDVLRPMVLGADKAKQVQNTNYLDALGLVITGTLPVFNITGQFENKTNLK 480

QY 481 NQILGVMGVDSLEDIKRLTPRFTLCPNGYIFAIDPNGYVLLHLPNLPKNPKSQBPVTL 540

Db 481 NQILGVMGVDSLEDIKRLTPRFTLCPNGYIFAIDPNGYVLLHLPNLPKNPKSQBPVTL 540

QY 541 DFLDALENDIKVEIRNKNMIDGESGKTRTLVKSDERYIDKGNRTYTPTVNGTDYSL 600

Db 541 DFLDALENDIKVEIRNKNMIDGESGKTRTLVKSDERYIDKGNRTYTPTVNGTDYSL 600

QY 601 ALVLPYSFYIYKAKLEETITQARSKKGMKDSITLKPNDNFESGYTFTIAPDYCNDLKI 660

Db 601 ALVLPYSFYIYKAKLEETITQARSKKGMKDSITLKPNDNFESGYTFTIAPDYCNDLKI 660

QY 661 SDNTEFLNFEFIDRKTTPNPNPCDMVQKPYRKGPDVCFNNVLEDYTDGCGVS 720

Db 661 SDNTEFLNFEFIDRKTTPNPNPCDMVQKPYRKGPDVCFNNVLEDYTDGCGVS 720

QY 721 FVYTDGGITRVPYKEAGENQWNPETYEDSFYKRSLDNDNYFTAPYFNKSGPGAYESGI 780

Db 721 FVYTDGGITRVPYKEAGENQWNPETYEDSFYKRSLDNDNYFTAPYFNKSGPGAYESGI 780

DB 721 FVVTGGITRVPKKEAGENWQENPETYEDSFYKRSLDNDNVYFTAPYFNKSGPGAYESGI 780

QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTKTSIRDPCAGVCDCKRNSVDVCVI 840

DB 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTKTSIRDPCAGVCDCKRNSVDVCVI 840

QY 841 LDGGFLLMANHDDVTNQIGRFFGEIDPSLRHLNIVSYAFNKSVDYQSVCEPGAAPKQ 900

DB 841 LDGGFLLMANHDDVTNQIGRFFGEIDPSLRHLNIVSYAFNKSVDYQSVCEPGAAPKQ 900

QY 901 GAGHSAYVPSVADILQIGWATAAAMSILQOFLSLFPRLLEAVEMEDDFTASLSKQ 960

DB 901 GAGHSAYVPSVADILQIGWATAAAMSILQOFLSLFPRLLEAVEMEDDFTASLSKQ 960

QY 961 SCITEQTOYFFNDKSFSGVLDCGNCGRIFHGEKLMNTNLIFIMVESKGTCPDTRLLI 1020

DB 961 SCITEQTOYFFNDKSFSGVLDCGNCGRIFHGEKLMNTNLIFIMVESKGTCPDTRLLI 1020

QY 1021 QAEQTSQGNPCDMVKQPRYKGPVCFNNVLEDYTDGCGVS 1063

DB 1021 QAEQTSQGNPCDMVKQPRYKGPVCFNNVLEDYTDGCGVS 1063

RESULT 4

008532 PRELIMINARY; PRT: 1103 AA.

AC 008532; 008533; 008534; 008535; 008536;

DT 01-JUN-1998 (Tremblrel. 06, Created)

DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)

DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)

DE DIHYDROPIRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-2/DELTA

DE SUBUNITS PRECURSOR.

GN CACNA2D1 OR CACNA2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi.

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_Taxid=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-BRAIN;

RX MEDLINE=97113514; PubMed=8955374;

RA Angelotti T. Hofmann F.;

RL FEBS Lett. 397:331-337(1996).

CC -1- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN EXCITATION-CONTRACTION COUPLING.

CC -1- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS: ALPHA-1, ALPHA-2, BETA AND GAMMA.

CC -1- SUBUNIT: ALPHA-2 AND DELTA FORM HETERODIMERS THAT ARE DISULFIDE-LINKED.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- ALTERNATIVE PRODUCTS: FIVE FORMS OF THE PROTEIN, ISOFORMS 2A-2E, ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THE SEQUENCE SHOWN HERE IS THAT OF ISOFORM 2A.

CC -1- TISSUE SPECIFICITY: ISOFORM 2A IS EXPRESSED IN SKELETAL MUSCLE AND AORTA, 2B IS EXPRESSED IN BRAIN, 2C IS EXPRESSED IN HEART. 2D IS EXPRESSED IN HEART AND SMOOTH MUSCLE, AND 2E IS EXPRESSED IN SMOOTH MUSCLE. ALL FIVE ISOFORMS ARE EXPRESSED IN THE CARDIOVASCULAR SYSTEM.

CC -1- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM A PRECURSOR FORM.

CC -1- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.

DR EMBL; U73484; AAB50139.1; -

DR EMBL; U73485; AAB50140.1; -

DR EMBL; U73483; AAB50138.1; -

DR EMBL; U73486; AAB50141.1; -

DR EMBL; U73487; AAB50142.1; -

DR MGI; 88295; CACNA2d1.

DR InterPro; IPR002035; -

DR Pfam; PF00092; vwa; 1.

KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;

KW Calcium channel; Glycoprotein; Phosphorylation; Signal;

KW Alternative splicing.

FT SIGNAL 1 24

FT CHAIN 25 957

FT CHAIN 958 1103

FT TRANSMEM 446 469

FT TRANSMEM 918 942

FT TRANSMEM 1079 1098

FT MOD_RES 501 501

FT MOD_RES 845 845

FT CARBOHYD 92 92

FT CARBOHYD 136 136

FT CARBOHYD 184 184

FT CARBOHYD 324 324

FT CARBOHYD 348 348

FT CARBOHYD 475 475

FT CARBOHYD 604 604

FT CARBOHYD 613 613

FT CARBOHYD 675 675

FT CARBOHYD 781 781

FT CARBOHYD 824 824

FT CARBOHYD 888 888

FT CARBOHYD 895 895

FT CARBOHYD 985 985

FT CARBOHYD 998 998

FT VARSPLIC 531 531

FT VARSPLIC 554 554

FT VARSPLIC 644 644

FT SQ SEQUENCE 1103 AA; 124629 MW; 103773BA735120D4 CRC64;

Query Match 96.1%; Score 5379; DB 11; Length 1103;

Best Local Similarity 94.3%; Pred. No. 0;

Matches 1020; Conservative 22; Mismatches 14; Indels 26; Gaps 2;

QY 1 MAAGCLLALTLFQSLILGPSSEEPSPSAVTIKSWDKMQEDLVTLAKTASGVNOLVDI 60

DB 1 MAAGCLLALTLFQSLILGPSSEEPSPSAVTIKSWDKMQEDLVTLAKTASGVNOLVDI 60

QY 61 YEKYQDLYTVEPNNAQQLVEIAARDIEKLISNRSKALVSLALEAEKVQAAHQRDPFAS 120

DB 61 YEKYQDLYTVEPNNAQQLVEIAARDIEKLISNRSKALVSLALEAEKVQAAHQRDPFAS 120

QY 121 EYVYNAKDDLPEDKNDSEPGSQRIKPVFTEDANFGRQISYQAAHVIPTDIYEGSTIVL 180

DB 121 EYVYNAKDDLPEDKNDSEPGSQRIKPVFTEDANFGRQISYQAAHVIPTDIYEGSTIVL 180

QY 181 NELNWTALDEVEKKNREDPSSLNQVFGSATGLARYYPASPVDNSRTNPKIDLYDVR 240

DB 181 NELNWTALDEVEKKNREDPSSLNQVFGSATGLARYYPASPVDNSRTNPKIDLYDVR 240

QY 241 RPWYIOGAASPKDMLILVDYSGVSGLTLLKIRTSVSEMLETSDDDFVNVPASNQAD 300

DB 241 RPWYIOGAASPKDMLILVDYSGVSGLTLLKIRTSVSEMLETSDDDFVNVPASNQAD 300

QY 301 VSCFHLVQAVNRNKKVLDKAVNNITAKGITYDKKGSFAFEQLLNTNVRANCNKIIML 360

DB 301 VSCFHLVQAVNRNKKVLDKAVNNITAKGITYDKKGSFAFEQLLNTNVRANCNKIIML 360

QY 361 FTGGEERAQEIFKNYKNDKRVFRFVSQGHYVERGPIQWACENKGYEIPISGAIR 420

DB 361 FTGGEERAQEIFKNYKNDKRVFRFVSQGHYVERGPIQWACENKGYEIPISGAIR 420

QY 421 INTQEYLDVLGRPMVLADGAKAQVQWNTNVLDALEGLVITGTLTPVENITGQFENKTNLK 480

DB 421 INTQEYLDVLGRPMVLADGAKAQVQWNTNVLDALEGLVITGTLTPVENITGQFENKTNLK 480

QY 481 NQLILGVMGVDVSLIEDIKRLTPFTLCPNGYFAIDPNGYVLLHPNLPKQKPIGVGPI 540

DB 481 NQLILGVMGVDVSLIEDIKRLTPFTLCPNGYFAIDPNGYVLLHPNLPKQKPIGVGPI 540

QY 531 -----NPKSQEPVTLDFDLAELENDIKVEIRNKMIDGESGEKFTLVKQSDERYI 581

DB 541 LRKRPNVQNPQSQEPVTLDFDLAELENDIKVEIRNKMIDGESGEKFTLVKQSDERYI 600

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QY 582 DKGNTYTWTPVNGTDYSLALVLPYSPYYIKAKLEETITQARSKKGMKDSKSETLKPNDF 641
Db 601 DKGNTYTWTPVNGTDYSLALVLPYSPYYIKAKLEETITQARY-----SETLKPND 653
QY 642 EESGTYTAPDYCNLDKISDNNTFLLNFNFIIDRKTPNPNPCNADLNINRVLLDAGFTN 701
Db 654 EESGTYTAPDYCNLDKISDNNTFLLNFNFIIDRKTPNPNPCNADLNINRVLLDAGFTN 713
QY 702 ELVQYWSKQKNIKGVKARFVVTGGITRVYPKEAGENQENPETEYDSFYKRSLDNDNY 761
Db 714 ELVQYWSKQKNIKGVKARFVVTGGITRVYPKEAGENQENPETEYDSFYKRSLDNDNY 773
QY 762 VETAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGIIKIDVNSWNIENFTKTSIRD 821
Db 774 VETAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGIIKIDVNSWNIENFTKTSIRD 833
QY 822 CAGPVCDCCKRNSDVMDCVTLDDGGFLMANHDDYTNQIGRFFGEIDPSPMLRHLVNI SYVA 881
Db 834 CAGPVCDCCKRNSDVMDCVTLDDGGFLMANHDDYTNQIGRFFGEIDPSPMLRHLVNI SYVA 893
QY 882 FNKSYDYSVCEPGAAPKOGAGHRSAYVPSVADIIQIGMWATAAASIIQQFLLSLTFFPR 941
Db 894 FNKSYDYSVCEPGAAPKOGAGHRSAYVPSVADIIQIGMWATAAASIIQQFLLSLTFFPR 953
QY 942 LLEAVEMEDDDFTASLSKQSCITEQTYFFDNDKSKFSGLDGCNCSRFHGEKLMNTNL 1001
Db 954 LLEAVEMEDDDFTASLSKQSCITEQTYFFDNDKSKFSGLDGCNCSRFHGEKLMNTNL 1013
QY 1002 IFIMVESGTCPCDTRLLIAEQTSQYFFDNDKSKFSGLDGCNCSRFHGEKLMNTNL 1061
Db 1014 IFIMVESGTCPCDTRLLIAEQTSQYFFDNDKSKFSGLDGCNCSRFHGEKLMNTNL 1073
QY 1062 VS 1063
Db 1074 VS 1075
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RESULT 5

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ID Q9UDQ3 PRELIMINARY; PRT; 745 AA.
AC Q9UDQ3;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE WUGSC:H_DJ0560014.1 PROTEIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99063792; PubMed=9847074;
RA Sulston J.E., Waterston R.;
RT "Toward a complete human genome sequence.";
RL Genome Res. 8:1097-1108(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Mead K., Bauer C.;
RT "The sequence of Homo sapiens PAC clone RP4-560014.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Waterston R.H.;
RT Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006145; AAD20938.1;
DR InterPro; IPR002035;
FT NON_TER 1
SQ SEQUENCE 745 AA; 84396 MW; BC07B53484B71E4A CRC64;
```

Query Match 68.3%; Score 3823; DB 4; Length 745;
Best Local Similarity 99.7%; Pred. No. 1.le-236;
Matches 715; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 347 YNVS RANCKIIIMLTDDGGEERAQEIFNKYKDKKVRVFRFVSGQHNVERGPIQWMACSN 406
Db 1 YNVS RANCKIIIMLTDDGGEERAQEIFNKYKDKKVRVFRFVSGQHNVERGPIQWMACSN 60
QY 407 KGYEYIPEISGAIRINTQYLDVLRPMVYLAGDKAKQVQWNTWYLDALBGLVITGTLPV 466
Db 61 KGYEYIPEISGAIRINTQYLDVLRPMVYLAGDKAKQVQWNTWYLDALBGLVITGTLPV 120
QY 467 FNITQGFENKTNLKNQILGVMGVDVSLDIKRLTPRFTLCPNGYFFAIDPNGYVLLHPN 526
Db 121 FNITQGFENKTNLKNQILGVMGVDVSLDIKRLTPRFTLCPNGYFFAIDPNGYVLLHPN 180
QY 527 LQPKPKSQEPVTLDFDLAELENDIKVEIRNKWIDGESGEKTFRLVKQSODERYIDKGNR 586
Db 181 LQPKPKSQEPVTLDFDLAELENDIKVEIRNKWIDGESGEKTFRLVKQSODERYIDKGNR 240
QY 587 TYTWTVPVNGTDYSLALVLPYSPYYIKAKLEETITQARSKKGMKDSKSETLKPNDEESY 646
Db 241 TYTWTVPVNGTDYSLALVLPYSPYYIKAKLEETITQARSKKGMKDSKSETLKPNDEESY 300
QY 647 TFIAPRDYCNLDKISDNNTFLLNFNFIIDRKTPNPNPCNADLNINRVLLDAGFTNELVN 706
Db 301 TFIAPRDYCNLDKISDNNTFLLNFNFIIDRKTPNPNPCNADLNINRVLLDAGFTNELVN 360
QY 707 YWSKQKNIKGVKARFVVTGGITRVYPKEAGENQENPETEYDSFYKRSLDNDNYVFTAP 766
Db 361 YWSKQKNIKGVKARFVVTGGITRVYPKEAGENQENPETEYDSFYKRSLDNDNYVFTAP 420
QY 767 YFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGIIKIDVNSWNIENFTKTSIRDPCAGPV 826
Db 421 YFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGIIKIDVNSWNIENFTKTSIRDPCAGPV 480
QY 827 CDCKRNSDVMDCVTLDDGGFLMANHDDYTNQIGRFFGEIDPSPMLRHLVNI SYAFNKSY 886
Db 481 CDCKRNSDVMDCVTLDDGGFLMANHDDYTNQIGRFFGEIDPSPMLRHLVNI SYAFNKSY 540
QY 887 DYQSVCEPGAAPKOGAGHRSAYVPSVADIIQIGMWATAAASIIQQFLLSLTFFPRLEAV 946
Db 541 DYQSVCEPGAAPKOGAGHRSAYVPSVADIIQIGMWATAAASIIQQFLLSLTFFPRLEAV 600
QY 947 EMEDDDDFTASLSKQSCITEQTYFFDNDKSKFSGLDGCNCSRFHGEKLMNTNLIFIMV 1006
Db 601 EMEDDDDFTASLSKQSCITEQTYFFDNDKSKFSGLDGCNCSRFHGEKLMNTNLIFIMV 660
QY 1007 ESKGTCPCDTRLLIAEQTSQYFFDNDKSKFSGLDGCNCSRFHGEKLMNTNLIFIMV 1063
Db 661 ESKGTCPCDTRLLIAEQTSQYFFDNDKSKFSGLDGCNCSRFHGEKLMNTNLIFIMV 717

RESULT 6

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ID Q9NY47 PRELIMINARY; PRT; 1150 AA.
AC Q9NY47;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE CALCIUM CHANNEL, ALPHA 2/DELTA SUBUNIT 2.
GN CACNA2D2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYROID;
RA Klugbauer N.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
```

RP	SEQUENCE FROM N.A.	
RC	TISSUE-THYROID;	
RA	Hobom M., Dai S., Marais E., Lacinova L.;	
RT	"Neuronal distribution and functional characterization of the calcium channel alpha2delta-2 subunit."	
RL	Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.	
DR	EMBL: AJ251368; CAB86193.1; -	
DR	InterPro: IPR002035; -	
SQ	SEQUENCE 1150 AA; 129875 MW; 37B75F687AFE573C CRC64;	
	Query Match 54.4%; Score 3045; DB 4; Length 1150;	
	Best Local Similarity 54.6%; Pred. No. 1.7e-186;	
	Matches 588; Conservative 172; Mismatches 286; Indels 30; Gaps 13;	
QY	7 LAITLTLFQSLIGPSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDIYEKYD 66	
DB	44 LWLLPLLLPLLAAPGASAYSFPQOQTHQHWARLEQEVGMRFQGVQQLREIYKDNRN 103	
QY	67 LYTVEPNNARQLVEIARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASNEVYYN 126	
DB	104 LFEVQENEPKLVKAGVAGDIESLLDRKQVQALKRLADAAENFQKARWQDNKEEDIVYD 163	
QY	127 AKDDL---DPEKNDSEPSQ--RIKPVFIEDANFGROISYQHAHVHPTDIYEGSTVLN 181	
DB	164 AKADAEELDDPESEDERGSKASTLRDLDFIEDPNFKKNVNTSYAAVQIPTDIYKGSTVLN 223	
QY	182 ELNWTALDEYFKKREEDPSLLQVFGSATGLARYYPASPWVDNSTRPNKIDLYDVRER 241	
DB	224 ELNWTALDENFVEMNRQDPTLLQVFGSATGVTRYIPATPW----RAPKKIDLYDVRER 279	
QY	242 PWYIOGAASPKDMLILVDVSGVSGSLTKLIRTSVSEMLETSLDDDFVNVASFNSAQDV 301	
DB	280 PWYIOGASSPKDMLIIVDVSGVSGSLTKLIRTSVSEMLETSLDDDFVNVASFNSAQDV 339	
QY	302 SCFOHLVQANVRNKKYLKADAVNNITAKGTDYKKGSPFAFEQLLNYNVSRANCKIIMLF 361	
DB	340 SCFTHLVQANVRNKKYKFAVQGVAKGTTGTGKAGFEYAFDQLQNSNITRANCKNIMMF 399	
QY	421 INTQYLDVLGRPMVLGADKAKQWNTNVLDALEGLVITGTLFPVFNITQGFENKTLK 480	
DB	460 INTQYLDVLGRPMVLGAKQWNTNVLDALEGLVITGTLFPVFNITQ--DGPGEKK 517	
QY	481 NQILILGVMDVSLIEDIKELTPRTFLPNGYYFAIDPNGYLLHPNLPKPKSQEPVTL 540	
DB	518 NQILILGVMDVSLIEDIKELTPRTFLPNGYYFAIDPNGYLLHPNLPKPKSQEPVTL 577	
QY	541 DFLDAELENDEKVEIRNKMIDGESKEFTLTKVKSODERYIDKGNRTYTWTVPVNGTDYSL 600	
DB	578 DFLDAELENDEKVEIRNKMIDGESKEFTLTKVKSODERYIDKGNRTYTWTVPVNGTDYSL 637	
QY	601 ALVLPYFYIYKALEETITQARKKGMKQSETLKPDPNFESGYTFTAPRDYNDLKI 660	
DB	638 GLVLPYFYIYKALEETITQARKKGMKQSETLKPDPNFESGYTFTAPRDYNDLKI 697	
QY	661 SDNTEFLNLFNEFIDRKTTPNPNPCNADILNVLVDAGFTNELVQVNSKQK-NIKGVKA 719	
DB	698 SDNTEFLNLFNEFIDRKTTPNPNPCNADILNVLVDAGFTNELVQVNSKQK-NIKGVKA 757	
QY	720 RFVVDGGITRVYKPEAGENMOENPTYEDSFYKRSLDNDNVFTAPYFNK-SGPCAYES 778	
DB	758 VFAATDGGITRVYKPEAGENMOENPTYEDSFYKRSLDNDNVFTAPYFNK-SGPCAYES 817	
QY	779 ---GIWYKAVEIYIOGKLLKPAVGVKIDVNSWIENF---TKTSIRDP--CAGP--- 825	
DB	818 DTGVLSTAVELSLGRRTLRPAVGVKIDVNSWIENF---TKTSIRDP--CAGP--- 876	
QY	826 -VCCKRNSDVMDCVILDDGGFLVLSNQNHQWQVGRFFSEYVDANLMLALYNNSTYTRKE 936	
	Query Match 53.9%; Score 3017.5; DB 4; Length 1143;	
	Best Local Similarity 54.5%; Pred. No. 9.5e-185;	
	Matches 586; Conservative 170; Mismatches 283; Indels 37; Gaps 14;	
QY	7 LAITLTLFQSLIGPSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDIYEKYD 66	
DB	44 LWLLPLLLPLLAAPGASAYSFPQOQTHQHWARLEQEVGMRFQGVQQLREIYKDNRN 103	
QY	67 LYTVEPNNARQLVEIARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASNEVYYN 126	
DB	104 LFEVQENEPKLVKAGVAGDIESLLDRKQVQALKRLADAAENFQKARWQDNKEEDIVYD 163	
QY	127 AKDDL---DPEKNDSEPSQ--RIKPVFIEDANFGROISYQHAHVHPTDIYEGSTVLN 181	
DB	164 AKADAEELDDPESEDERGSKASTLRDLDFIEDPNFKKNVNTSYAAVQIPTDIYKGSTVLN 223	
QY	182 ELNWTALDEYFKKREEDPSLLQVFGSATGLARYYPASPWVDNSTRPNKIDLYDVRER 241	
DB	224 ELNWTALDENFVEMNRQDPTLLQVFGSATGVTRYIPATPW----RAPKKIDLYDVRER 279	
QY	242 PWYIOGAASPKDMLILVDVSGVSGSLTKLIRTSVSEMLETSLDDDFVNVASFNSAQDV 301	
DB	280 PWYIOGASSPKDMLIIVDVSGVSGSLTKLIRTSVSEMLETSLDDDFVNVASFNSAQDV 339	
QY	302 SCFOHLVQANVRNKKYLKADAVNNITAKGTDYKKGSPFAFEQLLNYNVSRANCKIIMLF 361	
DB	340 SCFTHLVQANVRNKKYKFAVQGVAKGTTGTGKAGFEYAFDQLQNSNITRANCKNIMMF 399	
QY	421 INTQYLDVLGRPMVLGADKAKQWNTNVLDALEGLVITGTLFPVFNITQGFENKTLK 480	
DB	460 INTQYLDVLGRPMVLGAKQWNTNVLDALEGLVITGTLFPVFNITQ--DGPGEKK 517	
QY	481 NQILILGVMDVSLIEDIKELTPRTFLPNGYYFAIDPNGYLLHPNLPKPKSQEPVTL 540	
DB	518 NQILILGVMDVSLIEDIKELTPRTFLPNGYYFAIDPNGYLLHPNLPKPKSQEPVTL 577	
QY	541 DFLDAELENDEKVEIRNKMIDGESKEFTLTKVKSODERYIDKGNRTYTWTVPVNGTDYSL 600	
DB	578 DFLDAELENDEKVEIRNKMIDGESKEFTLTKVKSODERYIDKGNRTYTWTVPVNGTDYSL 637	
QY	601 ALVLPYFYIYKALEETITQARKKGMKQSETLKPDPNFESGYTFTAPRDYNDLKI 660	
DB	638 GLVLPYFYIYKALEETITQARKKGMKQSETLKPDPNFESGYTFTAPRDYNDLKI 697	
QY	661 SDNTEFLNLFNEFIDRKTTPNPNPCNADILNVLVDAGFTNELVQVNSKQK-NIKGVKA 719	
DB	698 SDNTEFLNLFNEFIDRKTTPNPNPCNADILNVLVDAGFTNELVQVNSKQK-NIKGVKA 757	
QY	720 RFVVDGGITRVYKPEAGENMOENPTYEDSFYKRSLDNDNVFTAPYFNK-SGPCAYES 778	
DB	758 VFAATDGGITRVYKPEAGENMOENPTYEDSFYKRSLDNDNVFTAPYFNK-SGPCAYES 817	
QY	779 ---GIWYKAVEIYIOGKLLKPAVGVKIDVNSWIENF---TKTSIRDP--CAGP--- 825	
DB	818 DTGVLSTAVELSLGRRTLRPAVGVKIDVNSWIENF---TKTSIRDP--CAGP--- 876	
QY	826 -VCCKRNSDVMDCVILDDGGFLVLSNQNHQWQVGRFFSEYVDANLMLALYNNSTYTRKE 936	


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QY 1003 FIVESKGTGCPDTRLLIQAEQ--TSDGNPCDMVKQPRYKRGPDVCFDNNVLEDYTDG 1060
Db 1057 FVVAERPLCSQCEAGRLQKETHCPADGPGQCELVQPRYRGRPHICFDYNATEDSDCG 1116

RESULT 9
QY268 ID Q9Y268 PRELIMINARY; PRT: 1145 AA.
AC Q9Y268;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE KIAA0558 PROTEIN.
GN KIAA0558.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN RNP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Sekido Y., Duh F.-M., Latif F., Ding J., Lin J., Mathis M.,
RA Minna J.D.;
RT "Gene 26, a new candidate human tumor suppressor gene located in the
RT 3p21.3 small cell lung cancer homozygous deletion region homologous to
RT a voltage gated calcium channel alpha 2/ delta subunit.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RN RNP SEQUENCE FROM N.A.
RA Wei M.-H., Latif F., Duh F.-M., Adreazoli-Angeloni D., Kashuba V.,
RA Zabarovsky E., Johnson B., Lerman M.I.;
RT "A new alpha 2 delta subunit of the L-type voltage gated calcium
RT channel resides in the lung cancer critical region on 3p21.3.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RN RNP SEQUENCE FROM N.A.
RA Nagase T., Ishikawa K., Miyajima N., Tanaka A., Kotani H., Nomura N.,
RA Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. IX.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro.";
RL DNA Res. 5:31-39(1998).
DR EMBL; AF040709; AAC70914.1; -
DR EMBL; AF042792; AAB96913.1; -
DR EMBL; AB011130; BAA25484.1; -
DR InterPro; IPR002035; -
SQ SEQUENCE 1145 AA; 129268 MW; 9ADRA4807FC70971B CRC64;

Query Match 53.7%; Score 3004.5; DB 4; Length 1145;
Best Local Similarity 54.3%; Pred. No. 6.5e-184;
Matches 585; Conservative 171; Mismatches 283; Indels 39; Gaps 15;

QY 7 LAULTLFOSLLIGPSSPPFSAVITKSWDKMGEDLVTLAKTAGVNLQVIEKYQD 66
Db 44 LMLLPLLLAAPGASAYSFQQHTMQHWARRLEQGVDMRIFGGVQQLREIYKDNEN 103
QY 67 LYTVPNNARQLVEIARDEIKLLNSRSLALAEKVAQAQHWREDFASNEVYYN 126
Db 104 LFEVQENEPQKLVKAGDIESLLDRKVALKRLDAEAENFQKAHRMQDNKEEDIVYD 163
QY 127 AKDDL--DPEKNDSPPGSO--RIKPVFTEDANFGRIQISYQAAAHVHPDIDYEGSTIVLN 181
Db 164 AKADAEIDPSESDVEKRGASTLRDLDFEDPNFKKNVSYAAVQIPDIYKGSVILN 223
QY 182 ELNWTGALDEVFKKNEEDPSLWQVFGSATGLARYYPASPPWVNSRTPNKLIDYVRRR 241
Db 224 ELNWTALENVFENRRQDPTLLAQVFGSATGVTYYYPATPW---RAPKKIDLYVRRR 279
QY 242 PWYIQGASPKDMLILVDVSGVSGVGLTKLIRTSVSEMLETLSDDDFVNVASNSNAQDV 301
Db 1003 FIVESKGTGCPDTRLLIQAEQ--TSDGNPCDMVKQPRYKRGPDVCFDNNVLEDYTDG 1060
Db 1057 FVVAERPLCSQCEAGRLQKETHCPADGPGQCELVQPRYRGRPHICFDYNATEDSDCG 1116
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Db 280 PWYIQGASPKDMLIVDVSGVSGVGLTKLIMKTSVCEMDLTSDDDYVNVASFNEKAQPV 339
QY 302 SCFOHLVQANVRNKKVLDKAVANNITAKGITDYKKGFSFAFEQLLNYNVRANCKIIMLF 361
Db 340 SCFTHLVQANVRNKKVFEKAVQGMVAKGTGYKAGFEYAFDQLQNSNITRANCKIMMF 399
QY 362 TDGGEERAQEIFNKYN-KDKKVVRFRFSVGQHNRYERGPTQWACENKNGYYEIPSPGAI 420
Db 400 TDGGEDRVQDVEKYNPNRTVRVFTFSVGQHNRYDVTPLQWACANNGYYEIPSPGAI 459
QY 421 INTQEVLDVLRPMVLGADKAKOVQNTNYLDALGLVITGTLGVFNITGQFENKTLK 480
Db 460 INTQEVLDVLRPMVLGAKAKOVQNTNYLDALGLVITGTLGVFNITGQFENKTLK 517
QY 481 NQILGVMGVDVSLIEDIKRLTPRTFPCNGYFFAIDPNGYVLLHLPNLPKNPKSQBPVTL 540
Db 518 NQILGVMGVDVSLIEDIKRLTPRTFPCNGYFFAIDPNGYVLLHLPNLPKNPKSQBPVTL 577
QY 541 DFLDAELENDIKVEIRNKMIDGESGKTFRTLVKSDQERYIDKGNRTYTWTPYNGTDSL 600
Db 578 DFLDAELENDIKVEIRNKMIDGESGKTFRTLVKSDQERYIDKGNRTYTWTPYNGTDSL 637
QY 601 ALVLPYTFYIYAKLEETITQARSKKGMKDSFETLAKPDNFEESGYTFIAPROYCNDLKI 660
Db 638 GLVLPYTFYIYAKLEETITQARSKKGMKDSFETLAKPDNFEESGYTFIAPROYCNDLKI 690
QY 661 SDNNTPELLNFEDIRKTPNPNPCNADLNVRLLDAGFTNELVQNYWSKQK-NIKGYKA 719
Db 691 SDNNTPELLNFEDIRKTPNPNPCNADLNVRLLDAGFTNELVQNYWSKQK-NIKGYKA 750
QY 720 RFVYTDGGITRVYKPEAGENQWENPTYEDSFYKRSLDNDNYVFTAPYFNK-SGPGAYES 778
Db 751 VFAATDGGITRVYKPEAGENQWENPTYEDSFYKRSLDNDNYVFTAPYFNK-SGPGAYES 810
QY 779 ---GIMYSKAVEIYIQKLLKAPVAVGKIDVNSWLENF-----TKTSIRDP--CAGP-- 825
Db 811 DTVGILVSTAVELSLGRITLTPAVVGVKLDLEAWAEKPKVLASNRTHQDQKQK-GPNSH 869
QY 826 -VCCCKNSDVMDCVILDDGGFLMANHDDVTNQGIRFEGEIDPSLMRHLNYSIYAFNK 884
Db 870 CEMDCEVNNEDLLCVLIDGGFLVLSNQHNQHWQVGRFSEVDANLMLALYNSFYTRKE 929
QY 885 SYDQSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAASILQOFLSLTFPRLE 944
Db 930 SYDQSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAASILQOFLSLTFPRLE 989
QY 945 AVEMEDDDFTASLSKQSCITEQTQYFFDNDKSFSGVLDGCGSRIFEGEKLMNLF 1004
Db 990 ADPAEAEQ-SPETRESSCMVKQTYIFGVSNAASYNAIIDCGNCSRLFAQRUTNLLFV 1048
QY 1005 MVESKGTGCPDTRLLIQAEQ--TSDGNPCDMVKQPRYKRGPDVCFDNNVLEDYTDG 1060
Db 1049 VAEKPLCSQCEAGRLQKETHCPADGPGQCELVQPRYRGRPHICFDYNATEDSDCG 1106

RESULT 10
QYUENO ID Q9UEWO PRELIMINARY; PRT: 1076 AA.
AC Q9UEWO;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE ALPHA 2 DELTA CALCIUM CHANNEL SUBUNIT ISOFORM II.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN RNP SEQUENCE FROM N.A.
RA Wei M.-H., Latif F., Duh F.-M., Adreazoli-Angeloni D., Kashuba V.,
RA Zabarovsky E., Johnson B., Lerman M.I.;
RT "A new alpha 2 delta subunit of the L-type voltage gated calcium
RT channel resides in the lung cancer critical region on 3p21.3.";
RN [2]
```


RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF042793; AB96914.1; -

DR InterPro: IPR002035; -

SQ SEQUENCE 1076 AA; 122116 MW; EBC474836B7EDA85 CRC64;

Query Match 53.3%; Score 2983.5; DB 4; Length 1076;

Best Local Similarity 54.8%; Pred. No. 1.3e-182;

Matches 576; Conservative 170; Mismatches 267; Indels 39; Gaps 15;

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QY 33 IKSHVQKQEDLVTLAKTASGVNOLVDIYKQDLYVEPNNAQLVEIAARQIEKLLSN 92
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MOHWARLEQEVGVCMRIFGVQVQLRIYKDRNMLFEVQENEPQKLVKVGADIESILDR 60

QY 93 RSKALVSLALEAKVQAAHQWREDFASNVYVYNAKDDL---DPEKNDSEPGSQ--RIKP 147
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 KVOALKRLADAENFQKAHQWQDNIKEEDIVYDADAKADAELDDPSESDVERGSKASTLRL 120

QY 148 VFTEDANFGQISYQHAHVHPTDIYEGSTIVLNELNWTLSALDVFYKKNREEDPSILWQV 207
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 DFTEDPNFKKNVSYAAVQIPTDIYKGSTVILNENWTALENVFMENRRQDPTLLWQV 180

QY 208 FGSATGLARYPPASPPVDNRSRTPNKIDLYVRRRPWTIOGAASPKDMLILVDVSGSYGL 267
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 181 FGSATGVTRYYPATPW----RAPKKIDLYVRRRPWTIOGAASPKDMLIVVDVSGSYGL 236

QY 268 TLKLIRTSVSEMLETLSDDDDFVNVASFNSNAQDVSFQHLVQANVRNKKVYLKDAVNNTA 327
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 237 TLKLMKTSVCEMLDLSDDDYVNVASFNEKAQPVSCFTHLVQANVRNKKVFEKAVQGVMA 296

QY 328 KGITDYKKGFSFAFEQLLNVSANCKIIMLETDGGERAQAQIFNKYN-KDKKVRVFR 386
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 297 KGITYKAGFEYAFDQLQNSNITRANCKNIMMPTDGGEDRVQDVFYKKNPNTVRYFT 356

QY 387 FSVQGHNYERGPQIOWMACENKGYIYFIPSGAIRNTQEVLDVLRPMVLADGAKOVQW 446
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 357 FSVQGHNYDVTPLQWMAKANKGYIFEIPSGAIRNTQEVLDVLRPMVLADGAKOVQW 416

QY 447 TNYVLDALGLVITGLPVFNITGQENKTNLKNQLILGVMGVDVLSLEDKRTPRTFL 506
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 417 TNYVEDALGLVITGLPVFNLTQ---DGPGEKKNQLILGVMGIDVALNDIKRTPNVTL 474

QY 507 CPNGYVFAIDPQGVLLHLPNLOPKNPKASQBPVTLDFLDAELENDIKYIRKNMIDGESGE 566
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 475 GANGYVFAIDPQGVLLHLPNLOPKNPKASQBPVTLDFLDAELENDIKYIRKNMIDGESGE 534

QY 567 KTFRTLVKSDERYIDKGNRTYVTPVNGDYSLALVLPYTSFYIYKAKLEETITQARSK 626
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 535 KQIRTLVKSLDERYIDVTRNYTWPIRSTNYSGLVLPYSTFYLQANLSDQILQ---- 590

QY 627 KGMKQDSETLKPDNFBESGYTFTIAPRYCNDLKTSDNNTBFLNFNFIIDRKTNNPSCN 686
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 591 ---VKYEFLLPSFSEGHVFTIAPREYCKDLNASDNNTBFLNFIELMEKVTPDSKQCN 647

QY 687 ADLNRVLLDAGFTNELVQVWSKQ--NIGVKARFVVTDDGITRVYPKEAGENQWENPE 745
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 648 NFLHNLILDTGTITQQLVVRVWRDQDLNTYSLAVFAATDGGITRVFPNKAEDWTNPE 707

QY 746 TYEDSFYKRSILDNDNYVFTAFYFNK--SGPGAYES---GIMVSKAVEYIYQGLKLPVAVG 801
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 708 PFNASFYRSLDNHGYVFKPPHQDALLRPLELENDYTGILVSTAVELSLGRTRLPVAVG 767

QY 802 IKIDVNSWIENF-----TKTSIRDP--CAGP----VDCCKRNSDVMDCVILDDGGFLLMA 850
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 768 VKLDLEAWAEKFKVLASNRTHQDQPKC--GPNSHCEMDCEVNNEDLLCVLIDDGGFVLVS 826

QY 851 NHDDYTNQIGRFGCEIDPSLMRHLVNTSVAFNKSYYQVSCPEGAAPKQAGHRSAYVP 910
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 827 NONHOWQVQRFSEVDANLMLALNNYSFYTRKESYDQACAPQPPGNCGLGAAPRGVFP 886

QY 911 SVADILQIGWAWAAWASLIQOFLLSLTFPRLLAEVEMEDDDFTFASLSKOSCIQTYQYF 970
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 887 TVADFLNLAWTSAWASLSLQOLLYGLIYHSWQADPAEAG--SPETRESSCYMKQTYQY 945
```

```
QY 971 FDNDKSFSGVLDGCGNCSRIPIHGEKLMNTNLIIFIMVBSKGTCPDTRLLIOAQE--TSDG 1028
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 946 FGSYNASYNAIIDCGNCSRLFQAQRLTNTNLLFYVAPLCSQCEAGRLQKETHCPADG 1005

QY 1029 PNPCDMYKOPRYRKGPVDFDNNVLEDYDCG 1060
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1006 PEQELVQRPRYRGRPHICFDYNATEDSDCG 1037
```

RESULT 11

Q9NSA6 PRELIMINARY; PRT: 975 AA.

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ID Q9NSA6 AC Q9NSA6; DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE LUAC11.1 (CALCIUM CHANNEL, VOLTAGE-DEPENDENT, L TYPE, ALPHA 2D SUBUNIT
DE (K1AA0558)) (FRAGMENT).
GN LUAC11.1. OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606; RN [1]
RP SEQUENCE FROM N.A.
RA Barlow K.; RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z84492; CAB41767.2; -
DR InterPro; IPR002035; -
FT NON_TER 1
SQ SEQUENCE 975 AA; 110192 MW; C7874D46B88242BF CRC64;
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Query Match 50.3%; Score 2814; DB 4; Length 975;
Best Local Similarity 56.9%; Pred. No. 8.1e-172;
Matches 541; Conservative 143; Mismatches 230; Indels 36; Gaps 14;

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QY 132 DPEKNDESPGSG--RIKPVFTEDANFGQISYQHAHVHPTDIYEGSTIVLNELNWTSA 189
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 2 DPESEDVERGSKASTLRLDFTEDPNFKKNVSYAAVQIPTDIYKGSTVILNENWTEAL 61

QY 190 DEVFKKREEDPSLLWQVFGSATGLARYPPASPPVDNRSRTPNKIDLYVRRRPWTIOGAA 249
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 62 ENVFENNRQDPTLLWQVFGSATGVTRYYPATPW----RAPKKIDLYVRRRPWTIOGAS 117

QY 250 SPKQMLILVDVSGVSGSLTLKLIRTSVSEMLETLSDDDDFVNVASFNSNAQDVSFQHLVQ 309
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 118 SPKQMLILVDVSGVSGSLTLKLIRTSVSEMLETLSDDDDFVNVASFNEKAQPVSCFTHLVQ 177

QY 310 ANVRNKKVLDVANNITAKGTDYKKGFSFAFEQLLNVSANCKIIMLETDGGERA 369
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 178 ANVRNKKVFEKAVQGVMAKGTGYKAGFEYAFDQLQNSNITRANCKNIMMPTDGGEDRV 237

QY 370 QEIFNKYN-KDKKVRVFRFSGVQHNVERGPIQWACENKGYIYFIPSGAIRNTQEVLD 428
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 238 QDVFYKKNPNTVRYFTFSVQGHNYDVTPLQWMAKANKGYIFEIPSGAIRNTQEVLD 297

QY 429 VLGRPMVLADGAKOVQWNTNYSGLVITGLPVFNITGQENKTNLKNQLILGVMA 488
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 298 VLGRPMVLADGAKOVQWNTNYSGLVITGLPVFNLTQ---DGPGEKKNQLILGVMA 355

QY 489 GVDVLSLEDKRTPRTFLCPNGYVFAIDPQGVLLHLPNLOPKNPKASQBPVTLDFLDAELE 548
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 356 GIDVALNDIKRTPNVTGLVNGYVFAIDPQGVLLHLPNLOPKNPKASQBPVTLDFLDAELE 415

QY 549 NDIKVEIRNKKMIDGESGEKTFRTLVKSDERYIDKGNRTYVTPVNGDYSLALVLPYTS 608
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 416 DENKEEIRRSIDNKGKHKQIRTLVKSLDERYIDVTRNYTWPIRSTNYSGLVLPYTS 475

QY 609 FFIYKAKLEETITQARSKKGMKQDSETLKPDNFBESGYTFTIAPRYCNDLKTSDNNTBFL 668
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 476 TFIYQANLSDQILQ-----VKYEFLLPSFSEGHVFTIAPREYCKDLNASDNNTBFL 528
```


QY	669	LNFEFIDRKTNNPNSONADLINRVLDAGFTNELVONYWSKOK-NIKGVKARFVVTDDG	727
Db	529	KNFTELMEKVTSPDSKOCNFFLNHLNLDITGITQOLVERVWRDQDLNTYSLLAVFAATDGG	588
QY	728	ITRVYPKEAGENQENPETEYDSFKRSLENDNYVETAPYFNK-SGPGAYES--GLMVS	783
Db	589	ITRVFPNKAADWTENPEFPNFSYRSLNDNHGTVFPHPHDDALLRPLELENDTVGLLVS	648
QY	784	KAVEIYTOGKLLKPAVGVIGIKIDVNSWTEF-----TKTSIRDP--CAGP-----VCDCRKN	832
Db	649	TAVELSGLRTRLRPAVGVKLDLEAWAEKFKVLASNETHODQPKC-GPNSHCEMDCEVN	707
QY	833	SDVMDCVILDDGGFLMANHDDYNTQIGRFFGEIDPSLMRHLVNISVYAFNKSVDYQSV	892
Db	708	NEDLLCVILDDGGFLVLSNQNHQWQVGRFFSEVDANLMLALYNNSFYTRKESDYQAA	767
QY	893	EPGAAPKQAGHRSAYVPSVADILQIGWATAAAWSILQOFLLSLTPTPRLLEAVEMEDDD	952
Db	768	APQPPGNLGAAPRGVFTVADFLNLAWMTSAAAWSLQOFLLYGLIYHSWFQADPAEAG	827
QY	953	FTASLSKQSCITEQTYFFONDNSFSGVLDGCGNCSRFHGEKLMNTNLIFIMVESKGT	1012
Db	828	-SPETRESSCVAKOTYFSGVNSYNALIDCGNCSRLFHAQRLTNLNFVVAEKPLCS	886
QY	1013	PCDFRLLIQAEQ--TSDGPNPCDMVKQPRYKRGPDVCFDNNVLEDDYDCG	1060
Db	887	QCEAGRLQKETHCPADGPEQCELVQRPRYRGPHICFDYNATEDTSDCG	936
RESULT 12			
ID	Q921L5	PRELIMINARY; PRT; 1091 AA.	
AC	Q921L5;		
DT	01-MAY-1999 (TREMBlrel. 10, Created)		
DT	01-MAY-1999 (TREMBlrel. 10, Last sequence update)		
DT	01-OCT-2000 (TREMBlrel. 15, Last annotation update)		
DE	CALCIUM CHANNEL ALPHA-2-DELTA-C SUBUNIT.		
GN	CACNA2D3.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=BRAIN;		
RX	MEDLINE=99098955; PubMed=9880589;		
RA	Klugbauer N., Lacinova L., Marais E., Hobom M., Hofmann F.;		
RT	"Molecular diversity of the calcium channel alpha2delta subunit.";		
RL	J. Neurosci. 19:648-691(1999).		
DR	EMBL; AJ010949; CAA09423.1; .		
DR	MGI; MGI:1338890; Caccna2d3.		
DR	InterPro; IPR002035; .		
SQ	SEQUENCE 1091 AA; 122777 MW; 7AE2BDAl0077A0A CRC64;		
Query Match			
Best Local Similarity 20.0%; Score 1119.5; DB 11; Length 1091;			
Matches 321; Conservative 230; Mismatches 443; Indels 131; Gaps 41;			
QY	3	AGCLALATLTFOSLLIGSPSEPPFSAVTIKSWDKMQEDLVTLAKTAGVNLVDIYE	62
Db	14	ASALLA-TALLYAALGDVVRSEQQIPLSV-VKLWASAFGEIKSIAAKYSGSOLLQKKYK	71
QY	63	KYQDLYTFEPNNARQLVEAARDIEKLLSNRSKALVSLALEAKYQAAHQRWEDFASNEV	122
Db	72	EYEKVAIEIDGLQLVKLAKIMEEFHKKSEAVRRLVEAEAEHLKHEFDADL---QY	128
QY	123	VYVNAK--DLDPEKNDSEPGSORIKPVFIEDANFR-QISYQAAVHIPTDIYEGSTV	179
Db	129	EYFNAVLIERNKDXGNFLGKEFI---LAPNDHFNNLPVNLISLSDVQVPTNWKNDPAI	185
QY	180	LNELNWTSLDVEFKKNREEDPSLLMQVFGSATGLARYYPASPWVDNSRTPNKIDLYDVR	239

OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
OC	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=BRAIN;
RA	Bugert P., Hanke S., Chudek J., Kovacs G.;
RT	"Analysis of a putative tumor suppressor gene region of 100 kb at chromosome 3p21.1 in conventional renal cell carcinoma."
RL	Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RT	EMBL; AJ272268; CAB75962.1; -
DR	InterPro: IPR002035; -
DR	SEQUENCE 997 AA; 112996 MW; B56D13133FD67B8D CRC64;
QY	Query Match 18.7%; Score 1045.5; DB 4; Length 997;
QY	Best Local Similarity 28.3%; Pred. No. 1.8e-58;
QY	Matches 293; Conservative 213; Mismatches 408; Indels 123; Gaps
QY	86 IEKLLNSRKALVSLALEAKVQAQHWREDFASNEVWYINAK--DDLDPKNDSPGSG 143
QY	1 MEENFHKKSEAVRLVEAAEAHLKHEFDADL---QYEFNAVLINERDKGNFLELGR 57
QY	144 RIRPVFIEDANFCR-QISQOHAHVHTPTDIYEGSTIVLNLNWTLSALDEVFKNREEDPS 202
QY	58 FI---LAPNDHFNNLPVNTLSLSDVQPTNMYNKOPAIWGVWSELSKVFVDNFDRODS 114
QY	203 LLWQVFGSATGLARYYPASPWVDNSRTPNKIDLYDVRRRPWYIQGAASPKDMLILVDVSG 262
QY	115 LIWQVFGSAKGFPRQYPGIKWEPDE---NGVTAFCDRNRKWTIQATSPDVVILVDVSG 171
QY	263 SVSGLTKLIRTSVSEMLETSLDDDDFVNVPASNQAQVYS-CFQ-HLVQANVRNKKVLKD 320
QY	172 SMKGLRTIAKQTVSSILDTGLDDDFNIAYNEELHYHVEPCLNGTLVQADRTNKEHFE 231
QY	321 AVNNITAKGITDYKKGFSAFEGOLLNMYNSRAN--CNKILMFLTDCGGERAQEIFKNYN- 377
QY	232 HLDKLFAGKIGMULDIALNEAFNLTSDFNHTGQSGICSAIMLITDGAVTYDTIFAKYNW 291
QY	378 KDKKVRFRSVGQHNVERGPIOWMACENKNGYYEIPSGIATRINTQEYLDVLGRPMVLA 437
QY	292 PDKRVFTVLIGREAFADNLAKWACANKGFTQISTLADQGVNWEVLHLVSRPKVI- 350
QY	438 GDKAKQVQWTVNYLDAL-----ELG--LVITGLTFVFNITGOFENKTLNKLILG 486
QY	351 -DQEHVDVWTEAYIDSTLPOAKLTDDQGPVMTTVAMPVES---KQNETRSKG-ILLG 404
QY	487 VMGVDSVLEDKILTRPFTPLCPNGYFYADPNQYVLLHPNLQ---PKNPKSQEP--VTLD 541
QY	405 VVGTDVPVKELLTIPKYLIGHYAFATNNNGYIITHPELRLLYEEGKRKRKNPYSSVD 464
QY	542 FLDAELENDIKVIRKNMIDGESSEKTRFLYKSDQERYIDKGNRT-----YVTWTPVNG 595
QY	465 LSEVEWEDRDV-LRNAWNRKTKG--FMSVEK---KTVDKGRVLVMTNDYYIDTIG 517
QY	596 TDYSALVLPT-YSFYIIKALEETITQARSKKGMKDSSETLKPDNFESGTYFTIAPRDY 654
QY	518 TPESLGVALSRGHGKYFF-----RGNVTIEEGL--HDLHPDYSLADSEWY 561
QY	655 CN-DLKISDNNTTEFLNFEFIDRKTPNPNPSCNADLINRVLLDAGTNNELVQNYWS---- 709
QY	562 CNTDLHPHRHLSQLAFLKLYLKGKEP-LLOCDKELIQLEVFA-VVSAPIEAYMTSLAL 619
QY	710 --KQKNIKYKGVKRVFVTDGITTVP-----KEAGENWQENPETVEDSDYFKRS 755
QY	620 NKSNSDKGVEVAFGLTRTGLSRNLNLFVGAEQVTNQDFUKAGDKENIFNADHPPLMYRA 679
QY	756 LDN--DNYVFTAPYFNKSGPGAYESGLWVSKAVEIYIQGKLLKPAVVGKIDVNSWENF 813
QY	680 AEQIPGGSFVYSIFP--STGPPVNSNVVTAISTSILLDERKSPVVAAGVGMKLEFFQRF 873
QY	814 TKTSIRDPDCAQVDCDKRNSDVMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRH 973

QY 89 LLSNRKALVSLALBAEKVQAQHQREDFA--SNEWVYNAKDDLDPEKNDSEPG-----S 142
 Db 71 ML-----ARKMDAVRCIQEFTYFSSYSTFNCSSELEPNEAEFAWYRN 117
 QY 143 QRIKPVFIEDANF-GROISYOHAAVHPTDIIEGFTIVILNELNWTSDALDEVFKKNEEDP 201
 Db 118 MELNP-----DTHFYNTVPDTHSSVHVFSNIWDRSERVLKTIWSEHLDEVERQNTQSDP 173
 QY 202 SLLWQVFGSATGLARYYPASPWVDNRTPNKIDLYDVRRRPWIQGAASPKDMLILVDVS 261
 Db 174 ALSWQYFGSDTGILRHYPAAQWTDTPNRDDADTYDCRKRWSYIETATCSKDIVILLDHS 233
 QY 262 GSVGLTLKLIKRTSVMLETLSDDDFNVASFNSNAQD-VSCFQ-HLVQANVRNKKVLK 319
 Db 234 GSWTGRHVRHAFRTIRSIDLTFSNDDFTILRYSEVNDIIFCFNGALVQATPENIEVEN 293
 QY 320 DAVNNI-TAKGTTDYKKGFSFAFOLLNYSNR---ANCKNIIMLFTDGGEEAQAEIF 373
 Db 294 QOIEQLDDPEGYANITLAYETAFQLLRKYDSRHCVTSTCNOAIMLVTDGVAGNTTEVF 353
 QY 374 NKYN-----KDKKVRVRFESVGOHNYERGIQWMAKENGYYEIPSIGAIRINTOE 425
 Db 354 QRYNNGENGTSQMDTRVFTYLLGKEVTKVREIQWMAKENGYYEIPSIGAIRINTOE 413
 QY 426 YLDVLGRPMVLADKAKQVQWNTNVDLAL-----ELGLVITGTLVPFNITQOFENK 476
 Db 414 YVDVATPLVLQNEQHPT-WTHAFTDKTYDKTSNEKRPRMLISVGPAPDFRYRHANS 472
 QY 477 TNLKQOLIIGLVNGVDVSLDKRLAPREFTLCPNGYFAIDPNGYVLLHNPLOP-----K 530
 Db 473 TNPRARL-LGVAGTDPVEDIDKLLPYKLGNGYSFVVSNNGYVLLHNPLOP-----K 531
 QY 531 NPKSOEPTVLDLDAE-LENDIK-----VEIRNMIDGESGE-KTPRTLKVSQDERY 580
 Db 532 NPNYN---SIDTVEHLFEDQS PREPGESILHIRNAMYHEANEFKSISVKFYDKMRR 588
 QY 581 IDKGNRTYTVPNGTDYSIALVLT-TSFYIYKAKLETTIQAARKKGMKDSKTLKPD 639
 Db 589 VSEERQDYFAPLNTPTGLVMPSEYKTKWIKVGEYD---KNKHKINISOFFIGE 644
 QY 640 NFE-----SGYTFIAP-----RDYC-----NDLKISDNNTFLLNFEFID--- 676
 Db 645 NKKVHPDWWYKYHLEGHEFTYPAELREFLAKWQNDKWKSEYAEDESDDDDKDLNC 704
 QY 677 -RTPNPS--CNADLINRVLDAETNELVQNYW-----SKQNKIKVKA--RFVYTDG 726
 Db 705 GRKTLGDDAYCNKELVNLIFDAKVNS-SYGVWRFESDEERQLIERFRADLRFFVATMS 763
 QY 727 GTRVYPKAENWQ-----ENPTYEDSFYKRSL-----DNDNYVFT 764
 Db 764 GLTR-----WQIFGEVEVDTRDFGDTHTTAIDETWYKSAILOHEDRAESFYVS 814
 QY 765 APVENKSGPGAYESGIMVSKAVEIYQGLKPAVVGVKIDVNSWTENFTKTSIRDPAC 824
 Db 815 VKYD-----DPMEDSEVKCNHCL 833
 QY 825 PVDCKRNSDMVDCVILDGGLMANHDDYTNQIGRFFGEIDPDSLMRHLVNIYSYAFNK 884
 Db 834 PIC-----TDDVDVCCVIDNNAYIVIGN--INTTKFFGEFGHDVMTAMVERGIFLSIE 886
 QY 885 STDYQSVQ--EPGAPKQAGHRSAYVPSVAD-ILQIGWATAAWSILQQFLLSLTFPR 941
 Db 887 VDYQEQCKEPEKAVNE-----YTDEIEYVAVGDKGKSSA----- 923
 QY 942 LLEAVEMEDDDTASLSK-----QSCITEQYFEDNDSKFSGLVDC--CNCSEIHF 992
 Db 924 --SKPKDDSDDENAMPDEPEPDYKACDKRSTLYAL--OPSALVGINDFVEAPSTRPFL 979
 QY 993 GEKLMNTNLIIFIVE----SKGTCPCDTRLIIQAEOTS-DGPNPCDWKQOPRY-RKGPDV 1046
 Db 980 VKKIPNSNLVVLVVNVLMPSR-----SVRLTTEPQRMEDKEFPCKLANMSFYERRIEE 1034
 QY 1047 CFDDNNVLEDYTD 1058

Db 1035 CY--TVHEDLSD 1044

Search completed: July 23, 2001, 07:47:50
 Job time: 636 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 23, 2001, 07:28:39 ; Search time 92.97 Seconds

(without alignments)

711.421 Million cell updates/sec

Title: US-09-397-548-14

Perfect score: 5748

Sequence: 1 MAGCLLALTLTFLQSLIG.....IIGIQFLLMLVSGSTRLL 1091

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_0601.*
1: /cgnl_9/gcgdata/geneseq/geneseq/AA1980.DAT.*
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22: /cgnl_9/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5748	100.0	1091	AA1980	Human neuronal cal
2	5748	100.0	1091	AA1981	Human neuronal cal
3	5748	100.0	1091	AA1982	Human neuronal cal
4	5748	99.9	1091	AA1983	Human neuronal cal
5	5742	99.9	1091	AA1984	Human neuronal cal
6	5728.5	99.7	1110	AA1985	Human neuronal cal
7	5708.5	99.3	1086	AA1986	Human neuronal cal
8	5708.5	99.3	1086	AA1987	Human neuronal cal
9	5708.5	99.3	1086	AA1988	Human neuronal cal
10	5691.5	99.0	1084	AA1989	Human neuronal cal
11	5691.5	99.0	1084	AA1990	Human neuronal cal

12	5691.5	99.0	1084	21	AA19589	Human calcium chan
13	5672	98.7	1103	16	AA19102	Human neuronal cal
14	5672	98.7	1103	19	AA19151	Human calcium chan
15	5672	98.7	1103	21	AA19586	Human calcium chan
16	5652	98.3	1079	19	AA19154	Human calcium chan
17	5652	98.3	1079	21	AA19588	Human calcium chan
18	5646	98.2	1079	16	AA19104	Human neuronal cal
19	5508.5	95.8	1106	18	AA19772	Rabbit skeletal ca
20	5508.5	95.8	1106	18	AA19389	Rabbit skeletal ca
21	5508.5	95.8	1106	21	AA19754	Rabbit skeletal ca
22	5487.5	95.5	1106	16	AA19305	Rabbit skeletal ca
23	5364.5	93.3	1100	10	AA19564	Rabbit skeletal mus
24	5364.5	93.3	1100	10	AA19322	Human alpha-2-delt
25	5341.5	92.8	1145	21	AA19322	(Alpha)-2 subunit
26	5281.5	92.8	1145	21	AA19322	Human skeletal cal
27	5281.5	92.8	1145	21	AA19322	Human alpha-2-delt
28	5281.5	92.8	1145	21	AA19322	Human alpha-2-delt
29	5281.5	92.8	1145	21	AA19322	Human alpha-2-delt
30	5281.5	92.8	1145	21	AA19322	Human alpha-2-delt
31	5281.5	92.8	1145	21	AA19322	Human alpha-2-delt
32	5281.5	92.8	1145	21	AA19322	Human alpha-2-delt
33	5281.5	92.8	1145	21	AA19322	Human alpha-2-delt
34	5281.5	92.8	1145	21	AA19322	Human alpha-2-delt
35	5281.5	92.8	1145	21	AA19322	Human alpha-2-delt
36	5281.5	92.8	1145	21	AA19322	Human alpha-2-delt
37	5281.5	92.8	1145	21	AA19322	Human alpha-2-delt
38	5281.5	92.8	1145	21	AA19322	Human alpha-2-delt
39	5281.5	92.8	1145	21	AA19322	Human alpha-2-delt
40	5281.5	92.8	1145	21	AA19322	Human alpha-2-delt
41	5281.5	92.8	1145	21	AA19322	Human alpha-2-delt
42	5281.5	92.8	1145	21	AA19322	Human alpha-2-delt
43	5281.5	92.8	1145	21	AA19322	Human alpha-2-delt
44	5281.5	92.8	1145	21	AA19322	Human alpha-2-delt
45	5281.5	92.8	1145	21	AA19322	Human alpha-2-delt

ALIGNMENTS

RESULT 1

AA191011
ID AA191011 standard; Protein; 1091 AA.
XX
AC AA191011;
XX
DT 01-DEC-1995 (first entry)
XX
DE Human neuronal calcium channel subunit alpha 2b.
XX
KW Calcium channel subunit; antagonist; agonist; diagnosis;
KW Lambert Eaton Syndrome.
XX
OS Homo sapiens.
XX
PN WO9504822-A.
XX
PD 16-FEB-1995.
XX
PF 11-AUG-1994; 94WO-US09230.
XX
PR 11-AUG-1993; 93US-0105536.
PR 05-NOV-1993; 93US-0149097.
XX
(SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
XX
PI Ellis SB, Gillespie A, Harpold MM, McCue AF, Williams ME;
XX
DR WPI; 1995-090900/12.
XX
DR N-PSDB; AAQ84664.
XX
PT DNA encoding human calcium channel sub-unit(s) - used for
PT developing prods. for studying calcium channels, e.g. for
PT obtaining agonists and antagonists

XX PS Claim 4; Columns 283-288; 166pp; English.

CC The present sequence represents the alpha-2 subunit of a human calcium channel. Calcium channels are membrane-spanning, multi-subunit proteins that allow controlled entry of calcium ions into cells. This leads to depolarisation events required for muscle contraction. The recombinant subunit, when expressed with nucleic acids encoding the complete calcium channel, can be used in assays for the detection and characterisation of compounds that modulate the channel. The DNA encoding the subunits can be alternatively spliced when transcribed, giving more than one form of the protein from the same transcript, each having slightly different properties. In addition, the reactivity of the alpha 1 subunit with IgG molecules from the serum of an individual with Lambert Eaton Syndrome (LES) can be used as a diagnostic for the disease.

XX SQ Sequence 1091 AA;

Query Match 100.0%; Score 5748; DB 19; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1091; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAAGCLLALTLTFLQSLILIGSPSEPPSAVTIKSWDKMOEDLVTLAKTAGVNLVDI 60
Db 1 maagcllaltltlflqslilgsssepppsavtlkswdkmqedlvtlaktasgvnlvdi 60

Qy 61 YEKYQDLYTEPNARQIVEAARDIEKLLNSRKALVSLALEAEKQAAHQWREDFASN 120
Db 61 yekyqdytvepnarqliveaardieklslsrkalvslaleaeqvaaahqwredfasn 120

Qy 121 EVVYNKADDDLPKDNSEPSQRIKPVIEDANFGROISYQHAHVHPTDIYEGSTVL 180
Db 121 evvynakddldpkdnsepsqrikpviedanfgroisyoahavhptdiyegstvl 180

Qy 181 NELNWTSLDVEFKNREDESLWVFGSATGLARYYPASPVVDNSRTPNKIDLYDVR 240
Db 181 nelnwtaldevfknreedsllwvfgsatglaryypaspvvdnsrtpnkidlydvr 240

Qy 241 RPWYIQGAASPKDMLILVDVSGVSGTLKLIKRTSVSEMLETSLDDDFNVNASFNSAQD 300
Db 241 rpyyiqgaaspkdmlilvdvsgvsgtlklirtsvsemlletisdddfnvvasfnsaqd 300

Qy 301 VSCFQHLVQANRKKVLKDAVNITAKGIDYKKGFSAFEOILLNYSRANCNKIIML 360
Db 301 vscfqlhvanrnkvkldavnnitakgidtykkgsfafeqllnysrancnkiiiml 360

Qy 361 FTDGGEERAQEIFNKNKDKRVFRFVSGVGHNYERGPIONMACENKGYEYIPEISGAIR 420
Db 361 ftdggeeeraqelfnknkdkrvfrfsvghnyergpiqwmacenkgyyeipisgaair 420

Qy 421 INTQBYLDVLRPMVLGDKAKQVQWNTNVLDAELGLVITGTLFVFNITQGFENKTNLK 480
Db 421 intqeyldvlgpmvlgdkakqvwnvnldeleglvgitgtlpvfnitqgfentnlnk 480

Qy 481 NQLILGVMGVDSLEDIKRLPRTLCPNGYFFAIDPNGVYLLHPNLPKPKSQEPVTL 540
Db 481 nqlilgvmgvdsledikrlprtlcpngyffaidpngvyllhpnlpkpkpsqepvltl 540

Qy 541 DFLDALENDLKVEIRKNKIDGSEKFTRLVKSDERYIDKGNRTYTWTPVNGTDYSL 600
Db 541 dflaelendlkveirknkidgsegekfrlvksqberyidkgnrtytwtpvngtdysl 600

Qy 601 ALVLPTYFYIKALEETITQAKSKGKMDSETLPKDPNFEESGYTFIAPRDYCNLDKI 660
Db 601 alvlptyfyikaleetiqarskgkmdsetlpkdpnfeesgytfiaprdyendiki 660

Qy 661 SDNTEFLLNFEIDRTPNPNPCNADLINRVLLDAGFTNELVQNYWSKOKNIKGVAR 720
Db 661 sdntefllnfeidrtppnpncnadlinrvllldagftnelvqnywskgnikgvkar 720

Qy 721 FVWTDGGITRVYPKAGENWQENPETYEDSFYKRSLODNDNVFTAPYFNKSGPGAYESGI 780
Db 721 fvwtdggitrvyypkagenwqenpetyedsfykrsldndnvftapyfnkspgpayesgi 780

Db 721 fvwtdggitrvyypkeagenwqenpetyedsfykrsldndnyvftapyfnkspgpayesgi 780

Qy 781 MYSKAVEIYIOGKLLKPAVVGIIKIDVNSWIENFTKTSRDPACAGPVCDCRNSDVMDCVI 840
Db 781 mvskaveiyyogkllkpaavgikidvnswieftktsrldpcagpvcdcxrnsdvmdcvi 840

Qy 841 LDGGFLMANHDDYTNIGIRFFGFEIDPSLMRHLVNIISVYAFNKSVDYQSVCEPGAAPKQ 900
Db 841 ldggflmanhddytndgrffgeidpslmrhlvnlvisyafnksydyqsvcepaapq 900

Qy 901 GAGHSAYVPSVADILQIGWATAAANSILOFLLSLTPRLEAVEMEDDDFTASLSKQ 960
Db 901 gaghsayvpsvadilqigwataaawsilqflsltpfrrleavemedddftaslskq 960

Qy 961 SCITEQTQYFFDNDKSKSPSGVLDGNCRSRIFHGEKLMNTNLIIFIMVESKGTCPCTRLLI 1020
Db 961 sciteqtqyffndsksfsgvldcgnrcsrifhgeklmntnlifimveskgtpcptrlll 1020

Qy 1021 QAEOTSDGNPCDMVKQPRYKGPDPVCFDNNVLEDTDCGGVSGNLPSLWYIIGIQFLLL 1080
Db 1021 qaeqtsdgnpcdmvkprryrgpdpvcfdnnvledytdcggvsgnlpslwyiigiqflll 1080

Qy 1081 WLVSQSTHRL 1091
Db 1081 wlvsqsthrll 1091

RESULT 3
AAB10576
ID AAB10576 standard; Protein; 1091 AA.
AC AAB10576;
XX DT 22-DEC-2000 (first entry)
XX DE Human calcium channel alpha-2 subunit protein.
XX KW Human; calcium channel; calcium channel subunit; diagnosis;
XX KW Lambert Eaton Syndrome; calcium channel subunit alpha-2.
XX OS Homo sapiens.
XX PN US6096514-A.
XX PD 01-AUG-2000.
XX PF 25-MAY-1995; 95US-0450562.
XX PR 04-APR-1988; 88US-0176899.
XX PR 02-FEB-1990; 90US-0482384.
XX PR 08-NOV-1990; 90US-0603751.
XX PR 30-NOV-1990; 90US-0620250.
XX PR 15-AUG-1991; 91US-0745206.
XX PR 10-APR-1992; 92US-0868354.
XX PR 13-JUL-1992; 92US-0914231.
XX PR 11-AUG-1993; 93US-0105536.
XX PR 05-NOV-1993; 93US-0149097.
XX PR 07-FEB-1994; 94US-0193078.
XX PR 04-APR-1994; 94US-0223305.
XX PR 11-AUG-1994; 94US-0290012.
XX PR 23-SEP-1994; 94US-0311363.
XX PR 28-SEP-1994; 94US-0314083.
XX PR 07-NOV-1994; 94US-0336257.
XX PR 13-MAR-1995; 95US-0404950.
XX PA (SIBI-) SIBIA NEUROSCIENCES INC.
XX PI Ellis SB, Williams ME, McCue AF, Harpold MM;
XX WIPI; 2000-548230/50.
XX DR N-ESDB; AAA71707.
XX XX Human calcium channel beta subunit polynucleotides, useful for

PT producing recombinant eukaryotic cells and for diagnosing Lambert Eaton
PS Syndrome

XX Example IV; Column 135-144; 153pp; English.

XX This invention describes a novel isolated DNA molecule (I) comprising a
CC sequence encoding a beta3-1 subunit of a human calcium channel.
CC Nucleic acid probes comprising 14-30 contiguous nucleotides of
CC beta3 subunit encoding DNA are useful for isolation and cloning of
CC calcium channel subunit-encoding DNA. Recombinant eukaryotic cells that
CC express heterologous calcium channel are useful for identifying compounds
CC that modulate calcium channel activity and in assays for identifying
CC agonists and antagonists of calcium channel activity in humans. Human
CC calcium channel subunit or eukaryotic cells expressing the channel are
CC useful for diagnosing Lambert Eaton Syndrome (LES) in a human. This
CC sequence represents the human calcium channel alpha-2 subunit which is
CC described in the method of the invention.

XX Sequence 1091 AA;

Query Match 100.0%; Score 5748; DB 21; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1091; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAAGCLLALTTLTQSLILIGSPSEPPPSATVTKSWVDKMQEDLVTLAKTASGVNQLVDI	60
Db	1	maagcillaaltltlqsliligspssepppsavtikswvdkmqedlvtlaktasgvnqlvdi	60
Qy	61	YEKYQDLTYVEPNARQLVEAARDIEKLLSNRSKALVSLALEKVOAAHQWREDFASN	120
Db	61	yekyqdltyvepnarqlveiaardieklslsrskalvslalesekvaahqwrdfasn	120
Qy	121	EVVYNKADLDPEKNDESPQSRIKPVFIEDANFGROISYOHAAVHIPTDIYEGSTIVL	180
Db	121	evvynakddldpekndepsqrikpvfiedanfrqisvghaahvhiptdiyegstivl	180
Qy	181	NELNWTSSALDEVEKKNREEDSLWQVSGSATGLARYYPASPWDNSRTPNKIDLYDVR	240
Db	181	nelnwtssaldevekknreedslwvsgsatglaryypaspwdnsrtpnkidydvrr	240
Qy	241	RPWYIQGAASPKDMLILVDVSGVSLGLTKLIRTSVSMLETLSDDDFVNVSFNSNAQD	300
Db	241	rpwyiqgaaspkdmlilvdvsgvsglklirtsvsmleltlstdddfvnvasfnasnaqd	300
Qy	301	VSCFOHLYQVANNRNKKVLKDAVNNTAKGIDTYKGFSAFEQLNLNYSRANCNKIIML	360
Db	301	vscfqlhlyqanvrnkvlkdavnnitakgitydkgfsafeqlnllynvsrancnkliiml	360
Qy	361	FTDGEERAQELFNKYNKDKVRFRFSVGOHNYERGPQWACENKGYEYIEPSIGAIR	420
Db	361	ftdgggeeraqeifnkynkdkvrfrfsvgqhnryergpqlwmacenkgyyieipsigair	420
Qy	421	INTQBYLDVLRPMVLADKAKQVNTNVLDALEGLVITGTLVPVFNITGQFNKTNLK	480
Db	421	intqeyldvlgprpmvladkkaqvntnvlaleglvigtltlpvfnitgqfknktnlk	480
Qy	481	NOLILGVMGVDVSLIEDIKRLTPRTFLCPNGYFYAIDPNGYVLLHPNLQPKPKSQEPVTL	540
Db	481	nqililgvmgvdvslaidikrltpftlcpngyfyaidpnyvllhpnlpkpkpqepvtl	540
Qy	541	DFLDAELENDIKVEIRNKMIDGSEKFRILVKSQDERYIDKGNRTYTWTPVNGTDYSL	600
Db	541	dflaelendikveirnmidgesektfrtlvksqderiyidkgnrtytwtpvngtdysl	600
Qy	601	ALVLPYSPYIKAKLEETITQARSKCKMKDSEFLKPDNFEESGYTFIAPRDCNDLKI	660
Db	601	alvlpyspyiakleecitqarskckmkdseclpdkpndfeesgytfiaprdcndlki	660
Qy	661	SDNTEFLNFEINFEIDRKTTPNPNPCNADLINRVLLDAGFTNELVQYWSKQKNKGVKAR	720
Db	661	sdnteflnfnfeidrkttpnpnpncnadlinrvlldagftnelvqywskqknkigvkar	720

Qy	721	FVYTDGGITRVYPKEAGENQENPETVEDSFYKRLSDNDNVFTAPYFNKSGPGAYESGI	780
Db	721	fvtydggitrvyypkeagenqenpetyedfsfyrslsdndnvyftapfynksppayesgi	780
Qy	781	MVSKAVIYIQQKLLKPAVVIGIKIDVNSWIENFTKTSIRDPACAGPVCDCRNSDVMDCVI	840
Db	781	mvskaveyiqgkllkpavvigikidvnswieenftktsirdpcagpvcdcrnsdvmdcvi	840
Qy	841	LDGGGFLMANHDDYTNQIGRFGCEIDPDSLMRHLVNI SVAFNKSVDYQSVCEPGAAPKQ	900
Db	841	lddggflmanhddytngirffgeidpslmrhlvnisvafnksydyqsvcepgaapkq	900
Qy	901	GAGHRSAYVPSVADILQIGWATAAASIIQQFTLSLTFPRLLEAVEMEDDDFTASLSKQ	960
Db	901	gaghrsayvpsvadilqigwataaawslqqfllstfprlleavemdddfstaslskq	960
Qy	961	SCITEQYQYFFDNDKSRFSGVLDGCGNSRIFPHGKLMNTNLIFIMVESKGPCCDTRLLI	1020
Db	961	sciteqtqyffndksksfsgvldcgncsrifhgeklmntnlifimveskgtpcdtrlli	1020
Qy	1021	QAEQTSQPNPCDMVKOPRYRKGPDCVCFDNNVLEDYTDGCGVSGNLPSLWIIIGIQFILL	1080
Db	1021	qaetsdgpnpdcdmvkprryrgkdpdcvcdnnvledytdcgvgsglnpslwyilqflll	1080
Qy	1081	WLVSGSTHRL 1091	
Db	1081	wlvsgsthrll 1091	

RESULT 4
AAW37879
ID AAW37879 standard; Protein; 1091 AA.
AC AAW37879;
XX XX
DT 28-AUG-1998 (first entry)
XX XX
DE Human calcium channel a2d subunit.
XX XX
KW Calcium channel; human; central nervous system disorder;
KW Lambert-Eaton syndrome; diagnosis; therapy.
XX XX
OS Homo sapiens.
XX XX
PN W09811131-A2.
XX XX
PD 19-MAR-1998.
XX XX
PF 11-SEP-1997; 97WO-US16146.
XX XX
PR 16-SEP-1996; 96US-0713118.
XX XX
PA (AMHP) AMERICAN HOME PROD CORP.
XX XX
PI Chen ARS, Franco R, Shuey DJ;
XX XX
DR WPI; 1998-207325/18.
XX XX
PT N-PSDB; AAV29060.
XX XX
PT DNA encoding human neuronal calcium channel subunit(s) - useful for
PT diagnosis of and treatment of central nervous system disorders, e.g.
PT Lambert-Eaton syndrome
XX XX
PS Disclosure; Fig 2; 89pp; English.
XX XX
CC This polypeptide comprises the a2d subunit of the human neuronal
CC calcium channel. cDNA clones (see AAV29059-61) encoding the a1b
CC subunit (see AAW37878), the a2d subunit and a b3 subunit (see AAW37880)
CC have been isolated. These have been inserted into expression
CC vectors and are stably expressed in transfected cell lines. The
CC transformed cells show omega-conotoxin GVIA binding activity,
CC and omega-conotoxin GVIA toxin sensitive potassium-stimulated
CC calcium uptake, indicating that the proteins expressed by the

CC clones are capable of forming a functioning calcium channel.
CC Nucleic acids encoding the 3 subunits, as well as vectors, host
CC cells and methods of isolating nucleic acids encoding related
CC calcium channels are disclosed. Fusion proteins incorporating the
CC subunit proteins, antibodies, and assays for identifying agents
CC that modulate calcium channel activity are also provided. Such
CC agents can be used to treat certain central nervous system
CC disorders by altering calcium channel activity. Methods of
CC diagnosing diseases associated with particular calcium channels,
CC such as Lambert-Eaton syndrome, are disclosed.
XX
SQ Sequence 1091 AA;

Query Match 99.9%; Score 5744; DB 19; Length 1091;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1090; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAGCLLALTTLTQSLIGPSSEPPFSAVTIKSWDKMQEDVTLAKTASGVNQLVDI 60
Db 1 maagcllaltltlqslilgspseepfbsavtikswdkmqedvltlaktasgvnqlvdi 60

QY 61 YEKYODLTVEPNNAQOLVETAAARDIEKLLSNRSKALVSLALEAEKVOAAHQRDFASN 120
Db 61 yekyodltyvepnnarqlvelaardieklslsnrskalvslaleaeekvqaahqrdfasn 120

QY 121 EYVYNNAKDDLDPEKNDESPQSRIKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180
Db 121 evvynnakddldpekndeespqsrirkpvfiedanfgroisqyhaavhiptdiyegstivl 180

QY 181 NELNWTSSALDEVFKNREDSLLMQVGSATGLARYPASPVWNSRTPNKIDLYDVR 240
Db 181 nelnwtssaldevfknreedsllmqvgsatglarypaspvwnsrtpnkidlydvr 240

QY 241 RPWYIOGAASPKDMLILVDVSGVSLGLKILRTSVSEMLETLSDDDFVNVAFSNSAQD 300
Db 241 rpwyiogaaspkdmlilvdvsgvsglklilrtsvsemlletlsdddfvnvasfnsaqd 300

QY 301 VSCFQHLVQANRNKVLKDAVNNTAKGIDTYKKGFSFAFQOLLNYSRANCNKIIML 360
Db 301 vscfqlvqanrnkvkldavnnitakgidtykkgfsfafqollnynsrancnkiiiml 360

QY 361 FTDGGEERAQELFNKYNKDKKVRFRFSGVQHNVERGPIQMACENKGYIYIPISGAIR 420
Db 361 ftdggeeraqelfnkynkdkkvrfrfsgvghnvergplqmacenkgyiyeipsigair 420

QY 421 INTQBYLDVLRPMVLADGAKOVQWTVNYLDALBELGVITGTLPVENITGOFENKTNLK 480
Db 421 intqbyldvgrpmvlagdakovqwtvnyldalbelgvitgtltpvenitgofenktnlk 480

QY 481 NQLILGVNGVDVSLDILKRLTPRFTLCPNGYFFAIDPNGYVLLHPLNLPKPKSQEPVTL 540
Db 481 nqlilgvngvdsledikrltpftlcpngyffaidpnyvllhplnlpkpkseqeptl 540

QY 541 DFLDAELENDIKVETRNKMDIGESEKFRILVKQDREYIDKGNRTYTWTPVNGTDSL 600
Db 541 dflaelendikveirnkmdigesekfrilvkqdreyidkgnrtytwtvpngtdysl 600

QY 601 ALVLPYFYIKAKLEETIQARSKGKMDSETLKPDPNPEESGYTFTAPRDYCNDLKI 660
Db 601 alvlpfyfyyikakleetiqarskkgkmdsetlkdnpnpeesgytftaprdycndlki 660

QY 661 SDNNTEFLNFEIDRTKTPNPNPCNADLINRVLLDAGFTNELVQNYWSKQKNKIGVKAR 720
Db 661 sdnnteflnfnfeidrtktpnppncnadlinrvllldagftnelvqnywskqknkigvkar 720

QY 721 FVVTGGITRYPPKAGENQWENPTYEDSFYKRSILDNDNYFTAPYFNKSPGAYESGI 780
Db 721 fvvtggitryvpkagenwqenpetyedsfyrksildndnyftapyfnkspgayesgi 780

QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTTSITRDCAGPVCDCKRNSDVMDCVI 840
Db 781 mvskaveiyyogkllkpaavgkldvnswnentfttsitrdcagpvcdckrnsdvmdcvi 840

QY 841 LDDGGFLLMANHDDTNTQIGRFFGEIDPSLMRHLNYSVAFNKSYDYOSVCEPGAAPKQ 900
Db 841 lddgffllmanhddtntqigrffgeidpslmrhlvnysvafnkdydyosvcepgaapkq 900

QY 901 GAGHSAYVPSVADILQIGWATAAAWSILOQFLLSLTPRLLAEVEMEDDDFTASLSKQ 960
Db 901 gaghsayvpsvadilqigwataaawsilqflsltprrlleavemedddftaslskq 960

QY 961 SCITEQTQYFFDNDKSFSGVLDGCGNCSRFHGEKLMNTNLIFIMVYESKGTCPDTRLLI 1020
Db 961 sciteqtqyffndksfsgvldcgncsrifhgeklmntnlifimveskgtcpdtrlli 1020

QY 1021 QAEQTSDDGNPCDMVKQPRYRKGPVCFDNNVLEDTDCGGVSGLNPSLWYIIGIOFLLL 1080
Db 1021 qaeqtsddgnpcdmvkqpryrkgpvcfdnnvledtdeggvsglnpslwyiigioflll 1080

QY 1081 WLVSNGTHLL 1091
Db 1081 wlvsngthll 1091

RESULT 5
AAR33553
ID AAR33553 standard; Protein; 1091 AA.
XX
AC AAR33553;
XX
DT 30-JUN-1993 (first entry)
XX
DE Sequence of the alpha 2 human calcium channel subunit.
XX
KW Human calcium channel subunit; diagnosis; agonist; antagonist;
KW Lambert Eaton syndrome.
XX
OS Homo sapiens.
XX
PN W09304083-A.
XX
PD 04-MAR-1993.
XX
PF 14-AUG-1992; 92WO-US06903.
XX
PR 15-AUG-1991; 91US-0745206.
PR 10-APR-1992; 92US-0868354.
XX
PA (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
XX
PI Brenner R, Ellis SB, Feldman DH, Harpold MM, Mccue AF;
PI Williams ME;
XX
XX WPI; 1993-093936/11.
DR N-PSDB; AAQ37821.
XX
PT DNA encoding specific human calcium channel sub-units - used for
PT identifying calcium channel agonists and antagonists and
PT diagnosing Lambert Eaton syndrome
XX
PS Disclosure; Page 134-138; 150pp; English.
XX
CC DNA encoding a human neuronal calcium channel alpha 2 subunit was
CC isolated from a human genomic DNA library probed under low and high
CC stringency conditions with a fragment of DNA encoding the rabbit
CC skeletal muscle calcium channel alpha 2 subunit. The fragment
CC included nucleotides having a sequence corresponding to the
CC nucleotide sequence between nucleotides 43 and 272 inclusive of
CC rabbit back skeletal muscle calcium channel alpha 2 subunit cDNA.
CC PCR analysis identified splice variants of the human calcium alpha
CC 2 subunit transcript. In particularly preferred embodiments, the
CC DNA encoding the alpha 2 subunit is produced by alternative
CC processing of a primary transcript that includes DNA encoding the
CC amino acids set forth in AAR33553 and the DNA of AAQ37823 inserted
CC between nucleotides 1624 and 1625 of AAQ37821.

Db	961	sciteqyffndsksfsgvldcncsrfifgheklmtnliffmveskgtcpdtrlli	1020
Qy	1021	QAEQTSQGNPCDMVKQPRYRKGPVCFDNNVLEDTDCGGVSGLNPSLWYLIIGIQELL	1080
Db	1021	qaeqtsdsgnpucdmvkqpryrkgpdcvfnvledytdcggvsglnpslwllylgiqflll	1080
Qy	1081	WLVSNGTHRL 1091	
Db	1081	wlvsgsthrll 1091	
RESULT 6			
AAW63148	AAW63148 standard; Protein; 1110 AA.		
XX	AAW63148;		
DT	12-OCT-1998 (first entry)		
DE	Human calcium channel alpha-2 subunit.		
XX	Alpha-2 subunit; human; calcium channel; assay; detection;		
KW	characterisation; Lambert Eaton Syndrome; LES; diagnosis.		
XX	Homo sapiens.		
OS			
XX	US5792846-A.		
PN			
XX	11-AUG-1998.		
PD			
XX	31-MAY-1995; 95US-0455543.		
PF			
XX	04-APR-1994; 94US-0223305.		
PR	04-APR-1988; 88US-0176899.		
PR	04-APR-1989; 89US-0603751.		
PR	04-APR-1989; 89WO-US01408.		
PR	20-FEB-1990; 90US-0482384.		
PR	30-NOV-1990; 90US-0620250.		
PR	15-AUG-1991; 91US-0745206.		
PR	31-MAY-1995; 95US-0455543.		
XX	(SIBI-) SIBIA NEUROSCIENCES INC.		
PA			
XX	Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;		
PI	Williams ME;		
PI			
XX	WPI; 1998-456192/39.		
DR	N-PSDB; AAV42694.		
XX	DNA encoding human calcium channel alpha 1B subunit protein -		
PT	useful for recombinant production of the channel for screening of		
PT	its modulators, and diagnosis of Lambert Eaton Syndrome		
XX	Disclosure; Columns 131-138; 166pp; English.		
PS			
XX	The present sequence represents the alpha-2 subunit of a human calcium		
CC	channel. Calcium channels are membrane-spanning, multi-subunit protein		
CC	that allow controlled entry of calcium ions into cells. This leads		
CC	to depolarisation events required for muscle contraction. The recombi		
CC	subunit, when expressed with nucleic acids encoding the complete calc		
CC	channel, can be used in assays for the detection and characterisation		
CC	compounds that modulate the channel. The DNA encoding the subunits ca		
CC	be alternatively spliced when transcribed, giving more than one form		
CC	the protein from the same transcript, each having slightly different		
CC	properties. In addition, the reactivity of the alpha 1 subunit with i		
CC	moles can be used as a diagnostic for the disease.		
CC	(LES) from the serum of an individual with Lambert Eaton Syndrome		
XX	Sequence 1110 AA;		
SQ			

Best Local Similarity 98.3%; Pred. No. 0;			
Matches 1091; Conservative 0; Mismatches 0; Indels 19; Gaps 1;			
QY	1	MAAGCLLATLTFLQSLIGSPSEPPFPSPATIKSWDKMOEDLVTLAKTAGSVNQLVDI	60
Db	1	maagcllatltlfgslilgspseepfsvatikswdkmqedlvtlaktasgvnqlvdi	60
QY	61	YEKQDLYTFPNARQLVETAAARDIEKLSNRSKALVSLAEKVOAAHQRDEFASN	120
Db	61	yekygdlytvepnnarqlvelaardiekllnsrskalvslaleakvqaahqrdefasn	120
QY	121	EWVYNNAKDDLPKNDSEPGSQRKPFIEANFGROIYSQHAHVHPTDIYEGSTIVL	180
Db	121	evvynnakddlpeknsepgsqrikpfiefanfgroisqghaavhptdiyegstivi	180
QY	181	NELNWTSADEVFKNKREDEPSLLQVFGSATGLARYYPASPDVNSRTPNKIDLYDVR	240
Db	181	nelnwtsealdevfknreedpsllwvfgsatglaryypaspdvnsrtpnkidydvrr	240
QY	241	RPWTIQGAASPKMLILVDVSGVSGGLTKLIRTSVSEMLETSLDDDFVNVASFNSAQD	300
Db	241	rpwyiqgaaspkdmlilvdvsgsvgltklirtsvsemlletlsdddfnvvasfnsaqd	300
QY	301	VSCFQHLVQANVRNKKVLKDAVNITAKGIDYKGFSPFAFEOILLNYSRANCNKIIML	360
Db	301	vscfghlvqanvrnkvlkdavnitakgitydkgfspfafeqillnynsvrancnkilml	360
QY	361	FTDGEERAQEIFNKYKDKKVRFRSVGQHNTERGPIOMACENKGYEYIEPSIGAIR	420
Db	361	ftdgeeraqeifnkynkdkkvrfrsvgqhnvtergpiqmacenkgyeyieipsigair	420
QY	421	INTQBYDLVGRPMVLGAKKAKQVQWNTNVLDALEGLVITGTLVPVFNITQGFENKTLK	480
Db	421	intqeydlvgrpmvlgakkakqvwnvnlalelglvitgtlvpvfnitqgfentknlk	480
QY	481	NQLILGVMGVDVSLIEDIKELTPRTLCPNGYFFAIDPNGYVLLHPNLOPK	540
Db	481	nqlilgvmgvdvsliekrltprtlcpngyffaidpngyvlhpnlpkpgvgiptin	540
QY	531	-----NPKSQBPVTLDFDALENDIKVEIRNKMIDGESGKTEPRTLVKSODERYI	581
Db	541	lkrprnlqnpksgpvtldfldaelendikvelnkmldgesgktrtlvksqderiyi	600
QY	582	DGNRTYTWTPVNGTDSLALVLPYFYIYKALEETITQARSKKGMKDSSETLKPDNF	641
Db	601	dkgnrtvtpvngtdyslalvlpysfyyikaleetitqarskkgmkdssetlkpdnf	660
QY	642	EESGYTFIAPRDYCNDLKISDNNTFELLNFNEFDIRKTPNPNPSNADLINRVLLDAGFTN	701
Db	661	eesgytfiaprdydcndlkisdnntefllnfnefidrktppnpscnadlinrvlldagftn	720
QY	702	ELVQNVYSKQKNIKVKARFVVTDGGITRVYPKBAENQWQENPETYEDSFYKRSILDNDNY	761
Db	721	elvqnywskqknikgvkarfvtdggitrvyppkeagenqwenpetyedsfykrslndndy	780
QY	762	VFTAPYFNKSGPGAYESGIMVSKAVEYIYQGLKLKPAVVGKIDVNSWNIENFTSIRDP	821
Db	781	vftapyfnksgpgayesgimvskaveiyiqgklkpkavvgikidvnswnienfttsirdp	840
QY	822	CAGPVCCKRNSYMDVCLDDGGLLMANHDDYTQIGRFFGEIDSLMRHLNWSIYVA	881
Db	841	cagpvcckrnsydmvclddgglmlmanhddytnglgrffgeidpslmrhlwnsiyva	900
QY	882	FNKSYDYQSVCEPAAKQAGHSAVPSVADILQIGWATAAASWTLQOFLSLTFPR	941
Db	901	fnsydyqsvceppaaqkqaghsavpsvadilqigwataaawslqqflsltfpr	960
QY	942	LLEAVEMEDDDFTASLSKQSCITEQTQYFFDNDSKFSVGLDGCNCRIFHGEKLMNTNL	1001
Db	961	lleavemedddftaslskqsciteqyffdnndskfsvglcncncrifgeklmntnl	1020
QY	1002	IFIMVESKGCPCDTRLLIQAEQTSQDGNPCDMYQKPRYKGPVDCFDNNVLEDTDCGG	1061
Db		ifimveskgcpcdtrlliqaeqtsdgnpcdmvqkpryrgpdcfdnnvledtydcgg	1080

Db	1021	ifimveskgtcpcdtrlllqaeqtsdgnpcdmvqkpryrgpdcfdnnvledtydcgg	1080
QY	1062	VSGNLPSLWYIIGIOFLILWLIVSGSTHRLI	1091
Db	1081	vsgnlpslwyiigiqflilwlivsgsthrll	1110
RESULT 7			
AA71013			
ID	AA71013	standard; Protein; 1086 AA.	
XX	AA71013;		
AC	AA71013;		
XX	01-DEC-1995	(first entry)	
DT			
XX	Human neuronal calcium channel subunit alpha 2c.		
DE			
XX	Calcium channel subunit; antagonist; agonist; diagnosis;		
KW	Lambert Eaton Syndrome.		
XX	Homo sapiens.		
OS			
XX	WO9504822-A.		
PN	16-FEB-1995.		
XX	11-AUG-1994;	94WO-US09230.	
PD			
XX	11-AUG-1993;	93US-0105536.	
PR	05-NOV-1993;	93US-0149097.	
XX	(SALK) SALK INST BIOTECHNOLOGY IND ASSOC.		
PA			
XX	Ellis SB, Gillespie A, Harpold MM, Mccue AF, Williams ME;		
PI			
XX	WPI; 1995-090900/12.		
DR	N-PSDB; AAQ84667.		
XX	DNA encoding human calcium channel sub-unit(s) - used for		
PT	developing prods. for studying calcium channels, e.g. for		
PT	obtaining agonists and antagonists		
XX	Disclosure; Page 237-242; 285pp; English.		
PS			
XX	Human neuronal alpha 2 coding sequence (AAQ84664) transcript is		
CC	differentially processed in skeletal muscle, aorta, and CNS in		
CC	the region corresp. to nt 1595-1942 of AAQ84664 in each of the		
CC	tissues. Five alternatively spliced variant transcripts that differ		
CC	in the presence or absence of one to three different portions of		
CC	this region. There are three sequences involved (see AAQ84664 FT		
CC	and AAQ84665 FT), sequence 1, sequence 2 and sequence 3. The five		
CC	alpha 2 encoding transcripts from the different tissues include		
CC	different combinations of the three sequences, except for one of		
CC	the alpha 2 transcripts expressed in aorta which lacks all three		
CC	sequences. The five alpha 2 forms identified are (1) a form that		
CC	lacks sequence 3 called alpha 2a, expressed in skeletal muscle		
CC	(2) one that lacks sequence 1 called alpha 2b, expressed in CNS		
CC	(3) one that lacks sequences 1 and 2 called alpha 2c, expressed in		
CC	aorta (4) one that lacks sequences 1, 2 and 3 called alpha 2d,		
CC	expressed in aorta and (5) one that lacks sequences 1 and 3		
CC	called alpha 2e. The DNA and AA sequences of alpha 2a - alpha 2e		
CC	are set forth in AAQ84666-Q84669 and AA71012-R71015 respectively.		
XX	Sequence 1086 AA;		
SQ			
Query Match 99.3%; Score 5708.5; DB 16; Length 1086;			
Best Local Similarity 99.5%; Pred. No. 0;			
Matches 1086; Conservative 0; Mismatches 0; Indels 5; Gaps 1;			
QY	1	MAAGCLLATLTFLQSLIGSPSEPPFPSPATIKSWDKMOEDLVTLAKTAGSVNQLVDI	60
Db	1	maagcllatltlfgslilgspseepfsvatikswdkmqedlvtlaktasgvnqlvdi	60

QY 61 YEKYQDLYTVEPNNAQOLVETAAEDIEKILNSRKALVSLALEAEKVQAAHQRWEDFASN 120
DB 61 yekyqdylytvepnnarqlvealaardieklinsrkalsvslaleakvqaahqredfasn 120
QY 121 EVVYNAKDDLDPEKNSEPGSQRIKPVFIEDANFGRIQISYQHAHVHIPTDIYEGSTIVL 180
DB 121 evvynakddldpekndsepgsqrikpvfiedanfgriqisyghaavhiptdiyegstivl 180
QY 181 NELNWTSSALDEVFKKNREEDPSLLWQVFGSATGLARYYPASPWVDNSTRPNKIDLYDVR 240
DB 181 nelnwtssaldevfkknreepdpsllwqvfgsatglaryypaspwvdnstrpnkidydvrr 240
QY 241 RPWYIQAASPKDMLILVDVSGVSGITLKLIRTSVSEMLETLSDDDFVNVSFNSNAQD 300
DB 241 rpwyiqaaaspkdmllilvdvsgvsgitlklirtsvsemlletlstdddfvnvsfnnaqd 300
QY 301 VSCFOHLVQANVRNKKVLDKADANNITAKGIDYKKGFSFAFEQLLNYNVSRANCKIIML 360
DB 301 vscfghlvqanvrnkvlkdavnnitakgidtykkgfsfafaqellnynvsranckiiiml 360
QY 361 FTDGEERAQELFNKYNKKVFRPERSVGOHNYERGPQIMACENKGYIYEISGAIR 420
DB 361 ftdgeeraaqelfnkynkdkvfrfsvgghnyergpqimacenkgyyiyeipsigair 420
QY 421 INTOEYLDVLRPMVLAGDKAKQVQWNTNVLDALELGLVITGLPVFNITGQFENKTNLK 480
DB 421 intoeyldvlrpmvlagdkakqvqwtntnvldalelglvigtglpvfnitgqfentnlnk 480
QY 481 NOLILGVMGVDSLEDKRLPRFTCLPNGYFYFAIDPNGYVLLHPNLPKNPKSQEPVTL 540
DB 481 nqililgvmgvdsledikrlprftclpngyfyfaldpnyvllbpnlqpk-----epvtl 535
QY 541 DFLDAELNDIKVEIRNKMIDGEGSEKTRFLVKSODERYIDKGNRYITWTVPNGTDYSL 600
DB 536 dfldaelndikveirnmidgesektrflvksoderyidkgnryitwtvpngtdysl 595
QY 601 ALVLPYFYIYKAKLEETIQAASKKMKMDSETLKPDPNEESGYTFIAPRDYCNLDKI 660
DB 596 alvlpysfyiykakleetiqarskkgmkmdsetlkdnpneesgytfiaprdycondlki 655
QY 661 SDNTEFLNFEIDRTPNPNCSNADLIRNVLLDAGFTNELYQVNSKOKNKGVKAR 720
DB 656 sdntefilnfeidrtppnpscnadlirnvlldagftnelvqnywskqknkgvkar 715
QY 721 FVWTDGGITRYVPKEAGNWEQENETVEDSYKSLDNDNVFTAPYFNKSGPCAYESGI 780
DB 716 fvttdggitryvpkeagenwqenpetyedsykrslndndnyvftapyfnksppayesgi 775
QY 781 MVSKAVEIYIOGKLLKPAVGIKIDVNSWIENFTKTSIRDPGAGPVCDCRNSDVMDCVI 840
DB 776 mvskaveiyiogkllkpaavgikidvnsvienftktsirdpcagpvcckrnsdvmdcvi 835
QY 841 LDGGFLLMANHDDYTNIGRFFGEIDPSLMRHLNIVSYAFNKSVDYQSVCEPGAAPKQ 900
DB 836 ldggfllmanhddytngirffgeidpslmrhlvnsyafnksydyqsvcepgaapkq 895
QY 901 GAGHRSAYVPSVADILQIGWATAAANSILOQFLLSLTFPRLLEAVENEDDDFTASLSKQ 960
DB 896 gaghrsayvpsvadilqigwataaansilqfllsltfprlleavenedddftaslskq 955
QY 961 SCITBQTYOFFDNDKSFSGVLDGNCNCSIRPFHGEKLMNTNIFITWVESKGTCPDTRLLI 1020
DB 956 sciteqtyoffdndksfsgvldcncnrsirfhgeklmntnifimveskgtpcdtrlli 1015
QY 1021 QAEQTSQDGNPCDMVQPRYRKGPVDCPDNNVLEDYTDGCGVSGNLPSLWYIIGIQFLLL 1080
DB 1016 qaeqtsqdpncdmvqpry-rkgpdcvcdnnvledytdcgvgvsgnlpslwyliqiflll 1075
QY 1081 WLVSQSTHRL 1091
DB 1076 wlvsqsthrll 1086

RESULT 8
AAW63153
ID AAW63153 standard; Protein; 1086 AA.
XX
XX AAW63153;
XX AC
XX 12-OCT-1998 (first entry)
XX DT
XX DE Human calcium channel alpha-2c subunit.
XX KW Alpha-2 subunit; human; calcium channel; assay; detection;
XX KW characterisation; Lambert Eaton Syndrome; LES; diagnosis.
XX OS Homo sapiens.
XX PN US5792846-A.
XX PD 11-AUG-1998.
XX PF 31-MAY-1995; 95US-04555543.
XX PR 04-APR-1994; 94US-0223305.
XX PR 04-APR-1988; 88US-0176899.
XX PR 04-APR-1989; 89US-0603751.
XX PR 04-APR-1989; 89WO-US01408.
XX PR 20-FEB-1990; 90US-0482384.
XX PR 30-NOV-1990; 90US-0820250.
XX PR 15-AUG-1991; 91US-0745206.
XX PR 31-MAY-1995; 95US-04555543.
XX PA (SIBI-) SIBIA NEUROSCIENCES INC.
XX PI Brenner R, Ellis SB, Feldman DR, Harpold MM, McCue AF;
PI Williams ME;
XX WPI; 1998-456192/39.
XX DR N-PSDB; AAV42702.
XX PT DNA encoding human calcium channel alpha 1B subunit protein -
XX PT useful for recombinant production of the channel for screening of
XX PT its modulators, and diagnosis of Lambert Eaton Syndrome
XX PS Claim 3; Columns 293-300; 166pp; English.
XX CC The present sequence represents the alpha-2c subunit of a human calcium
XX CC channel. Calcium channels are membrane-spanning, multi-subunit proteins
XX CC that allow controlled entry of calcium ions into cells. This leads
XX CC to depolarisation events required for muscle contraction. The recombinant
XX CC subunit, when expressed with nucleic acids encoding the complete calcium
XX CC channel, can be used in assays for the detection and characterisation of
XX CC compounds that modulate the channel. The DNA encoding the subunits can
XX CC be alternatively spliced when transcribed, giving more than one form of
XX CC the protein from the same transcript, each having slightly different
XX CC properties. In addition, the reactivity of the alpha 1 subunit with IgG
XX CC molecules from the serum of an individual with Lambert Eaton Syndrome
XX CC (LES) can be used as a diagnostic for the disease.
XX SQ Sequence 1086 AA;

Query Match 99.3%; Score 5708.5; DB 19; Length 1086;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1086; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 1 MAACGLIALTLTLOSLLIGPSSEPPSPVATIKSWDKMQEDLVTLAKTAGVGNQLVDI 60
DB 1 maagclialtltlfqslligpsseepfsvatikswdkmqedlvtlaktasgvnqlvdi 60
QY 61 YEKYQDLYTVEPNNAQOLVETAAEDIEKILNSRKALVSLALEAEKVQAAHQRWEDFASN 120
DB 61 yekyqdylytvepnnarqlvealaardieklinsrkalsvslaleakvqaahqredfasn 120

QY 121 EVYYNAKDDLDPEKNDSEGGQRIKPVFIEDANFORQISYOHAAVHIPTDIYEGSTIVL 180
Db 121 evvynakddldpekndsepgsqrikpvfiedanforqisghaavhiptdiyegstivl 180
QY 181 NELNWTSAIDVFKKREDEPSSLLWQVCSAGCLARYYPASPHVDSRPNKIDLDVRR 240
Db 181 nelnwtসাঈদব্ফক্ক্রেদেপ্সল্লব্ফসাগক্লার্য্যপস্ফব্ফদস্ফপ্নকিঈদব্ফ 240
QY 241 RPYWIGAAAPKMDLILVDVSGVSLGTLKLRITSVSEMLETSLDDDFVNVASFNSNAOD 300
Db 241 rpywigaaapkdmlilvdvsgvslgtlklritsvsemlletlsldddfvnvasfnasnaod 300
QY 301 VSCFOHLVQANVRNKKVLKADVNNITAKGIDYKKGFSFAFEOQLNLYNSRANCNKIIML 360
Db 301 vscfghlvqanvrnkkvlkdavnnitakgidykkgfsfafeoqlnlynvsrancnkiiml 360
QY 361 FVDTGGERAQEIFNKYNDKVRVRFSGVGHNYERGPIOWMACENKGYYYEIPSGAIR 420
Db 361 fdtggeraqeifnkyndkvrvfsvghnyergpigmwmacenkgyyyeipsigair 420
QY 421 INTQEYLDVLRPMVLGDKAKQVQNTVYLDALGLVITGTLPVFNITGQENKTNLK 480
Db 421 intqeyldvlgprmvlgdkakqvqntvnyldaleglvitgtlvpfnitgqenktnlk 480
QY 481 NQILGVMGVDSLEDIKRLTPRTLCPNGYFPAIDPNGVYLLHPNLQPNKPSQEPVTL 540
Db 481 nqilgvmgvdsledikrltpftlcpngyypaidpngvylhpnlpknpsqepvtl 540
QY 541 DFLDAELENDIKVEIRNKNMDGESGKRTLVKSDERYIDKGNRTYTWTPVNGTDYSL 600
Db 541 dfldalendikveirnkndgesgkrtlvksderyidkgnrtytwtvpngtdysl 600
QY 595 DFLDAELENDIKVEIRNKNMDGESGKRTLVKSDERYIDKGNRTYTWTPVNGTDYSL 595
QY 601 ALVLPYSFYIKAKLEETITQARSKKGMKDSKTLKPNFESGYTFIAPRDCNDLKI 660
Db 596 alvlpysfyyikaleetitqarskkgmkdsktlkpnfesytyfiaprdcndlki 660
QY 661 SONTEFLNFEIDRKPNNPSCNADINRVLLDAGFTNELVQNSKQNIKGVKAR 720
Db 656 sdntefllnfeidrktppnpscnadinrvlldagftnelvqnywskqnikgvkar 715
QY 721 FVDTGGITRVYPKEAGENWENPETYEDSFYKRSIDNDNYVTPATYFNKSGPAYESGI 780
Db 716 fvtddgitrvypkeagenwenpetyedsfykrsidndnyvtapyfnksgpayesgi 775
QY 781 MYSKAVEIYIQGLKLPVAVGVIKIDVNSNIENFTKTSIRDPACAGPVCDCKRNSDVMDCVI 840
Db 776 myskaveiyiqglklpavvgvikidvnsnienfktksirdpcagpvcdckrnsdvmdevi 835
QY 841 LDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNSVYAFNKSVDYOSVCEPGAAPKQ 900
Db 836 ldggfllmanhddyntnqigrffgeidpslmrhlvnsyafnksydyosvcepgaapkq 895
QY 901 GAGHSAYVPSVADILQGWATAAASILQOFLLSLTPRLLEAVEMEDDDFTASLSKQ 960
Db 896 gaghsayvpsvadilqgwataaasilqflsltprlleavemedddftaslskq 955
QY 961 SCITEQTOFFNDKDSFSGVLDGNCRSIFHGKELMNTNLIFIMVESKGTCTCDTRLII 1020
Db 956 sciteqtqffndkdsfsgvldgncrsifhgekmlntnlifimveskgtcpcdtrlll 1015
QY 1021 QAEQTSQGNPCDMVKQPKRYKGPVCFNNVLEDYTDGCGVSGGLNPSLWYIIGIQLLL 1080
Db 1016 qaeqtsdgnpcdmvkqpryrykgpvcfnnvledytdcgvgsgglnpwlyiigiqflll 1075
QY 1081 WLVSSTHRL 1091
Db 1076 wlvssthrll 1086

RESULT 9

AAB10587

ID AAB10587 standard; Protein; 1086 AA.

XX

AC AAB10587;
XX 22-DEC-2000 (first entry)
DT Human calcium channel alpha-2c subunit protein.
XX Human; calcium channel; calcium channel subunit; diagnosis;
KW Lambert Eaton Syndrome; calcium channel subunit alpha-2c.
XX Homo sapiens.
OS US6096514-A.
PN 01-AUG-2000.
PD 25-MAY-1995; 95US-0450562.
PF 04-APR-1988; 88US-0176899.
PR 02-FEB-1990; 90US-0482384.
PR 08-NOV-1990; 90US-0603751.
PR 30-NOV-1990; 90US-0620250.
PR 15-AUG-1991; 91US-0745206.
PR 10-APR-1992; 92US-0868354.
PR 13-JUL-1992; 92US-0914231.
PR 11-AUG-1993; 93US-0105536.
PR 05-NOV-1993; 94US-0149097.
PR 07-FEB-1994; 94US-0193078.
PR 04-APR-1994; 94US-0223305.
PR 11-AUG-1994; 94US-0290012.
PR 23-SEP-1994; 94US-0311363.
PR 28-SEP-1994; 94US-0314083.
PR 07-NOV-1994; 94US-0336257.
PR 13-MAR-1995; 95US-0404950.
XX (SIBI-) SIBIA NEUROSCIENCES INC.
XX Ellis SB, Williams ME, McCue AF, Harpold MM;
PI WPI; 2000-548230/50.
XX N-PSDB; AAA71725.
XX Human calcium channel beta subunit polynucleotides, useful for
PT producing recombinant eukaryotic cells and for diagnosing Lambert Eaton
PT Syndrome
XX Disclosure; Column 237-244; 153pp; English.
XX This invention describes a novel isolated DNA molecule (I) comprising a
CC sequence encoding a beta3-1 subunit of a human calcium channel.
CC Nucleic acid probes comprising 14-30 contiguous nucleotides of
CC beta.3 subunit encoding DNA are useful for isolation and cloning of
CC calcium channel subunit-encoding DNA. Recombinant eukaryotic cells that
CC express heterologous calcium channel are useful for identifying compounds
CC that modulate calcium channel activity and in assays for identifying
CC agonists and antagonists of calcium channel activity in humans. Human
CC calcium channel subunit or eukaryotic cells expressing the channel are
CC useful for diagnosing Lambert Eaton Syndrome (LES) in a human. This
CC sequence represents the human calcium channel alpha-2c subunit which is
CC described in the method of the invention.
XX Sequence 1086 AA;
SQ

Query Match 99.3%; Score 5708.5; DB 21; Length 1086;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1086; Conservative 0; Mismatches 0; Indels 5; Gaps 1;
QY 1 MAAGCLALTLTFLQSLIGPSSSEFPSPSAVTIKSWVDKMQEDLVTLAKTAGSYGNQLVDI 60
Db 1 maagclalaltltflqslilgppssefpssavtikswvdkmqedlvtlaktasgynqlvdi 60
QY 61 YEKYQDLTYTFEPNNARQLVEIAARDTEKLLSNRSKALVSLALEAEKVQAAHQHREDPASN 120
XX

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Db 61 yekyqdltyvepnarqlveiaardieklisrskalsvlsialeaeqvqaahqwrefasn 120
QY 121 EVVYNKADDDLPKNDSEPGSQRIKPVFTEDANFGQISQYHAAVHIPTDIYEGSTIVL 180
Db 121 evvynakddlpekdndsepgsgrikpvfiedanfgqisqyhaavhiptdiyegstivl 180
QY 181 NEUNWTSALDEVFKKNEEDPSLLQVFGSATGLARYYPASPWVDNSRTPNKIDLDVRR 240
Db 181 neunwtsaldevfkneedpsllqvfsgatglaryypaspwvdnsrtpnkidldvrr 240
QY 241 RPWYIOGAASPDKMLILVDVSGVSGLTGLKIRTSVSEMLETSLDDDFVNVASFNSAQD 300
Db 241 rpwyiogaaspdkmlilvdvsgvsgltlklirtsvsemletlssdddfvnvasfnsaqd 300
QY 301 VSCFQHLVQANVRNKKVLDVANNITAKGTTDYKGFSPAFEOILLNINVRANCNKIIML 360
Db 301 vscfqlhvanvrnkvladvannitakgttdykkgfspafoillnynvrancnkliml 360
QY 361 FTDGGEERAQEIFNKYKOKKVRFRFSVQGHNYERGPIQWACENKGYIYEIPSIGAIR 420
Db 361 ftdggeeraqeifnkykdkkvrfrfsvqghnyergpiqwmacenkgyyeipsigair 420
QY 421 INTQEVLDVLRPMVLGAKAKOVQWNTNVLDALELGLVITGTLPVFNITGQFENKTNLK 480
Db 421 intqeyldvlgpmvlagkakovqwnvnyldalelglvltgtlplvfnitgqfenktnlk 480
QY 481 NOLILGVMGVDSLEDIKRLTRFTLCPNGCYFAIDPNGVLLHLPNLOPKNPKSQBPVIL 540
Db 481 nolilgvmgvdsleedikrltrftlcpngcyfaidpngvllhlpnlqpk-----epvll 540
QY 541 DFLDAELNDIKYIERNKIDMGSEKFTRTLKQSDERYIDKGNRTYWTVPVNGDYSL 600
Db 541 dfldaelndikyeirnkidmgsektftlksqderydkgnrtytwtvpvngdyasl 600
QY 595 DFLDAELNDIKYIERNKIDMGSEKFTRTLKQSDERYIDKGNRTYWTVPVNGDYSL 595
QY 601 ALVLPYISFYIYAKLEETITQARSKGKMKDSETLKPNFESSGYTFIAPRDYCNLKI 660
Db 596 alvlpysfyiyakleetitqarskgkmdsetlkdndfessgytfiaprdyendlki 655
QY 661 SDNNTTEFLNFEIDRKTPNPNPCNADLINRVLLDAGFTNELVQWYKOKNKGVKAR 720
Db 656 sdntteflnfeidrktpnpncnadlinrvlldagftnelvqwkknkgvkar 715
QY 721 FVVTGGITRVYPKEAGENQENPETYEDSFYKRSILDNDNYFTAPYFNKSGPGAYESGI 780
Db 716 fvtddggitrvypkeagenqenpetyedsfykrsldndnyftapyfnksgpgayesgi 775
QY 781 MYSKAVEIIOGKLLPNAVVGKIDVNSWENFTKTSIRDPCAGPVCDCKRNSDVMDCVI 840
Db 776 mvsakaveiioqkllpnavvgikidvnswnftktsirdpcagpvcdckrnsdvmdevi 835
QY 841 LDGPGFLMANHDDYTNQIGRPFGEITDPSLMRHLNIVSYAFNKSYDYOSVCEPGRAPKQ 900
Db 836 ldgpgflmanhdycnqigrfgeitdpslmrhlvnsyafnksydyosvcepgsapkq 895
QY 901 GAGHSAYVPSVADIQIGWATAAWSILQOFLSLTFPRLLAEVEMEDDDFTASLSKQ 960
Db 896 gaghsayvpsvadiiqgwataawsilqflsltfprlleavemedddftaslskq 955
QY 961 SCITEQTOFFDNDKSFSGVLDCGNCISFIFGHEKLMNTNLIIFIMVESKGTCPDTRLLI 1020
Db 956 scitedqtoffndksfsgvldcgnscisfifgheklmntnllifimveskgtcpdtrlli 1015
QY 1021 QAEOTSDGPNPCDMVKOPRYRKGPVCFDNNVLEDYTDGCGVSGLNPSLWYIIGTQFLLL 1080
Db 1016 qaeotsdgpnpcdmvpkpryrkgpvcfdnnvledytdcgvgsglnpslwyiigiqflll 1075
QY 1081 WLVSNGTHRL 1091
Db 1076 wlvsngthrll 1086
RESULT 10
AAR71015
```

```
ID AAR71015 standard; Protein; 1084 AA.
XX
AC AAR71015;
XX
DT 01-DEC-1995 (first entry)
XX
DE Human neuronal calcium channel subunit alpha 2e.
XX
KW Calcium channel subunit; antagonist; agonist; diagnosis;
KW Lambert Eaton Syndrome.
XX
OS Homo sapiens.
XX
PN W09504822-A.
XX
PD 16-FEB-1995.
XX
PF 11-AUG-1994; 94WO-US09230.
XX
PR 11-AUG-1993; 93US-0105536.
PR 05-NOV-1993; 93US-0149097.
XX
PA (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
XX
PI Ellis SB, Gillespie A, Harpold MM, McCue AF, Williams ME;
XX
DR WPI; 1995-090900/12.
DR N-PSDB; AA084669.
XX
PT DNA encoding human calcium channel sub-unit(s) - used for
PT developing prods. for studying calcium channels, e.g. for
PT obtaining agonists and antagonists
XX
PS Disclosure; Page 248-253; 285pp; English.
XX
CC Human neuronal alpha 2 coding sequence (AA084664) transcript is
CC differentially processed in skeletal muscle, aorta, and CNS in
CC the region corresp. to nt 1595-1942 of AA084664 in each of the
CC tissues. Five alternatively spliced variant transcripts that differ
CC in the presence or absence or one to three different portions of
CC this region. There are three sequences involved (see AA084664 FT
CC and AA084665 FT), sequence 1, sequence 2 and sequence 3. The five
CC alpha 2 encoding transcripts from the different tissues include
CC different combinations of the three sequences, except for one of
CC the alpha 2 transcripts expressed in aorta which lacks all three
CC sequences. The five alpha 2 forms identified are (1) a form that
CC lacks sequence 3 called alpha 2a, expressed in skeletal muscle
CC (2) one that lacks sequence 1 called alpha 2b, expressed in CNS
CC (3) one that lacks sequences 1 and 2 called alpha 2c, expressed in
CC aorta (4) one that lacks sequences 1, 2 and 3 called alpha 2d,
CC expressed in aorta and (5) one that lacks sequences 1 and 3
CC called alpha 2e. The DNA and AA sequences of alpha 2a - alpha 2e
CC are set forth in AA084666-Q84669 and AAR71012-R71015 respectively.
XX
SQ Sequence 1084 AA;
Query Match 99.0%; Score 5691.5; DB 16; Length 1084;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1083; Conservative 0; Mismatches 1; Indels 7; Gaps 1;
QY 1 MAAGCLLATLTLFQSLIGPSEPPFPSPAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
Db 1 maagcllatlftlfgsligpsseepfpavtikswdkmqedlvtlaktasgvnqlvdi 60
QY 61 YEKYQDLYTVEPNARQLVEIAARDIEKLISNRKALSVLSIALEAEKVQAHHQWREFASN 120
Db 61 yekyqdltyvepnarqlveiaardieklisnrskalsvlsialeaeqvqaahqwrefasn 120
QY 121 EVVYNKADDDLPKNDSEPGSQRIKPVFTEDANFGQISQYHAAVHIPTDIYEGSTIVL 180
Db 121 evvynakddlpekdndsepgsgrikpvfiedanfgqisqyhaavhiptdiyegstivl 180
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QY 181 NELNWT SALDEVFKKNEEDPSLLQVFGSATGLARYYPASPMWNSRPNKIDLYDVR 240
Db 181 nelnwt saldevfkknredpsllqvfgsatglaryypaspmwvnsrtpnkidlydvrr 240
QY 241 RPWYIOGAASPKDMLILVDVSGSVGLTLKLRITSVSEMLETSLDSDDFVNVASFNSNAQD 300
Db 241 rpwyiogaaspkdmlilvdvsgsvgltlklirtsvesemletlsdddfvnvasfnsnaq 300
QY 301 VSCFOHLVQANVKNKVLDAVNNTAKGTDYKKGFSFAPEQLLNNYSRANCKIIML 360
Db 301 vscfhlvqanvknkvlkdaannicakgtdykkgsfafeqllnynvranckikiml 360
QY 361 FTDGGERAQEIFNKYKDKKRVFRFSVQGNHYERGPIQWACENKGYVEIPSGAIR 420
Db 361 ftdggearsaqeifnkykdkkrrvfrfsvqgnhyergpiqwmacenkgvyvelpsgair 420
QY 421 INTQEVLDVLRPMVLGAKAKOVQNTNYYLDALGLVITGTLPVFNITGQFENKTNLK 480
Db 421 intqeyldvlgprmvlagkakqvntnyldalelgvltgtpvfnitgqfenktnlk 480
QY 481 NQLILGVMGVDSLEDIKRLTRFTLCPNGYFAIDPNGYVLLHPLNPKSKQEPVIL 540
Db 481 nqlilgvmgvdsledikrltrftlcpngyfaidpngyvilhplnqpkpsqepvtil 540
QY 541 DELDAELNDIKVEIRKMKIDGESGKTRTLVKSDERYIDKGNRTYTTPVNGTDYSL 600
Db 541 deldaelndikveirkmkidgesgktrtlvksderyidkgnrtytwpvngtdysl 600
QY 601 ALVLPYSFYIKAKLEETITOARSKKMKDSETLKPDNFEESGYTFIAPRDYCNLDKI 660
Db 601 alvlpysfyikakleetitqary-----setlkdndfeesgytfiaprdydcndk 653
QY 661 SDNNTFELNFEIDRTPNPNPCNADLINRVLLDAGFTNELVQYKQKNIKGVKAR 720
Db 654 sdnteflnfneidrtktpnpncnadlinrvlldagftnelvqykwaknikgvkar 713
QY 721 FVYTDGGITRVYPKBAGENQENPEYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
Db 714 fvtddggitrvypkageenqenpetyedsfykrsldndnyvftapynkspgpaysgi 773
QY 781 MYSKAVEIYIOGKLKPAVVGIKIDVNSNIENFTKTSIRDPCAGPVCDCKRNSDVMDCVI 840
Db 774 mvskaaveiyigklkpaavgikidvnsnienvftktsirdpcagpvcckrnsdvmcvi 833
QY 841 LDGQFLLMANHDDTYNQIRGFEIDPSLMRHLVNSIVAFNKSVDYOSVCEPGAAPKQ 900
Db 834 ldgqfllmanhddytngirfgeidpslmrhlvnsivafnksydyosvcepgaapkq 893
QY 901 GAGHRSAYVPSVADILQIGWATAAAMSTLQOFLLSLTPRLEAVEMEDDDFTASLSKQ 960
Db 894 gaghrsayvpsvadllqigwataaawslqqlslstprlleavemedddftaslskq 953
QY 961 SCITEQTYFFDNDSKFSGLVDCGNCSEIFHGEKLMNTNLIFIMVESKGTCPCTRLLI 1020
Db 954 sciteqtyffdnkskfsvglcdncseifhgeklmntnlifimveskgtcpctrlli 1013
QY 1021 QAEQSDGNPCDMVKQPRYRGPVCDPNNVLEDTDCGGVSGNLNPSLWYIIGIOFLLL 1080
Db 1014 qaeqsdgnpcdmvkqpryrgpvcddpnnvledtdcggvsgnlpslwyiigioflll 1073
QY 1081 WLVSGSTHRL 1091
Db 1074 wlvsgsthrll 1084

RESULT 11
ID AAW63155
XX AAW63155 standard; Protein; 1084 AA.
AC AAW63155;
XX
DT 12-OCT-1998 (first entry)
XX

DE Human calcium channel alpha-2e subunit.
XX Alpha-2 subunit; human; calcium channel; assay; detection;
KW characterisation; Lambert Eaton Syndrome; LES; diagnosis.
XX Homo sapiens.
XX US5792846-A.
XX 11-AUG-1998.
XX 31-MAY-1995; 95US-0455543.
XX 04-APR-1994; 94US-0223305.
XX 04-APR-1988; 88US-0178899.
XX 04-APR-1989; 89US-0603751.
XX 04-APR-1989; 89WO-US01408.
XX 20-FEB-1990; 90US-0482384.
XX 30-NOV-1990; 90US-0620250.
XX 15-AUG-1991; 91US-0745206.
XX 31-MAY-1995; 95US-0455543.
XX (SIBI-) SIBIA NEUROSCIENCES INC.
XX Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;
PI Williams ME;
XX WPI; 1998-456192/39.
XX N-PSDB; AAV42704.
XX DNA encoding human calcium channel alpha 1B sub-unit protein -
PT useful for recombinant production of the channel for screening of
PT its modulators, and diagnosis of Lambert Eaton Syndrome
XX Claim 3; Columns 305-310; 166pp; English.
XX The present sequence represents the alpha-2e subunit of a human calcium
CC channel. Calcium channels are membrane-spanning, multi-subunit proteins
CC that allow controlled entry of calcium ions into cells. This leads
CC to depolarisation events required for muscle contraction. The recombinant
CC subunit, when expressed with nucleic acids encoding the complete calcium
CC channel, can be used in assays for the detection and characterisation of
CC compounds that modulate the channel. The DNA encoding the subunits can
CC be alternatively spliced when transcribed, giving more than one form of
CC the protein from the same transcript, each having slightly different
CC properties. In addition, the reactivity of the alpha 1 subunit with IgG
CC molecules from the serum of an individual with Lambert Eaton Syndrome
CC (LES) can be used as a diagnostic for the disease.
XX Sequence 1084 AA;
SQ

Query Match 99.0%; Score 5691.5; DB 19; Length 1084;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1083; Conservative 0; Mismatches 1; Indels 7; Gaps 1;
QY 1 MAAGCLLATLTLFOSLLIGPSEEPFSAVTIKSWDKMQEDLVTLAKTAGSVNOLVDI 60
Db 1 maagcllatltlfqslligpsseepfsavtikswdkmqedlvtlaktagsvnglvd 60
QY 61 YEKYQDLTYVEPNNAQOLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120
Db 61 yekyqdltyvepnnarqlveiaardiekllsnrskalvslaleaeqvqahqwfedasn 120
QY 121 EVVYVNAKDDLDPEKNDSEPGSORIKPVFIEDANFGRQISYQHAHVHPTDIYEGSTIVL 180
Db 121 evvyvnaakddldpekndsepgsqrikpvfiedanfgriqsyqhaavhiptdiyegstivl 180
QY 181 NELNWT SALDEVFKKNEEDPSLLQVFGSATGLARYYPASPMWNSRPNKIDLYDVR 240
Db 181 nelnwt saldevfkknredpsllqvfgsatglaryypaspmwvnsrtpnkidlydvrr 240
QY 241 RPWYIOGAASPKDMLILVDVSGSVGLTLKLRITSVSEMLETSLDSDDFVNVASFNSNAQD 300


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Db 241 rpwyigaaapdkmlllvavsvsgltklirtsvsemletisdddfvnvasfnsnagd 300
QY 301 VSCFQHLVQANVRNKKVZKADANNITAKGIDYKKGFSAFQELLNINVRANCNKIIML 360
Db 301 vscfghlvqanvrnkklvavnnitakgidykkgfafaeqllynvstancnkiml 360
QY 361 FTDGGEERAQETFNKYNKDKKVRFRFVSQGHYRGPIQWMACENKGYEIPSGAIR 420
Db 361 ftdggeeraqeifnkynkdkkvrfrfvsqghnyergplqwmacenkgyyeipsaigair 420
QY 421 INTQSYLDVLRPMVLADGKAKOVQWTVNVLDAELGLVITGTLVPVNITQGFENKTNLK 480
Db 421 intqsyldvlgprpmvladgkakqvwtvnyldalelgvltgtlvpvnitqgfentnlk 480
QY 481 NOLILGVGVDSVLEDEIKRLPRFTCLPNGYFAIDPNGYVLLPNLQPKNPKSOEPTVL 540
Db 481 nqlilgvmgdvsledikrlprfclpngyfaidpnyvllhpnlpknkpsqepvtl 540
QY 541 DFLDAELENDIKVEIRNMWIDGESGKTRFLVLKSDQDRYTDKGNRTYTWTPVNGTDYSL 600
Db 541 dfldaelendikvelrnmwidgesektfrtlvksqderytdkgnrtytwtpvngtdysl 600
QY 601 ALVPTYFYFYKAKLETTIOAKSKGKMDSETLKPDPNEESGYTFIAPRDYCNLDKI 660
Db 601 alvptysfyfykakleetitqary-----selkpdnfeesgytfiaprdydcndlki 653
QY 661 SDNTEFLNPNFIDRKTNPNSCNADLINRVLLDAGFTNELVQWWSKOKIKGVKAR 720
Db 654 sdnntefllnfnidrktpnpscnadlinrvlldagftnelvqywsqknkkgvkar 713
QY 721 FVVDGGITRYPKAEAGNWQENPETYEDSYKRSLONDNVYFTAPYFNKSGPGAYESGI 780
Db 714 fvtvdggitrpypkaeagwnqenpetyedsfyrslndnvvyftapyfnksgpgayesgl 773
QY 781 MVSKAVEIYIGKLLKPAVVGKIDVNSWTENFTKTSIRDPKAGPVCDCRNSDVMDCVI 840
Db 774 mvskaveiyigkllkpaavgikidvnswtentfktksirpcagpvcdcrnsdvmdcvi 833
QY 841 LDDGGFLMANHDDYTQIGRFFGEIDPISLMRHLVNI SVYAFNKSXDYQSVCEPGAAPKQ 900
Db 834 ldggflmanhddytqigrffgeidpslmrhlvnsvyafnksydyqsvcepgaapkq 893
QY 901 GAGHRSYVPSVADIIGWATAAASILQFLLSLTFPRLLAEVMEDEDDFTASLSKQ 960
Db 894 gaghrsypsvadilqgwataaasilqfllsltfprlleavmedddftaslskq 953
QY 961 SCITEQTYEFDNDKSFSGVLDCGNCSTPFGHEKLMNTNLIIFIMVESKGTCPDTRLLI 1020
Db 954 sciteqtqyifdndksfsgvlcgcncstpfhgekmlntnlifimveskgtcpdtrlli 1013
QY 1021 QAEQTSQPNPCDMVKOPRYRKGPDVCFDNNVLEDYTDGGSGLNPSLWYIIGIQFLLL 1080
Db 1014 qaeqtsqpnpcdmvkpryrkgpdvcfdnnvledytdcggsvglpslwyiigiqflll 1073
QY 1081 WLVSNGTHRL 1091
Db 1074 wlvsngthrll 1084
```

RESULT 12

AAB10589

ID AAB10589 standard; Protein; 1084 AA.

XX

AC AAB10589;

XX

DT 22-DEC-2000 (first entry)

XX

DE Human calcium channel alpha-2e subunit protein.

XX

KW Human; calcium channel; calcium channel subunit; diagnosis;

KW Lambert Eaton Syndrome; calcium channel subunit alpha-2e.

XX

OS Homo sapiens.

XX US6096514-A.

PN

XX 01-AUG-2000.

PD

XX 25-MAY-1995; 95US-0450562.

XX

XX 04-APR-1988; 88US-0176899.

XX 02-FEB-1990; 90US-0482384.

PR

PR 08-NOV-1990; 90US-0603751.

PR

PR 30-NOV-1990; 90US-0620250.

PR

PR 15-AUG-1991; 91US-0745206.

PR

PR 10-APR-1992; 92US-0868354.

PR

PR 13-JUL-1992; 92US-0914231.

PR

PR 11-AUG-1993; 93US-0105536.

PR

PR 05-NOV-1993; 93US-0149097.

PR

PR 07-FEB-1994; 94US-0193078.

PR

PR 04-APR-1994; 94US-0223305.

PR

PR 11-AUG-1994; 94US-0290012.

PR

PR 23-SEP-1994; 94US-0311363.

PR

PR 28-SEP-1994; 94US-0314083.

PR

PR 07-NOV-1994; 94US-0336257.

PR

PR 13-MAR-1995; 95US-0404950.

XX

XX (SIBI-) SIBIA NEUROSCIENCES INC.

PA

XX

XX Ellis SB, Williams ME, McCue AF, Harpold MW;

PI

PI WPI; 2000-548230/50.

DR

DR N-PSDB; AAA71727.

XX

XX Human calcium channel beta subunit polynucleotides, useful for

XX

XX producing recombinant eukaryotic cells and for diagnosing Lambert Eaton

XX Syndrome

XX

XX Disclosure; Column 253-260; 153pp; English.

XX

XX This invention describes a novel isolated DNA molecule (I) comprising a

XX

XX sequence encoding a beta3-1 subunit of a human calcium channel.

XX

XX Nucleic acid probes comprising 14-30 contiguous nucleotides of

XX

XX beta.3 subunit encoding DNA are useful for isolation and cloning of

XX

XX calcium channel subunit-encoding DNA. Recombinant eukaryotic cells that

XX

XX express heterologous calcium channel are useful for identifying compounds

XX

XX that modulate calcium channel activity and in assays for identifying

XX

XX agonists and antagonists of calcium channel activity in humans. Human

XX

XX calcium channel subunit or eukaryotic cells expressing the channel are

XX

XX useful for diagnosing Lambert Eaton Syndrome (LES) in a human. This

XX

XX sequence represents the human calcium channel alpha-2e subunit which is

XX

XX described in the method of the invention.

XX

XX Sequence 1084 AA;

SQ

Query Match 99.0%; Score 5691.5; DB 21; Length 1084;

Best Local Similarity 99.3%; Pred. No. 0;

Matches 1083; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY 1 MAAGCLLALTTLTFLQSLIGPSSEEPFSAVTIKSWDKMQEDLVTLAKTAGSNOLVDI 60

Db 1 maagcllaltltlfgsligpsseepfpaavtikswdkmqedlvtlaktasgvnqlvdi 60

QY 61 YEKYQDLTYVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALEAEKVAQAHQWREDFASN 120

Db 61 yekyqdltyvepnnaqlveiaardieklslrskalvslaleaeakvgaahqwrdfasn 120

QY 121 EVVYVYNAKDDLPKNDSEPGSORIKPVEDANFGRQISYOHAAVHIPTDIYEGSTIVL 180

Db 121 evvyvynakddlpeknndsepgsqrikpvedanfgrqisyhaavhiptdiyegstivl 180

QY 181 NELNNTSALDVEYFKKNREDDPSLLQVFGSATGLARYYPASWPVNSRTPNKIDYDVR 240

Db 181 nelnntsaldevfkknreedpsllqvfgsatglaryypaswpvnsrtpnkidydvrr 240

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

QY 241 RPWYIQAASPKDMLILVDVSGSVSGLTLKLRISVSEMLETISDDDFVNVASFNSNAQD 300
Db 241 rpwyiqaaspkdmlilvdvsgsvsgltlklrtsvsemletisdddfvnnvasfnasqd 300
QY 301 VSCFOHLVQANVRNKKVLKDAVNNITAKITDYKKGFSFAFOLLNINVSANRANKIIML 360
Db 301 vscfghlvqanvrnkvlkdavnnitakitdykkgfsfafellnynvsanranciiml 360
QY 361 FTDGGEERAQEIFNKNYKDKKVRFRFSVGOHNYERGPIONMACENKGYEYIPISGAIR 420
Db 361 ftdggeeeraqeifnknkdkkvrfrfsvgghnyergpionmacenkgyeypisgaair 420
QY 421 INTQEVLDVLRPMVLGAKAKOVQWNTVYLDALLEGVLITGLPVFNITGOFENKTNLK 480
Db 421 intqevldvlgprmvlagkakqvntvnyldalelgvlitgltpvfnitgofenktnlk 480
QY 481 NQILIGVMGVDSLEIDIKRLTFRFLCPNGYVFAIDPNGYVLLHNPLOKPKNSQEPVTL 540
Db 481 nqililgvmgvdsleidikrltfrflcpngyvfaiidpnyvllhnploqpknpksqepvtl 540
QY 541 DFLDALENDIKVEIRNKMIDGSEKFTRLVLVKSQDERYIDKGNRTYTWTPVNGTDSL 600
Db 541 dfldaelendikveirnkmidgesektftlrvksqderiyidkgnrtwtvtpvngtdysl 600
QY 601 ALVLTYSFYIKALEETITQARSKKGMKDSFLKPDNFEESGYTFIAPRDYCNLDKI 660
Db 601 alvltysfyikaleetitqarskkgmkdslkpdnfeesgytfiaprdyicndlki 660
QY 661 SDNNTEFLNFEIDRTKPNPNCNADLINRVLLDAGFTNELVONYSKOKNIKGVKAR 720
Db 661 sdnnteflnfeidrtkpnnpncnadlinrvllldagftnelvonyksoknikgvkar 720
QY 721 FVVTGGITRVYPKEAGENWQENPETYEDSFYKSLDNDNYYFTAPYFNKSGPGAYESGI 780
Db 721 fvtvgtgtrvypkeagenwqenpetyedsfykrsldndnyftapyfnkspggayesgi 780
QY 781 MYSKAVEYIYQGLKLPVAVGKIDVNSWENFTYSTRDPCAGVCDCKRNSDVMDCVI 840
Db 781 mvskaaveiyigkllkpvavgkidvnswnftystdrpcagvcdckrnsdvmdcvi 840
QY 841 LDGDFLLMANHDDYTNOIGRFEGIDPSLMRHLNYSVYAFNKSVDYQSVCEPGAAPKQ 900
Db 841 ldgdfllmanhddytnoigrfegidpslmrhlvnysvyafnksvdyqsvcepgaapkq 900
QY 901 GAGHRSAYVPSVADILQIGWATAAASWILQOFLSLTFPRLLEAVEMEDDDFTASLSKQ 960
Db 901 gaghrsayvpsvadilqigwataaawilqoqlsltfprlleavemedddftaslskq 960
QY 961 SCITQTOYFFDNDKSGSVGLDCGNCRIHFGEKLMNTNLFIMVESKGTGCPDTRLLI 1020
Db 961 sciteqtqoyffndksfsgvldcgnrcrifhgeklmntnlfimveskgtgcpdtrlli 1020
QY 1021 OAEQTSQGNPCDMVKQPRYRKGPVCFDNNVLEDTGCGVSGINPSLWYIIGIQFLLI 1080
Db 1021 oaeqtsqgnpcdmvkqpryrkgrpvcfdnnvledtgcgvsginpslwyiigiqflll 1080
QY 1081 WLVSQSTHRL 1091
Db 1081 wlvsqsthrll 1091
QY 1091 WLVSQSTHRL 1094
Db 1094 wlvsqsthrll 1094

RESULT 13
AAR71012
ID AAR71012 standard; Protein: 1103 AA.
XX
AC AAR71012;
XX
DT 01-DEC-1995 (first entry)
XX Human neuronal calcium channel subunit alpha 2a.
XX
XX Calcium channel subunit; antagonist; agonist; diagnosis;
KW

Lambert Eaton Syndrome.
XX Homo sapiens.
XX W09504822-A.
XX 16-FEB-1995.
XX 11-AUG-1994; 94WO-US09230.
XX 11-AUG-1993; 93US-0105536.
XX 05-NOV-1993; 93US-0149097.
XX (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
XX Ellis SB, Gillespie A, Harpold MM, McCue AF, Williams ME;
XX WPI; 1995-090900/12.
XX N-PSDB; AAQ84666.
XX DNA encoding human calcium channel sub-unit(s) - used for
XX developing prods. for studying calcium channels, e.g. for
XX obtaining agonists and antagonists
XX Disclosure; Page 231-236; 285pp; English.
XX Human neuronal alpha 2 coding sequence (AAQ84664) transcript is
XX differentially processed in skeletal muscle, aorta, and CNS in
XX the region corresp. to nt 1595-1942 of AAQ84664 in each of the
XX tissues. Five alternatively spliced variant transcripts that differ
XX in the presence or absence of one to three different portions of
XX this region. There are three sequences involved (see AAQ84664 FT
XX and AAQ84665 FT), sequence 1, sequence 2 and sequence 3. The five
XX alpha 2 encoding transcripts from the different tissues include
XX different combinations of the three sequences, except for one of
XX the alpha 2 transcripts expressed in aorta which lacks all three
XX sequences. The five alpha 2 forms identified are (1) a form that
XX lacks sequence 3 called alpha 2a, expressed in skeletal muscle
XX (2) one that lacks sequence 1 called alpha 2b, expressed in CNS
XX (3) one that lacks sequences 1 and 2 called alpha 2c, expressed in
XX aorta (4) one that lacks sequences 1, 2 and 3 called alpha 2d,
XX expressed in aorta and (5) one that lacks sequences 1 and 3
XX called alpha 2e. The DNA and AA sequences of alpha 2a - alpha 2e
XX are set forth in AAQ84666-084669 and AAR71012-R71015 respectively.
XX Sequence 1103 AA;

Query Match 98.7%; Score 5672; DB 16; Length 1103;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 1083; Conservative 0; Mismatches 1; Indels 26; Gaps 2;

QY 1 MAAGCLLALTTLFQSLIGPSSEPPFSAVTIKSWDKMQEDLVTLAKTAGVNLQVLDI 60
Db 1 maagcllalttlfqlsligpsseppfsvavtikswdkmqedlvtlaktaagvnlqldi 60
QY 61 YEKYQDLYTVEPNNAQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120
Db 61 yekyqdytvepnnarqlveiaardieklslsnrskalvslaleaekvqaahqwredfaen 120
QY 121 EVVYNNAKDDLDPKNDSEPGSQRIKPFVIEDANRGRQISYQHAHVHPTDIYEGSTIVL 180
Db 121 evvynnakddldekndsepgsqrikpvfiedanrgrqisyqhaahvhtptdiyegstivl 180
QY 181 NELNWTSAIDVFKKNREEDPSLLWQVFGSATGLARYYPASVPWNSRTPNKNIDLYDVR 240
Db 181 nelnwtaldevfkknreedpsllwqvfgsatglaryypasvpwnsrtpnknidlydvrr 240
QY 241 RPWYIQAASPKDMLILVDVSGSVSGLTLKLRISVSEMLETISDDDFVNVASFNSNAQD 300
Db 241 rpwyiqaaspkdmlilvdvsgsvsgltlklrtsvsemletisdddfvnnvasfnasqd 300
QY 301 VSCFOHLVQANVRNKKVLKDAVNNITAKITDYKKGFSFAFOLLNINVSANRANKIIML 360
Db 301 vscfghlvqanvrnkvlkdavnnitakitdykkgfsfafellnynvsanranciiml 360

Db 301 vscfhlvqanvknkvlkdavnnitakgtdykgkfsfafeqllnynvsrancnkiml 360
QY 361 FTGGEERAQEIENKYNKDKKVRFRFSVGQHNHYERGPIOMMACENKGYEYIEPSIGAIR 420
Db 361 ftdggeeraqeifnkynkdkkvrfrfsvgqhnhyergpiqwmacenkgyyeypsiga 420
QY 421 INTQEVLDVLRPNVLGADKAKOVQNTNYLDALGLVITGLPVFNITQEPENTNLK 480
Db 421 intqeyldvlgpnmvlagdkakvgntnyldaleiglvtglpvnitgqfenktnlk 480
QY 481 NQILGVMGVYDLSLEDKRTPFTLCPNGYFAIDPNGVLLHPNLQPK----- 530
Db 481 nqilgvmgvdsledkrltpftlcpngyfaidpngvllhpnlpkpgvgiptin 540
QY 531 -----NPKSQEPVTLDFDAELNDIKVEIRNMKIDGESGERTFPLVKSQDERYI 581
Db 541 lrrrpnqpksgqevtlfdlaelndikveirnmkldgesgkrtfplvksqgeryl 600
QY 582 DKGNRVTWTPVNGTDSLALVLPYTFYFKAKLEETITQARSKGKMKDSETLKPDNF 641
Db 601 dkgnrvtwtpvngtdyslaivtpysfyfakleettqary-----setlkpdnf 653
QY 642 EESGYTFIAPRDYCNLDIKISDNNTEFLNNEFIDRKTPNNPSCNADLINRVLLDAGFTN 701
Db 654 eesgytfiaprdycndlikisdnteflnnefidrktppnpscnadlinrvlldagftn 713
QY 702 ELVONWYSKNTKGVKARVVTGGITRVYPREAGENWOENPETTEDSYKKSLONDNY 761
Db 714 elvqnywskqknlgkavrtvtdggitrvypkeagenwdenpetyedsfyrksldndy 773
QY 762 VFTAPYENKSGPAGYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKSTRDP 821
Db 774 vftapyfnksgpaysgimvskaveiyigkllkpavvgikidvnswiefnfktstirdp 833
QY 822 CAGPVCCKRNSDMVCVILDDGFLLMANHDDYTNOIGRFFGEIDPMSLRHLVNTSVYA 881
Db 834 cagpvcckrnsdvmcdevliddgflmlanhddytngirffgeidpslmlrhlvntsvya 893
QY 882 FNKSYDYQSVCEGAPKQAGHRSAYVPSVADILQGWATAAASILQOFLLSLTFPR 941
Db 894 fnksydyqsvcegaapkqaghsayvpsvadilqgwataaasilqqlsltfpr 953
QY 942 LLEAVEMEDDDFTASLSKQSCITEOTOFYFDNDKSKFSGLDCGNCRIPIHGEKLMNTNL 1001
Db 954 lleavemedddftaslskqsciteqtgyffondsksfsgvldcncsrifhgeklmntnl 1013
QY 1002 IFIMVESKGTCPCDTRLIIQAQETS DGNPCDMVKOPRYRKGPDPVCFDNNVLEDTDCGG 1061
Db 1014 ifimveskgtcpdtrliiqaqetsdgnpcdmvkopryrkgpdcfdnnvledydcgg 1073
QY 1062 VSGUNPSLWIIIGIOFLLWLVSGSTHRL 1091
Db 1074 vsgunpslwiiigiofllwlvsgsthrll 1103
RESULT 14
AAW63151
ID AAW63151 standard; Protein; 1103 AA.
XX
AC AAW63151;
XX
XX 12-OCT-1998 (first entry)
XX Human calcium channel alpha-2a subunit.
XX Alpha-2 subunit; human; calcium channel; assay; detection;
KW characterisation; Lambert Eaton Syndrome; LES; diagnosis.
XX Homo sapiens.
XX US5792846-A.
XX

PD 11-AUG-1998.
XX 31-MAY-1995; 950S-0455543.
XX 04-APR-1994; 940S-0223305.
PR 04-APR-1988; 880S-0176899.
PR 04-APR-1989; 890S-0603751.
PR 04-APR-1989; 89WO-US01408.
PR 20-FEB-1990; 900S-0482384.
PR 30-NOV-1990; 900S-0620250.
PR 15-AUG-1991; 910S-0745206.
PR 31-MAY-1995; 950S-0455543.
XX (SIBI-) SIBIA NEUROSCIENCES INC.
XX Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;
PI Williams ME;
XX WPI; 1998-456192/39.
DR N-PSDB; AAV42700.
XX DNA encoding human calcium channel alpha 1B subunit protein -
PT useful for recombinant production of the channel for screening of
PT its modulators, and diagnosis of Lambert Eaton Syndrome
XX
XX Claim 3; Columns 287-294; 166pp; English.
XX The present sequence represents the alpha-2a subunit of a human calcium
CC channel. Calcium channels are membrane-spanning, multi-subunit proteins
CC that allow controlled entry of calcium ions into cells. This leads
CC to depolarisation events required for muscle contraction. The recombinant
CC subunit, when expressed with nucleic acids encoding the complete calcium
CC channel, can be used in assays for the detection and characterisation of
CC compounds that modulate the channel. The DNA encoding the subunits can
CC be alternatively spliced when transcribed, giving more than one form of
CC the protein from the same transcript, each having slightly different
CC properties. In addition, the reactivity of the alpha 1 subunit with IgG
CC molecules from the serum of an individual with Lambert Eaton Syndrome
CC (LES) can be used as a diagnostic for the disease.
XX Sequence 1103 AA;
SQ
Query Match 98.7%; Score 5672; DB 19; Length 1103;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 1083; Conservative 0; Mismatches 1; Indels 26; Gaps 2;
QY 1 MAAGCLLALTLTLFQSLILIGPSSSEPPPSAVTTKSWVDKMQEDLVTAKTAGVGNQLVDI 60
Db 1 maagcllaltltlftqslilgppsseepfppsavtikswvdkmqedlvtlaktasgvnqlvdi 60
QY 61 YEKYODLYTVEPNAROLVETAAARDIEKLLSNRSKALVSLALEAEKYQAAHOREDFASN 120
Db 61 yekyodlytvepnarqlveaardieklslsnrskalvslaleaekyqaahqrwdfasn 120
QY 121 EVVYNAKDDLDPEKNDSEPCSORIKPFVIEDANFRGQISYQHAHVHIPTDIYEGSTIVL 180
Db 121 evvyinakddldpekndsepgsqrikpfiedanfrqisyqhaavhiptdiyegstivl 180
QY 181 NELNWTSSALDEVFKKNEEDPSLLVQVFGSATGLARYYPASPWVDNSTRTPNKIDLYDVR 240
Db 181 nelnwtssaldevfkknreedpsllwqvfgsatglaryypaspwvdnstrtpnkidlydvr 240
QY 241 RPWYIOGAASPDKMLILVDYVSGSVSGLTALKLIRTSVEMLETLSDDDFVNVSNSNAQD 300
Db 241 rpwyiogaaspdkmllilvdvsgsvsgltalklirtsvemletlsdddfvnvsnasnaqd 300
QY 301 VSCFOHLVQANVRNKKVYLKDAVNNITAKGITYDKKGFSAFEPQLLNYSRANCNKIIML 360
Db 301 vscfhlvqanvrnknkylkdavnnitakgitydkkgsfafeqllnynvsrancnkiml 360
QY 361 FTGGEERAQEIENKYNKDKKVRFRFSVGQHNHYERGPIOMMACENKGYEYIEPSIGAIR 420
Db 361 ftdggeeraqeifnkynkdkkvrfrfsvgqhnhyergpiqwmacenkgyyeypsiga 420

Db 361 ftdggeeraqefnkynkdkkvrfrfsvqghnyergpqlqmacenkgyyypisgair 420
Qy 421 INTQBYLDVLRPMVLGAKAKQVQWNTVYLDALBELGLVITGTLVPVFNITGOFENKTNLK 480
Db 421 Intqeyldvlgprpmvlagdkakqvqtnvyldalelgivigtltlpvfnitgqfenktnlk 480
Qy 481 NQLILGVNGVDVSLIEDIKRLPRFTLPCNGYFYFADPNQYVLLHNPLOPK-----530
Db 481 nqlilgvngvdsvedikrlprftlpcngyfyfaldpnygvllhnpkplgvipptn 540
Qy 531 -----NPKSQPVTLDLDALENDIKVEIRNKMIDGSGEKTFRTLVKSODERYI 581
Db 541 lrrkrrpnlnqpkseqpvtldfldaelndikveirnkmidgesgkttftrlvksqderiy 600
Qy 582 DKGNTYTWTPVNGDYSLALVLPYSFYIKAKLEETITQARSKGKMKDSETLKPDNF 641
Db 601 dkgnrtwtvpngtdyslalvlpysfyikakleetitgary-----setlkpdnf 653
Qy 642 EESGYTFIAPRDCYCNLKSNDNTEFLNFEFIDRKTNNPNSCNADLINRVLLDAGFTN 701
Db 654 eesgytfiaprdydcnldkisdnteflnfnefidrktppnpscnadlinrvlldagftn 713
Qy 702 ELVQNWSKQKNIKGVKARFVVTGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNY 761
Db 714 elvqywskqknikgvkarfvvtggitrvypkeagenwqenpetyedsfykrsldndny 773
Qy 762 VETAPYFNKSGPAYESGIMSKAVEIYIYQGLKLPVAVVGIKIDVNSWTENTKTSIRDP 821
Db 774 vftapyfnksgpayesgimskaveiyiqgkllkpavvgikidvnswnlentktsirp 833
Qy 822 CAGPVCDCRNSDNDVNDVTLDDGGFLMANHDDYTNQIGRFFGETDPSLMRHLVNLISVA 881
Db 834 cagpvcdcrcnsdndvndvtdldggflmanhddytngqgrffgetdpslmrhlvnlisva 893
Qy 882 FNKSYDYQVCPGAPKOGAGHRSAYVPSVADILQIGWATAAAMSILQOFLLSLTFFR 941
Db 894 fnskdyqsvcepapkgaghrasypvadilqigwataaawsilqflsiltfr 953
Qy 942 LLEAVEMEDDDFTASLSKOSCITEQTQYFFDNDKSFSGVLDGCGNSRIFHGEKLMNTNL 1001
Db 954 lleavemedddftaslskscitegtqyffndksksfgvldcgnscrifhgeklmntnl 1013
Qy 1002 IFTWESKGTCPDCTELLQAEQTSQGNPCDMVQPRYKGPDYCFDNNVLEDYDTCGG 1061
Db 1014 iftweskgtcpdctrlliqaegtsgpnpdmvqprykgpdycfdhnvledydcgg 1073
Qy 1062 VSGLPNLTWYIIGIOPFLLEWLVSGSTHRL 1091
Db 1074 vsglpnlwyiigiqfllwlvsgsthrll 1103

RESULT 15

AA10586
ID AA10586 standard; Protein; 1103 AA.
XX
AC AA10586;
XX
DT 22-DEC-2000 (first entry)
XX
DE Human calcium channel alpha-2a subunit protein.
XX
KW Human; calcium channel; calcium channel subunit; diagnostics;
KW Lambert Eaton Syndrome; calcium channel subunit alpha-2a.
XX
OS Homo sapiens.
XX
PN US6096514-A.
XX
PD 01-AUG-2000.
XX
PF 25-MAY-1995; 95US-0450562.
XX
PR 04-APR-1988; 88US-0176899.

PR 02-FEB-1990; 90US-0482384.
PR 08-NOV-1990; 90US-0603751.
PR 30-NOV-1990; 90US-0620250.
PR 15-AUG-1991; 91US-0745206.
PR 10-APR-1992; 92US-0868354.
PR 13-JUL-1992; 92US-0914231.
PR 11-AUG-1993; 93US-0105536.
PR 05-NOV-1993; 93US-0149097.
PR 07-FEB-1994; 94US-0193078.
PR 04-APR-1994; 94US-0223305.
PR 11-AUG-1994; 94US-0290012.
PR 23-SEP-1994; 94US-0311363.
PR 28-SEP-1994; 94US-0314083.
PR 07-NOV-1994; 94US-0336257.
PR 13-MAR-1995; 95US-0404950.
XX
PA (SIBI-) SIBIA NEUROSCIENCES INC.
XX
PI Ellis SB, Williams ME, McCue AF, Harpold MM;
XX
XX WPI; 2000-548230/50.
DR N-PSDB; AAA711724.
XX
PT Human calcium channel beta subunit polynucleotides, useful for
PT producing recombinant eukaryotic cells and for diagnosing Lambert Eaton
PT Syndrome -
XX
XX Disclosure: Column 229-236; 153pp; English.
XX
XX This invention describes a novel isolated DNA molecule (I) comprising a
CC nucleic acid encoding a beta3-1 subunit of a human calcium channel.
CC Nucleic acid probes comprising 14-30 contiguous nucleotides of
CC beta3 subunit encoding DNA are useful for isolation and cloning of
CC calcium channel subunit-encoding DNA. Recombinant eukaryotic cells that
CC express heterologous calcium channel are useful for identifying compounds
CC that modulate calcium channel activity and in assays for identifying
CC agonists and antagonists of calcium channel activity in humans. Human
CC calcium channel subunit or eukaryotic cells expressing the channel are
CC useful for diagnosing Lambert Eaton Syndrome (LES) in a human. This
CC sequence represents the human calcium channel alpha-2a subunit which is
CC described in the method of the invention.
XX
SQ Sequence 1103 AA;

Query Match 98.7%; Score 5672; DB 21; Length 1103;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 1083; Conservative 0; Mismatches 1; Indels 26; Gaps 2;
Qy 1 MAAGCILLALTTLTFLQSLLIGPSSEEPFSAVTIKSVKMOEDLVTLAKTAGVGNOLVDI 60
Db 1 maagcillaltltlflqslligpsseepfsavtiksvdkmqedvltlaktagvgnlvdI 60
Qy 61 YEKYQDLYTVEPNARQOLVEIAARDIEKLISNRSKALVSLALEAEKVQAAHQRDFASN 120
Db 61 yekyqdytvepnarqlveiaardieklisnrskalvslaleaekvqaahqrdfasn 120
Qy 121 EYVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFRQISYQHAHVHPIPDIEGSTIVL 180
Db 121 evvyynakddldpekndsepgsqrikpvfiedanfrqisyqhaavhiptdiyegstivl 180
Qy 181 NELNWTSALEDVEPKNREDEPSLLWQVFGSATGLARYYPASPWVDNSRTNKKIDLYDVR 240
Db 181 nelnwtaldevfkureedpsllwqvfgsatglaryypaspwvdnsrtnpkidiydvrr 240
Qy 241 RPWYIOGAASPKDMLILVDVSGVSGITLKLIRTSVSEMLETSLDDDFNVASFNSNAQD 300
Db 241 rpwyiogaaspkdmlilvdvsgvsgitlklirtsvsemletisdddfnvvasfnasqd 300
Qy 301 VSCFQHLVQANVRNKKVLDVANNITAKGITDYKKGFSFAEQLLNYSRANCNKIIML 360
Db 301 vscfqlhvqanvrnkvlkdvannitakgitdykkgfsfafeqllnynvrancnkiiml 360

QY 361 FTDGGERAEIFNKYNKDKVVRFRFSVGOHNYERGPIONMACENKGYYYEIPSIGAIR 420
 Db 361 fcdgggeeraqelfnkynkdkkvrfrfsvgqumyergpionmacenkgyyyeipsigair 420
 QY 421 INTQBYLDVLRPMVLGAKQKQVOMTNYVLDALGLVITGTLFVFNITGQFENKTNLK 480
 Db 421 intqeyldvlgprpmvlgakqkqvomtnvyldaleglvltgtlpvfnitgqfenktnlk 480
 QY 481 NQLILGVWGVDSLEDDIKRLPRFTLCPNGYFFAIDPNNGYVLLHPNLQPK----- 530
 Db 481 nqlilgvwgvdsledikrltprftlcpngyvyfaidpnyvllhpnlpkpgvgiptin 540
 QY 531 -----NPKSQBPVTLDFDLDALENDIKVEIRNMIDGESGEKTFRTLVKSODERYI 581
 Db 541 lkrtrpnlpnqpksgqepvldfldaelendikveirnmidgesgektftrlvksoderyi 600
 QY 582 DRGNRTYTWTPVNGTDYSLALVLPYSYIIKAKLEETITQARSKKGMKDSSETLKPDNF 641
 Db 601 dkgnrtytwpngtdyslalvlpysyiyiakleetitqary-----setlkpdnf 653
 QY 642 EESGYTFIAPROYCNDLKISDNTEFLLNFEFIDRKTPNPNPCNADLINRVLLDAGFTN 701
 Db 654 eesgytfiaproycndlkisdntefllnfefidrktppnpscnadlinrvlldagftn 713
 QY 702 ELVQNYWKQKNIKGVKARFVVTDGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNY 761
 Db 714 elvqnywkqknikgvkarfvvtdggitrvyypkeagenwqenpetyedsfykrsldndny 773
 QY 762 VETAPYFNKSGPAYESGIMVSKAVEIYIQGLKLPVAVVGIKIDVNSWIENFTKTSIRD 821
 Db 774 vftapyfnksgpayesglmvskaveiyiqgkllkpavvgikidvnswienvftktsirdp 833
 QY 822 CAGPVCDCKRNSDVMDCVILDDGGFLMANHDDYTNQIGRPFGEIDPSLMRHLNYSVYA 881
 Db 834 cagpvcckrnsdvmdcvilddggflmanhddytngigrffgeidpslmrhlvnisvya 893
 QY 882 FNKSYDYQSVCEPAAKQAGHRSAIYVPSVADILQIGWATAAAWSILQOFLLSLTTPR 941
 Db 894 fnksydyqsvcepaaqaghrsayvpsvadilqigwataaawsilqfllsiltfpr 953
 QY 942 LLEAVEMEDDDFTASLSKQSCITEQTQYFFDNDKSFSGVLDGNCSCRFHGEKLMNTNL 1001
 Db 954 lleavemedddftaslskqsciteqtqyffndnksfsgvldcncsrfhgeklnmtnl 1013
 QY 1002 IFTMVESKGTCPDTRLLIQAEQTSDEGNPCDMVKQPYRKGPDPVCFDNNVLEDYDCGG 1061
 Db 1014 iftmveskgtcpdtrlliqaeqtsdgnpcdmvkpyrkpdpvcfdnnvledydcgg 1073
 QY 1062 VSGLNPSLWYIIIGIOFLLLWLVSNGTHRL 1091
 Db 1074 vsghlpslwyiigiofllllwlvsngthrll 1103

Search completed: July 23, 2001, 07:36:05
 Job time: 446 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 23, 2001, 07:30:13 ; Search time 37.55 Seconds
(without alignments)
585.294 Million cell updates/sec

Title: US-09-397-548-14
Perfect score: 5748
Sequence: 1 MAAGCLLALTTLFQSLIG.....IIGIQFLLWLVSQSHRLL 1091

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgnl_7/ptodata/1/1aa/5A_COMB.pap.*
2: /cgnl_7/ptodata/1/1aa/5B_COMB.pap.*
3: /cgnl_7/ptodata/1/1aa/6A_COMB.pap.*
4: /cgnl_7/ptodata/1/1aa/6B_COMB.pap.*
5: /cgnl_7/ptodata/1/1aa/PTUS_COMB.pap.*
6: /cgnl_7/ptodata/1/1aa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5748	100.0	1091	1	US-07-745-206A-25
2	5748	100.0	1091	1	US-08-455-543A-52
3	5748	100.0	1091	2	US-08-223-305C-52
4	5748	100.0	1091	2	US-08-311-363-25
5	5744	99.9	1091	3	US-08-713-118-4
6	5744	99.9	1091	4	US-09-452-007-4
7	5708.5	99.3	1086	1	US-08-455-543A-54
8	5708.5	99.3	1086	2	US-08-223-305C-54
9	5691.5	99.0	1084	1	US-08-455-543A-56
10	5691.5	99.0	1084	2	US-08-223-305C-56
11	5672	98.7	1103	1	US-08-455-543A-53
12	5672	98.7	1103	2	US-08-223-305C-53
13	5652	98.3	1079	1	US-08-455-543A-55
14	5652	98.3	1079	2	US-08-223-305C-55
15	5508.5	95.8	1106	1	US-08-435-675B-5
16	5490.5	95.5	1106	1	US-08-336-257A-8
17	5257.5	91.5	1086	6	5386025-8
18	2581.5	44.9	508	1	US-08-435-675B-6
19	182	3.2	885	3	US-09-074-579-5
20	182	3.2	885	4	US-09-388-774-5
21	159.5	2.8	946	3	US-09-074-579-3
22	159.5	2.8	946	4	US-09-388-774-3
23	154	2.7	903	1	US-08-021-601-12
24	154	2.7	903	1	US-08-082-849B-12
25	154	2.7	903	5	PCT-US94-01624-12
26	152.5	2.7	789	1	US-08-471-033-32
27	152.5	2.7	789	2	US-08-471-044-32

28	152.5	2.7	789	2	US-08-463-483A-32	Sequence 32, Appl
29	152.5	2.7	789	2	US-08-471-046A-32	Sequence 32, Appl
30	152.5	2.7	789	2	US-08-470-566B-32	Sequence 32, Appl
31	152.5	2.7	789	2	US-08-838-219B-4	Sequence 4, Appl
32	152.5	2.7	789	2	US-08-469-334-32	Sequence 32, Appl
33	152.5	2.7	789	3	US-09-300-529-32	Sequence 32, Appl
34	152.5	2.7	789	3	US-09-233-336A-4	Sequence 4, Appl
35	152.5	2.7	789	4	US-09-233-752A-4	Sequence 4, Appl
36	150.5	2.6	789	4	US-08-960-780-6	Sequence 6, Appl
37	150.5	2.6	789	4	US-09-073-898-6	Sequence 6, Appl
38	148.5	2.6	790	4	US-08-960-780-4	Sequence 4, Appl
39	148.5	2.6	790	4	US-09-073-898-4	Sequence 4, Appl
40	147.5	2.6	746	2	US-08-838-219B-6	Sequence 6, Appl
41	147.5	2.6	746	3	US-09-233-336A-6	Sequence 6, Appl
42	147.5	2.6	746	4	US-09-233-752A-6	Sequence 6, Appl
43	145.5	2.5	790	4	US-08-960-780-8	Sequence 8, Appl
44	145.5	2.5	790	4	US-09-073-898-8	Sequence 8, Appl
45	141.5	2.5	789	1	US-08-471-033-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-07-745-206A-25
; Sequence 25, Application US/07745206A
; Patent No. 5429921
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: McCue, Ann
; APPLICANT: Feldman, Daniel
; TITLE OF INVENTION: Human Calcium Channel Compositions and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitch, Even, Tabin & Flannery
; STREET: 135 S. LaSalle
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/745.206A
; FILING DATE: 19910815
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Feder, Scott B
; REFERENCE/DOCKET NUMBER: 51504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-372-7842
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1091 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-745-206A-25

Query Match 100.0%; Score 5748; DB 1; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1091; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAGCLLALTTLFQSLIGPSSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
DB 1 MAAGCLLALTTLFQSLIGPSSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

61 YEKYQDLYTVEPNNAQVIAAARDIEKLSNRKALVSLALEAEKVQAAHQWREDFASN 120
121 EVVYNAKDDLDPEKNDSEPGSQRIPKFVIEDANFRQISYQHAHVHPDIDYEGSTIVL 180
181 NELNWTISALDEVKKNREEDPSLLQVFGSATGLARYYPASPWVNSRTPNKIDLDYVRR 240
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241 RPYVIOGAASPDKMLILDVYSGVSGLTILRTSVSEMLETSLDDDFVNVASFNSNAQD 300
241 RPYVIOGAASPDKMLILDVYSGVSGLTILRTSVSEMLETSLDDDFVNVASFNSNAQD 300
301 VSCFQHLVQANVRNKKVLDKAVNNITAKGTDYKGFSPFAFEQOLLNVNSRANCNKIIML 360
361 FTGGERAEQIEFNKYNKKVRFVRSVQHNHYERGPIQWACENKGYIYEIPSGAIR 420
361 FTGGERAEQIEFNKYNKKVRFVRSVQHNHYERGPIQWACENKGYIYEIPSGAIR 420
421 INTQEYLDVLRPMVLGADKAKOVQWNTVYLDALGLVITGTLPVFNITGQFENKTNLK 480
421 INTQEYLDVLRPMVLGADKAKOVQWNTVYLDALGLVITGTLPVFNITGQFENKTNLK 480
481 NQILTVGMGVDSLEDIKRLTPFTLCPNGYFAIDPDPNGYVLLHLPNLPKNPKSQBPVTL 540
481 NQILTVGMGVDSLEDIKRLTPFTLCPNGYFAIDPDPNGYVLLHLPNLPKNPKSQBPVTL 540
541 DFLDAELNDIKVEIRNKMIDGSGEKTFTLVKQSDERYIDKGNRTYTTPVNGTDYSL 600
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601 ALVLPYTFYIIKAKLEETITQARSKGKMKDSETLKPDNFEESGYTFIAPRYCNDLKI 660
601 ALVLPYTFYIIKAKLEETITQARSKGKMKDSETLKPDNFEESGYTFIAPRYCNDLKI 660
661 SDNTEFLNFEFIDRKTTPNPNNSCNADLINRVLLDAGFTNELVQWYWSKQKNIKVYKAR 720
661 SDNTEFLNFEFIDRKTTPNPNNSCNADLINRVLLDAGFTNELVQWYWSKQKNIKVYKAR 720
721 FVYTDGGITVYKAEAGNKOENPETIYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
721 FVYTDGGITVYKAEAGNKOENPETIYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
781 MYSKAVIYIQQKLLKPAVVGIKIDVNSWIENTFTKTSIRDPGAGPVCDCKRNSDVMDCVI 840
781 MYSKAVIYIQQKLLKPAVVGIKIDVNSWIENTFTKTSIRDPGAGPVCDCKRNSDVMDCVI 840
841 LDGSGFLMANHDDYTNQIGRFFGEIDPDLMLHLNLSVYAFNKSVDYQSVCEPFGAPKQ 900
841 LDGSGFLMANHDDYTNQIGRFFGEIDPDLMLHLNLSVYAFNKSVDYQSVCEPFGAPKQ 900
901 GAGHRSYVPSVADILQIGWATAAANSILQOFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960
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961 SCITEQTYFDDNDKSFSGVLDGCGNSRIFPHGKLMNTNLIIFTWESKTCPCDTRLLI 1020
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1021 QAEQTSQDPNCPDMVKQPRYKKGPDVCFDNNVLEDYTDGCGVSGLNPSLWYIIGIQFLLL 1080
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1081 WLVSQSTHRL 1091
1081 WLVSQSTHRL 1091

RESULT 2
US-08-455-543A-52
Sequence 52 Application US/08455543A
Patent No. 5752846
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA: US/08/455,543A
APPLICATION NUMBER: US/08/455,543A
FILING DATE: May 31, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-455-543A-52

Best Local Similarity 100.0%; Pred. No. 0;		Matches 1091; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	MAAGCLLATLTQSLIGPSSEEPSPSATTIKSWDKMQEDLVTLAKTASGVNQLVDI	60
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Db	121	EVVYNAKDDLPEDKNDSEPGSRIKPIPVFIEDANFRQISYQAAHVHPIDIYEGSTIVL	180
QY	181	NELNWTSALEDEVEKKREEDPSLLWVFGSATGLARYYPASPWDNSRTNPKIDLDVRR	240
Db	181	NELNWTSALEDEVEKKREEDPSLLWVFGSATGLARYYPASPWDNSRTNPKIDLDVRR	240
QY	241	RPWYIOGAASPDKMLILVDVSGSVGLTLKLI RTSVSEMLETISDDDFVNVASFNSNAQD	300
Db	241	RPWYIOGAASPDKMLILVDVSGSVGLTLKLI RTSVSEMLETISDDDFVNVASFNSNAQD	300
QY	301	VSCFQHLVQANVNKKVLKDAVNNTAKGITDYKKGFSFAPEQLLNYNVSRANCKIIML	360
Db	301	VSCFQHLVQANVNKKVLKDAVNNTAKGITDYKKGFSFAPEQLLNYNVSRANCKIIML	360
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Db	361	FTDGGERAQEIENKYNKDKKRVFRFSVGOHNYERGPIOWMACENKGYIYEIPSGAIR	420
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Db	421	INTQEYLDVLRPMVLADGAKAKOVQNTNVYDLALEGLVITGLPVFNITGQFENKTNLK	480
QY	481	NQILGVMGVDSLEIDIKRLTPFTICPNGYIFAIDPNGVYLLHPNLQPNKPSQEPVTL	540
Db	481	NQILGVMGVDSLEIDIKRLTPFTICPNGYIFAIDPNGVYLLHPNLQPNKPSQEPVTL	540
QY	541	DFLDALENDIKYIENKMKIDGSGEKTFTLVKSDERYIDKGNRTYTWTPVNGTDYSL	600
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QY	601	ALVLPYSFYIYKAKLEETITQARSKKGMKDSSETLKPDNFESGYTFIAPRDYCNLDKI	660
Db	601	ALVLPYSFYIYKAKLEETITQARSKKGMKDSSETLKPDNFESGYTFIAPRDYCNLDKI	660
QY	661	SDNTEFLNFNEFIDRKTPNPNPNSCHADLINRVLLDAGFTNELVQNYWSQKNKGVKAR	720
Db	661	SDNTEFLNFNEFIDRKTPNPNPNSCHADLINRVLLDAGFTNELVQNYWSQKNKGVKAR	720
QY	721	FVYTDGTRVYKPEAGENQENPEYDSFYKRSLDNDNVFTAPYFNKSGPGAYESGI	780
Db	721	FVYTDGTRVYKPEAGENQENPEYDSFYKRSLDNDNVFTAPYFNKSGPGAYESGI	780
QY	781	MVSKAVEIYIQGLKLLPAVVGIRKIDVNSWTFNFTKSIRDPACAGPVCDCRNSDVMDCVI	840
Db	781	MVSKAVEIYIQGLKLLPAVVGIRKIDVNSWTFNFTKSIRDPACAGPVCDCRNSDVMDCVI	840
QY	841	LDDGGLLMANHDYDYNQIGRFFGEIDPSLMRHLVNIISVYAFNKSVDYQSVCEPGAAPKQ	900
Db	841	LDDGGLLMANHDYDYNQIGRFFGEIDPSLMRHLVNIISVYAFNKSVDYQSVCEPGAAPKQ	900
QY	901	GAGHRSAYPSVADILQIGWATAAASILQOFLLSITTPRLLEAVEMEDDDFTASLSKQ	960
Db	901	GAGHRSAYPSVADILQIGWATAAASILQOFLLSITTPRLLEAVEMEDDDFTASLSKQ	960
QY	961	SCITEQTQFFDNDKDSFSGVLDCGNCRSRIFHGEKLMNTNLIIFIMVESKTCPCDTRLLI	1020
Db	961	SCITEQTQFFDNDKDSFSGVLDCGNCRSRIFHGEKLMNTNLIIFIMVESKTCPCDTRLLI	1020
QY	1021	QAEQTSQDGPNCPCDMVKOPRYRKGPVCFDNNVLEDYTDGCGVSGLNPSLWYIIGIOFLLL	1080
Db	1021	QAEQTSQDGPNCPCDMVKOPRYRKGPVCFDNNVLEDYTDGCGVSGLNPSLWYIIGIOFLLL	1080

Db	1021	QAEQTSQDGPNCPCDMVKOPRYRKGPVCFDNNVLEDYTDGCGVSGLNPSLWYIIGIOFLLL	1080
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Db	1081	WLVSGSTHRL 1091	
RESULT 3			
US-08-223-305C-52			
: Sequence 52, Application US/08223305C			
: Patent No. 5851824			
: GENERAL INFORMATION:			
: APPLICANT: Harpold, Michael			
: APPLICANT: Ellis, Steven			
: APPLICANT: Williams, Mark			
: APPLICANT: Feldman, Daniel			
: APPLICANT: McCue, Ann			
: APPLICANT: Brenner, Robert			
: TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND			
: TITLE OF INVENTION: METHODS			
: NUMBER OF SEQUENCES: 57			
: CORRESPONDENCE ADDRESS:			
: ADDRESSEE: Brown, Martin, Haller & McClain			
: STREET: 1660 Union Street			
: CITY: San Diego			
: STATE: California			
: COUNTRY: USA			
: ZIP: 92101-2926			
: COMPUTER READABLE FORM:			
: MEDIUM TYPE: Diskette			
: COMPUTER: IBM Compatible			
: OPERATING SYSTEM: DOS			
: SOFTWARE: FastSEQ Version 1.5			
: CURRENT APPLICATION DATA:			
: APPLICATION NUMBER: US/08/223,305C			
: FILING DATE: April 4, 1994			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: 07/868,354			
: FILING DATE: April 10, 1992			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: US 07/745,206			
: FILING DATE: 15-AUG-1991			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: US 07/620,250			
: FILING DATE: 30-NOV-1990			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: US 07/482,384			
: FILING DATE: 20-FEB-1990			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: US 07/603,751			
: FILING DATE: 04-APR-1989			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: WO PCT/US89/01408			
: FILING DATE: 04-APR-1989			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: US 07/176,899			
: FILING DATE: 04-APR-1988			
: ATTORNEY/AGENT INFORMATION:			
: NAME: Seidman, Stephanie L.			
: REGISTRATION NUMBER: 33,779			
: REFERENCE/DOCKET NUMBER: 52516 (P519739)			
: TELECOMMUNICATION INFORMATION:			
: TELEPHONE: (619)238-0999			
: TELEFAX: (619)238-0062			
: INFORMATION FOR SEQ ID NO: 52:			
: SEQUENCE CHARACTERISTICS:			
: LENGTH: 1091 amino acids			
: TYPE: amino acid			
: STRANDEDNESS: single			
: TOPOLOGY: linear			
: MOLECULE TYPE: protein			
: FRAGMENT TYPE: internal			
US-08-223-305C-52			

Query Match 100.0%; Score 5748; DB 2; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1091; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MAAGCLLALTLTFLFOSLLIGPSSPEPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

QY 61 YEKYODLYTVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALEAEKVAQAHHQWREDFASN 120
DB 61 YEKYODLYTVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALEAEKVAQAHHQWREDFASN 120

QY 121 EYVYNKADLLDPKNDSEPGSORIKPVFIEDANFGRIQISYQAAHVHIPTDIYEGSTIVL 180
DB 121 EYVYNKADLLDPKNDSEPGSORIKPVFIEDANFGRIQISYQAAHVHIPTDIYEGSTIVL 180

QY 181 NELNWTALDEVFKNKNEEDPSLLQWVGSGATGLARYYPASPWVDNSRTNPKIDLYDVR 240
DB 181 NELNWTALDEVFKNKNEEDPSLLQWVGSGATGLARYYPASPWVDNSRTNPKIDLYDVR 240

QY 241 RPYWIOGAASPDKMLILVDYSGVSGLTLLKIRTSVSEMLETISDDDFVNVASFNSNAQD 300
DB 241 RPYWIOGAASPDKMLILVDYSGVSGLTLLKIRTSVSEMLETISDDDFVNVASFNSNAQD 300

QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKGFSPAFEQLLNYSRANCNKIIML 360
DB 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKGFSPAFEQLLNYSRANCNKIIML 360

QY 361 FTGGEERAQEIENKYNKKVRFVFSVQGHYERGPQIOWMACENKGYIYEIPSGAIR 420
DB 361 FTGGEERAQEIENKYNKKVRFVFSVQGHYERGPQIOWMACENKGYIYEIPSGAIR 420

QY 421 INTQEYLDVLRGWLWLAGDKAKOVQNTNVLDALEGLVITGTLPVFNITGQFENKTNLK 480
DB 421 INTQEYLDVLRGWLWLAGDKAKOVQNTNVLDALEGLVITGTLPVFNITGQFENKTNLK 480

QY 481 NQILGVMGVDVSLDKRLTPRTLCNPGYYFAIDPNGYVLLHPNLQKNPKSQEPVTL 540
DB 481 NQILGVMGVDVSLDKRLTPRTLCNPGYYFAIDPNGYVLLHPNLQKNPKSQEPVTL 540

QY 541 DFLDAELNDIKVEINKNMIDGESGKFTLVKSDERYIDKGNRTYTWTPVNGTDYSL 600
DB 541 DFLDAELNDIKVEINKNMIDGESGKFTLVKSDERYIDKGNRTYTWTPVNGTDYSL 600

QY 601 ALVLPYTSFYIIKALEETITQARSKGKMDSETLKPONFESGYTFTAPRDYCNLDKI 660
DB 601 ALVLPYTSFYIIKALEETITQARSKGKMDSETLKPONFESGYTFTAPRDYCNLDKI 660

QY 661 SONTEFLNNEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQNYWSKQKNKGVKAR 720
DB 661 SONTEFLNNEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQNYWSKQKNKGVKAR 720

QY 721 FVYTDGGLTRVYPKEAGENQWNPETIYDSFKRSLDNDNYFTAPYFNKSGPAYESGI 780
DB 721 FVYTDGGLTRVYPKEAGENQWNPETIYDSFKRSLDNDNYFTAPYFNKSGPAYESGI 780

QY 781 MYSKAVEIYIOGKLLPAPVVGKIDVNSNIENFTKTSIRDPGAGPVCCCKRNSDVMDCVI 840
DB 781 MYSKAVEIYIOGKLLPAPVVGKIDVNSNIENFTKTSIRDPGAGPVCCCKRNSDVMDCVI 840

QY 841 LDGGLFLMANHDDYTNQIGRFFGEIDPSLMRHLVNIISYAFNKSVDYQSVCEPGAAPQ 900
DB 841 LDGGLFLMANHDDYTNQIGRFFGEIDPSLMRHLVNIISYAFNKSVDYQSVCEPGAAPQ 900

QY 901 GAGHSAYPSVADIIQIGWATAAWSIILOQFLSLTFRLEAVEMEDDDFTASLSQ 960
DB 901 GAGHSAYPSVADIIQIGWATAAWSIILOQFLSLTFRLEAVEMEDDDFTASLSQ 960

QY 961 SCITEQTYFFDNDKSFSGVLDGNCNCSIFHGEKLMNTNLIIFIMVESKGTCPCTRLLI 1020
DB 961 SCITEQTYFFDNDKSFSGVLDGNCNCSIFHGEKLMNTNLIIFIMVESKGTCPCTRLLI 1020

QY 1021 QAEQTSQDPNCPDMVKQPRYRKGPVCFDNNVLEDYTDGCGVSGNLNPSLWYIIGIQFLL 1080
DB 1021 QAEQTSQDPNCPDMVKQPRYRKGPVCFDNNVLEDYTDGCGVSGNLNPSLWYIIGIQFLL 1080

QY 1081 WLYSGSTHRL 1091
DB 1081 WLYSGSTHRL 1091

RESULT 4
US-08-311-363-25
; Sequence 25, Application US/08311363
; Patent No. 5876958
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: Human Calcium Channel Compositions and
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,363
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-51506
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1091 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-311-363-25

Query Match 100.0%; Score 5748; DB 2; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1091; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLTFLFOSLLIGPSSPEPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
DB 1 MAAGCLLALTLTFLFOSLLIGPSSPEPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

QY 61 YEKYODLYTVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALEAEKVAQAHHQWREDFASN 120
DB 61 YEKYODLYTVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALEAEKVAQAHHQWREDFASN 120

QY 121 EYVYNKADLLDPKNDSEPGSORIKPVFIEDANFGRIQISYQAAHVHIPTDIYEGSTIVL 180
DB 121 EYVYNKADLLDPKNDSEPGSORIKPVFIEDANFGRIQISYQAAHVHIPTDIYEGSTIVL 180

181 NELNWTSALEDEVEFKKREDDPSLLMQVFGSATGLARYYPASPVWDNSRTPNKIDLDYDVR 240
181 NELNWTSALEDEVEFKKREDDPSLLMQVFGSATGLARYYPASPVWDNSRTPNKIDLDYDVR 240
241 RPWYIOGAASPKDMLLDVDSVSGSLTKLRTSVSEMLETSDDDFVNVSFNSNAQ 300
241 RPWYIOGAASPKDMLLDVDSVSGSLTKLRTSVSEMLETSDDDFVNVSFNSNAQ 300
301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFQQLNLYNSRANCNKIIML 360
301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFQQLNLYNSRANCNKIIML 360
361 FTDGGEERAQEIFNKYKDKKRVFRFVSQGHNYERGPQIOWMACENKGYIYEIPSGAIR 420
361 FTDGGEERAQEIFNKYKDKKRVFRFVSQGHNYERGPQIOWMACENKGYIYEIPSGAIR 420
421 INTQEYLDVLGRPMVLGAKAKOVQNTNVLDALEGLVITGTLPVFNITGQFENKTNLK 480
421 INTQEYLDVLGRPMVLGAKAKOVQNTNVLDALEGLVITGTLPVFNITGQFENKTNLK 480
481 NQLILGVMGVDSLEDIKRLTPFTLCPNGYYPADPNQVYLLHPLNLPKNPKSQBPVTL 540
481 NQLILGVMGVDSLEDIKRLTPFTLCPNGYYPADPNQVYLLHPLNLPKNPKSQBPVTL 540
541 DFLDAELNDIKVEIRKMKIDGESGKTRTLVKSQDERYIDKGNRTYTWTVPNGTDYSL 600
541 DFLDAELNDIKVEIRKMKIDGESGKTRTLVKSQDERYIDKGNRTYTWTVPNGTDYSL 600
601 ALVLPYSFYIKAKLEETITQARSKGKMDSETLKPDNFESGYTFTAPRDYCNLDKI 660
601 ALVLPYSFYIKAKLEETITQARSKGKMDSETLKPDNFESGYTFTAPRDYCNLDKI 660
661 SDNTEFLNFEFIDRKTPNPNNSCNADLNRYLLDAGFTNELVQNYWSKQNKIKGVKAR 720
661 SDNTEFLNFEFIDRKTPNPNNSCNADLNRYLLDAGFTNELVQNYWSKQNKIKGVKAR 720
721 FVYTDGGITRVYKPEAGENQWENPEYEDSFYKRSLDNDNYVETAPYFNKSGPGAYESGI 780
721 FVYTDGGITRVYKPEAGENQWENPEYEDSFYKRSLDNDNYVETAPYFNKSGPGAYESGI 780
781 MVSKAVEIYIOGKLLPAPVGIKIDVNSWJENFTKTSIRDPACGVCDCRNSDVMDCVI 840
781 MVSKAVEIYIOGKLLPAPVGIKIDVNSWJENFTKTSIRDPACGVCDCRNSDVMDCVI 840
841 LDDGGFLMANHDDYTNQIGRFGEIDPISLMRHLVNI SVYAFNKSXYDQSVCEPGAAPKQ 900
841 LDDGGFLMANHDDYTNQIGRFGEIDPISLMRHLVNI SVYAFNKSXYDQSVCEPGAAPKQ 900
901 GAGHRSAYVPSVADILQIGWATAAASILQQLLSLTPFRLLEAVEMEDDDFTASLSKQ 960
901 GAGHRSAYVPSVADILQIGWATAAASILQQLLSLTPFRLLEAVEMEDDDFTASLSKQ 960
961 SCITEQYEFDDNDKSFSGVLDCGNCRIFFHGEKLMNTNLIIFIMVESKGTCPDTRLLI 1020
961 SCITEQYEFDDNDKSFSGVLDCGNCRIFFHGEKLMNTNLIIFIMVESKGTCPDTRLLI 1020
1021 QAEQTSQGNPCDMVKQPRYRKGPVDCFDNNVLEDYTDGCGVSGSLNPSLWYIIGIQFLLL 1080
1021 QAEQTSQGNPCDMVKQPRYRKGPVDCFDNNVLEDYTDGCGVSGSLNPSLWYIIGIQFLLL 1080
1081 WLVSNGTHRL 1091
1081 WLVSNGTHRL 1091

RESULT 5
US-08-713-118-4
; Sequence 4, Application US/08713118
; Patent No. 604036
; GENERAL INFORMATION:
; APPLICANT: Franco, Rodrigo
; APPLICANT: Sun Chen, Ai Ru

APPLICANT: Suey, David J.
TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL
TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,118
FILING DATE: 16-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mata, Elizabeth W.
REGISTRATION NUMBER: 38,236
REFERENCE/DOCKET NUMBER: ACC96-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-713-118-4

Query Match 99.9%; Score 5744; DB 3; Length 1091;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1090; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAGCLIALTLTFLQSLIGPSEEPFPPSAVTIKSWDKMQEDLVTLAKTAGSYNQVLVDI 60
DB 1 MAAGCLIALTLTFLQSLIGPSEEPFPPSAVTIKSWDKMQEDLVTLAKTAGSYNQVLVDI 60
QY 61 YEKYQDLYTVEPNARQVLEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQHREDFASN 120
DB 61 YEKYQDLYTVEPNARQVLEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQHREDFASN 120
QY 121 EVVYINAKDLDPEKNDSEPGSORIKPVFTEDANFGRIQISYQAAVHIPTDIEGSTITV 180
DB 121 EVVYINAKDLDPEKNDSEPGSORIKPVFTEDANFGRIQISYQAAVHIPTDIEGSTITV 180
QY 181 NELNWTSALEDEVEFKKREDDPSLLMQVFGSATGLARYYPASPVWDNSRTPNKIDLDYDVR 240
DB 181 NELNWTSALEDEVEFKKREDDPSLLMQVFGSATGLARYYPASPVWDNSRTPNKIDLDYDVR 240
QY 241 RPWYIOGAASPKDMLLDVDSVSGSLTKLRTSVSEMLETSDDDFVNVSFNSNAQ 300
DB 241 RPWYIOGAASPKDMLLDVDSVSGSLTKLRTSVSEMLETSDDDFVNVSFNSNAQ 300
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFQQLNLYNSRANCNKIIML 360
DB 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFQQLNLYNSRANCNKIIML 360
QY 361 FTDGGEERAQEIFNKYKDKKRVFRFVSQGHNYERGPQIOWMACENKGYIYEIPSGAIR 420
DB 361 FTDGGEERAQEIFNKYKDKKRVFRFVSQGHNYERGPQIOWMACENKGYIYEIPSGAIR 420
QY 421 INTQEYLDVLGRPMVLGAKAKOVQNTNVLDALEGLVITGTLPVFNITGQFENKTNLK 480
DB 421 INTQEYLDVLGRPMVLGAKAKOVQNTNVLDALEGLVITGTLPVFNITGQFENKTNLK 480
QY 481 NQLILGVMGVDSLEDIKRLTPFTLCPNGYYPADPNQVYLLHPLNLPKNPKSQBPVTL 540

Db 481 NOLILGVNGVDVSLDIEKRLTPRTLCFNGYFAIDPNGYALLHPNLQPKNPKSQEPVTL 540
Qy 541 DFLDAELNDIKVEIRNMIDGEGEKTFRTLVKSQDERYIDKGNRTYTTPVNGTDSL 600
Db 541 DFLDAELNDIKVEIRNMIDGEGEKTFRTLVKSQDERYIDKGNRTYTTPVNGTDSL 600
Qy 601 ALVLPYTFYIYKAKLEETITQARSKKMKDSETLKPDPNFEESGYTFIAPRDYCNLKI 660
Db 601 ALVLPYTFYIYKAKLEETITQARSKKMKDSETLKPDPNFEESGYTFIAPRDYCNLKI 660
Qy 661 SDNTEFLNFEEDIRKTPNPNPCNADLINRVLLDAGFTNELVQYWSKOKNIKVYKAR 720
Db 661 SDNTEFLNFEEDIRKTPNPNPCNADLINRVLLDAGFTNELVQYWSKOKNIKVYKAR 720
Qy 721 FVWTDGGITRVYKPEAGENQWENPETEDSFYKRSLDNDNVFTAPYFNKSGPGAYESGI 780
Db 721 FVWTDGGITRVYKPEAGENQWENPETEDSFYKRSLDNDNVFTAPYFNKSGPGAYESGI 780
Qy 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPGAPVCDCKRNSDVMDCVI 840
Db 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPGAPVCDCKRNSDVMDCVI 840
Qy 841 LDDGGFLLMANHDDYTNOIGRFEIDPDLRHLVNI SVYAFNKSVDYQSVCEPGRAPKQ 900
Db 841 LDDGGFLLMANHDDYTNOIGRFEIDPDLRHLVNI SVYAFNKSVDYQSVCEPGRAPKQ 900
Qy 901 GAGHSAYVPSVADILQIGWATAAASIIQQFLLSLTFPRLLLEAVEMEDDDFTASLSKQ 960
Db 901 GAGHSAYVPSVADILQIGWATAAASIIQQFLLSLTFPRLLLEAVEMEDDDFTASLSKQ 960
Qy 961 SCITEQYQYFFDNDKSFSGVLDGNGSRIFHGEKLMNTNLIIFIMVESKGTCPCDTRLII 1020
Db 961 SCITEQYQYFFDNDKSFSGVLDGNGSRIFHGEKLMNTNLIIFIMVESKGTCPCDTRLII 1020
Qy 1021 QAEQTSQPNPCDMVKOPRYKGPVDFCDNNVLEDYTDGCGVSGLNPSLWYIIGIQFLLL 1080
Db 1021 QAEQTSQPNPCDMVKOPRYKGPVDFCDNNVLEDYTDGCGVSGLNPSLWYIIGIQFLLL 1080
Qy 1081 WLVSQSTHRL 1091
Db 1081 WLVSQSTHRL 1091

RESULT 6

US-09-452-007-4

Sequence 4, Application US/09452007

Patent No. 6140485

GENERAL INFORMATION:

APPLICANT: Franco, Rodrigo

APPLICANT: Sun Chen, Ai Ru

APPLICANT: Suey, David J.

TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: MA

COUNTRY: USA

ZIP: 02173-4799

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/452,007

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/713,118

FILING DATE: 16-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mata, Elizabeth W.
REGISTRATION NUMBER: 38,236
REFERENCE/DOCKET NUMBER: ACC96-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-452-007-4

Query Match 99.9%; Score 5744; DB 4; Length 1091;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1090; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MAAGCLLALTTLTFLQSLIGPSSSEEPFPPSAVTIKSWYDKMQEDLVTLAKTASGVNQLVDI 60
Db 1 MAAGCLLALTTLTFLQSLIGPSSSEEPFPPSAVTIKSWYDKMQEDLVTLAKTASGVNQLVDI 60
Qy 61 YEKYQDLTYVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDEPASN 120
Db 61 YEKYQDLTYVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDEPASN 120
Qy 121 EYVYNAKDDLDPEKNDSEPGSQRIKPVFTEDANFGRQISYQAAHVIPTDIYEGSTIVL 180
Db 121 EYVYNAKDDLDPEKNDSEPGSQRIKPVFTEDANFGRQISYQAAHVIPTDIYEGSTIVL 180
Qy 181 NELNWTALDEVEFKKREEDPSLLQVFGSATGLARYYPASPWDNSRTPNKKIDLYDVR 240
Db 181 NELNWTALDEVEFKKREEDPSLLQVFGSATGLARYYPASPWDNSRTPNKKIDLYDVR 240
Qy 241 RPWYIOGAASPKDMLILVDVSGSVGLTLKIRTSVSEMLETSLDDDFVNVASFNSNAQD 300
Db 241 RPWYIOGAASPKDMLILVDVSGSVGLTLKIRTSVSEMLETSLDDDFVNVASFNSNAQD 300
Qy 301 VSCFQHLVQANVRNKKVLDAVNNITAKGITYDKGFSFAFQOLLNYSRANCNKIIML 360
Db 301 VSCFQHLVQANVRNKKVLDAVNNITAKGITYDKGFSFAFQOLLNYSRANCNKIIML 360
Qy 361 FTDGGEERAQEIFNKYKNDKKVFRFSGVQHNYERGIOMMACENKGYIYEIPSGAIR 420
Db 361 FTDGGEERAQEIFNKYKNDKKVFRFSGVQHNYERGIOMMACENKGYIYEIPSGAIR 420
Qy 421 INTOEYLDVLGRPMVLGAKAKOVQNTNYLDALEGLVITGTLPVFNITGQFNKTNLK 480
Db 421 INTOEYLDVLGRPMVLGAKAKOVQNTNYLDALEGLVITGTLPVFNITGQFNKTNLK 480
Qy 481 NQLILGVNGVDVSLDIEKRLTPRTLCFNGYFAIDPNGYALLHPNLQPKNPKSQEPVTL 540
Db 481 NQLILGVNGVDVSLDIEKRLTPRTLCFNGYFAIDPNGYALLHPNLQPKNPKSQEPVTL 540
Qy 541 DFLDAELNDIKVEIRNMIDGEGEKTFRTLVKSQDERYIDKGNRTYTTPVNGTDSL 600
Db 541 DFLDAELNDIKVEIRNMIDGEGEKTFRTLVKSQDERYIDKGNRTYTTPVNGTDSL 600
Qy 601 ALVLPYTFYIYKAKLEETITQARSKKMKDSETLKPDPNFEESGYTFIAPRDYCNLKI 660
Db 601 ALVLPYTFYIYKAKLEETITQARSKKMKDSETLKPDPNFEESGYTFIAPRDYCNLKI 660
Qy 661 SDNTEFLNFEEDIRKTPNPNPCNADLINRVLLDAGFTNELVQYWSKOKNIKVYKAR 720
Db 661 SDNTEFLNFEEDIRKTPNPNPCNADLINRVLLDAGFTNELVQYWSKOKNIKVYKAR 720
Qy 721 FVWTDGGITRVYKPEAGENQWENPETEDSFYKRSLDNDNVFTAPYFNKSGPGAYESGI 780
Db 721 FVWTDGGITRVYKPEAGENQWENPETEDSFYKRSLDNDNVFTAPYFNKSGPGAYESGI 780

QY 781 MVSKEVEIYIOGKLLKPAVVGIIKIDVNSWIENTKTSIRDPACGVCDCRNSDVMDCVI 840
Db 781 MVSKEVEIYIOGKLLKPAVVGIIKIDVNSWIENTKTSIRDPACGVCDCRNSDVMDCVI 840
QY 841 LDGSGFLLMANHHDDYTNQIGRFFGEIDPDLMLRLVNSVYAFNKSVDYQSVCEPGAAPKQ 900
Db 841 LDGSGFLLMANHHDDYTNQIGRFFGEIDPDLMLRLVNSVYAFNKSVDYQSVCEPGAAPKQ 900
QY 901 GAGHRSAYVPSVADIQIGWATAAAMSIIQQFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960
Db 901 GAGHRSAYVPSVADIQIGWATAAAMSIIQQFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960
QY 961 SCITEQYQFFDNDKSFSGVLDCGNCRIHFHGEKLMNTNLIIFIMVESKGTCTCDTRLII 1020
Db 961 SCITEQYQFFDNDKSFSGVLDCGNCRIHFHGEKLMNTNLIIFIMVESKGTCTCDTRLII 1020
QY 1021 QAEQSDGPNPCDMVKOPRYRKGPVDFVCFDNNVLEDYDTCGVSGLNPSLWYIIGIQFLLL 1080
Db 1021 QAEQSDGPNPCDMVKOPRYRKGPVDFVCFDNNVLEDYDTCGVSGLNPSLWYIIGIQFLLL 1080
QY 1081 WLVSNGTHRL 1091
Db 1081 WLVSNGTHRL 1091

RESULT 7

US-08-455-543A-54
; Sequence 54, Application US/0845543A
; Patent No. 5792846

GENERAL INFORMATION:

APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA

COMPUTER READABLE FORM:

ZIP: 92101-2926
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,543A

FILING DATE: May 31, 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/223,305
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 1086 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-455-543A-54

Query Match 99.3%; Score 5708.5; DB 1; Length 1086;

Best Local Similarity 99.5%; Pred. No. 0; Mismatches 0; Indels 5; Gaps 1;
Matches 1086; Conservative 0;

QY 1 MAAGCLLALTLTLFQSLIGPSSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
Db 1 MAAGCLLALTLTLFQSLIGPSSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
QY 61 YEKYQDLYTVEPNNAQOLVEIAARDIEKLSNRSKALVSLALEAEKVQAAHQWREDFASN 120
Db 61 YEKYQDLYTVEPNNAQOLVEIAARDIEKLSNRSKALVSLALEAEKVQAAHQWREDFASN 120
QY 121 EVVYVNAKDDLPDKNDSEPGSORIKPVFIEDANFGQISYQAAHVHPTDIYEGSTIVL 180
Db 121 EVVYVNAKDDLPDKNDSEPGSORIKPVFIEDANFGQISYQAAHVHPTDIYEGSTIVL 180
QY 181 NELNWTSSALDEVEFKKNEEDPSLLQWVFGSATGLARYYPASPVWDSNRTNPKIDLYDVR 240
Db 181 NELNWTSSALDEVEFKKNEEDPSLLQWVFGSATGLARYYPASPVWDSNRTNPKIDLYDVR 240
QY 241 RPWYIOGAASPDKMLILVDVSGSVGLTLKLTSTVSEMLETSLDDDFVNVASFNSNAQD 300
Db 241 RPWYIOGAASPDKMLILVDVSGSVGLTLKLTSTVSEMLETSLDDDFVNVASFNSNAQD 300
QY 301 VSCFOHLVQANVRNKKVLDVANNITAKGTDYKGFSAFEQILLNYSRANCNKTIIML 360
Db 301 VSCFOHLVQANVRNKKVLDVANNITAKGTDYKGFSAFEQILLNYSRANCNKTIIML 360
QY 361 FTGGEERAQEIFNKYNKDKKRVFRFVSQGHNYERGPIQWACENKGYIYEIPSGAIR 420
Db 361 FTGGEERAQEIFNKYNKDKKRVFRFVSQGHNYERGPIQWACENKGYIYEIPSGAIR 420
QY 421 INTQEYLDVLGRPMVLGAKAKOVQMTNVYDLALELGLVTGTLPLVFNITGQENKTNLK 480
Db 421 INTQEYLDVLGRPMVLGAKAKOVQMTNVYDLALELGLVTGTLPLVFNITGQENKTNLK 480
QY 481 NQLILGVMGVDSLEDIKRLTPRFTLCPNGIYFAIDPBGVYLHPNLPKNPKSQEPVTL 540
Db 481 NQLILGVMGVDSLEDIKRLTPRFTLCPNGIYFAIDPBGVYLHPNLPKNPKSQEPVTL 540
QY 541 DFLDAELENDIKVEIRNKMIDGESGKTFRTLVKSODERYIDKGNRTYTWTPVNGTDYSL 600
Db 541 DFLDAELENDIKVEIRNKMIDGESGKTFRTLVKSODERYIDKGNRTYTWTPVNGTDYSL 600
QY 601 ALVLPYTSFYIYKAKLEETITQARSKKGMKDSITLKPONFESGYTFTIAPRDYCNLDKI 660
Db 601 ALVLPYTSFYIYKAKLEETITQARSKKGMKDSITLKPONFESGYTFTIAPRDYCNLDKI 660
QY 661 SONNTEFLNPFNEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQNVSKQKIKGVKAR 720
Db 661 SONNTEFLNPFNEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQNVSKQKIKGVKAR 720

Db 656 SDNTEFLLNFNEFIDRKTNNPSCNADLINRVLLDAGFTNELVQNTWSKQKNIKVKAR 715
QY 721 FVWTDGGITRYVPKEAGNWOENPETYEDSYKRSLDNDNTVETAPYFNKSGPGAYESGI 780
Db 716 FVWTDGGITRYVPKEAGNWOENPETYEDSYKRSLDNDNTVETAPYFNKSGPGAYESGI 775
QY 781 MYSAVEYIIQGLKLPKPAVGIKIDVNSWIEFTKTSIRDPFCAGPVCDCCKRNSDVMDCVI 840
Db 776 MYSAVEYIIQGLKLPKPAVGIKIDVNSWIEFTKTSIRDPFCAGPVCDCCKRNSDVMDCVI 835
QY 841 LDDGGFLMAHNDYTNQIGRFFGEIDPSLMRHLVNTSVYAFNKSVDYQSVCEPGAAPKQ 900
Db 836 LDDGGFLMAHNDYTNQIGRFFGEIDPSLMRHLVNTSVYAFNKSVDYQSVCEPGAAPKQ 895
QY 901 GAGHSAYVPSVADILQIGWATAAANSILOQFLLSLTFEPRLLEAVEMDDDFASLSKQ 960
Db 896 GAGHSAYVPSVADILQIGWATAAANSILOQFLLSLTFEPRLLEAVEMDDDFASLSKQ 955
QY 961 SCITEQTYFFDNDSKFSFSGVLDGCGNSRIFPHGKLMNTNLIFIMVESKGTGCPDTRLLI 1020
Db 956 SCITEQTYFFDNDSKFSFSGVLDGCGNSRIFPHGKLMNTNLIFIMVESKGTGCPDTRLLI 1015
QY 1021 QAEQTSQGNPCDMVKOPRYRKGPDVCFDNNVLEDYTDGCGVSGNLPSLWYIIQIFLL 1080
Db 1016 QAEQTSQGNPCDMVKOPRYRKGPDVCFDNNVLEDYTDGCGVSGNLPSLWYIIQIFLL 1075
QY 1081 WLVSSTHRL 1091
Db 1076 WLVSSTHRL 1086

RESULT 8
US-08-223-305C-54
; Sequence 54, Application US/08223305C
; Patent No. 5851824
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/223,305C
; FILING DATE: April 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,250
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA: WO PCT/US89/01408
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 52516 (P519739)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1086 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-223-305C-54

Query Match 99.3%; Score 5708.5; DB 2; Length 1086;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1086; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 1 MAAGCLIALTLTFLQSLIGPSSPEPPSAVTIKSWDKMQEDLVTLAKTAGSGVNLVDI 60
Db 1 MAAGCLIALTLTFLQSLIGPSSPEPPSAVTIKSWDKMQEDLVTLAKTAGSGVNLVDI 60
QY 61 YEKYQDLYTVEPNNAQVLEIAARDEKLLSNRSKALVSLALEAEKYQAAHQWREDFASN 120
Db 61 YEKYQDLYTVEPNNAQVLEIAARDEKLLSNRSKALVSLALEAEKYQAAHQWREDFASN 120
QY 121 EVVYNAKDDLDPEKNDSEPGSORIKPVFIEDANFGQISYQHAHVHIPTDIYEGSTIVL 180
Db 121 EVVYNAKDDLDPEKNDSEPGSORIKPVFIEDANFGQISYQHAHVHIPTDIYEGSTIVL 180
QY 181 NELNWT-SALDEVEFKNREEDPSLLWQVFGSATGLARYYPASPWVDSNRTNPKIDLYDVR 240
Db 181 NELNWT-SALDEVEFKNREEDPSLLWQVFGSATGLARYYPASPWVDSNRTNPKIDLYDVR 240
QY 241 RPWYIOGAASPKDMLILVDVSGSVGLTLKIRTSVSEMLETLSDDDFVNVASFNSNAQD 300
Db 241 RPWYIOGAASPKDMLILVDVSGSVGLTLKIRTSVSEMLETLSDDDFVNVASFNSNAQD 300
QY 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGITYDKKGFSAFEQQLNLYNVRANCKNKLIML 360
Db 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGITYDKKGFSAFEQQLNLYNVRANCKNKLIML 360
QY 361 FTGGEERAQEIENKYNKDKKVRVFRFVSQHNHYERGPQIOWMACENKGYIYEPSIGAIR 420
Db 361 FTGGEERAQEIENKYNKDKKVRVFRFVSQHNHYERGPQIOWMACENKGYIYEPSIGAIR 420
QY 421 INTQEYLDVLGRPMVLADKAKOVQNTNVYLDALGLVITGTLVPVFNITGQFENKTNLK 480
Db 421 INTQEYLDVLGRPMVLADKAKOVQNTNVYLDALGLVITGTLVPVFNITGQFENKTNLK 480
QY 481 NQILGVMGVDVSLIEDIKRLTPFTLCPNGIYFAIDPNGYVLLHPNLPKNPKSQBPVTL 540
Db 481 NQILGVMGVDVSLIEDIKRLTPFTLCPNGIYFAIDPNGYVLLHPNLPKNPKSQBPVTL 535
QY 541 DFLDAELENDIKVEIRNKMIDGESGKFTFTLVKSDERYIDKGNRTYTWTPVNGTDYSL 600
Db 536 DFLDAELENDIKVEIRNKMIDGESGKFTFTLVKSDERYIDKGNRTYTWTPVNGTDYSL 595
QY 601 ALVLPYTSFYIKAKLEETITQARSKKGMKDSSETLKPDPNFESGYTFTIAPRDYCNLDKI 660
Db 596 ALVLPYTSFYIKAKLEETITQARSKKGMKDSSETLKPDPNFESGYTFTIAPRDYCNLDKI 655

QY 661 SNNTEFLNFEIDRKTTPNPNPCNADLINRVLLDAGFTNBLVONYSKQNKIKGVKAR 720
DB 656 SNNTEFLNFEIDRKTTPNPNPCNADLINRVLLDAGFTNBLVONYSKQNKIKGVKAR 715
QY 721 FVVTGGITRVYPKKAGENWQENPETYEDSFYKRSIDNDNVYFTAPYFNKSGPGAYESGI 780
DB 716 FVVTGGITRVYPKKAGENWQENPETYEDSFYKRSIDNDNVYFTAPYFNKSGPGAYESGI 775
QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTKTSIRDPCAGVPCDCRNSDVMDCVI 840
DB 776 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTKTSIRDPCAGVPCDCRNSDVMDCVI 835
QY 841 LDDGGFLLMANHDDYTNQIGRFEGIDPSLRHLNYSVIAFNKSYDYQSCEPGAAPKQ 900
DB 836 LDDGGFLLMANHDDYTNQIGRFEGIDPSLRHLNYSVIAFNKSYDYQSCEPGAAPKQ 895
QY 901 GAGHSAYVPSVADILQIGWATAAWSILOQFLSLTFPRLEAVEMEDDDFTASLSKQ 960
DB 896 GAGHSAYVPSVADILQIGWATAAWSILOQFLSLTFPRLEAVEMEDDDFTASLSKQ 955
QY 961 SCITEQTOYFFDNDKSGVGLDCGNCRIHGEKLMNTNLFIMVESKGTGCPDTRLLI 1020
DB 956 SCITEQTOYFFDNDKSGVGLDCGNCRIHGEKLMNTNLFIMVESKGTGCPDTRLLI 1015
QY 1021 QAEQSDGPNPCDMYKQPRYKGPVCFDNNVLEDYTDGCGVSGNLNPSLWYIIGIOFLLL 1080
DB 1016 QAEQSDGPNPCDMYKQPRYKGPVCFDNNVLEDYTDGCGVSGNLNPSLWYIIGIOFLLL 1075
QY 1081 WLVSSTHRL 1091
DB 1076 WLVSSTHRL 1086

RESULT 9

US-08-455-543A-56

; Sequence 56, Application US/08455543A

; Patent No. 5792846

; GENERAL INFORMATION:

; APPLICANT: Harpold, Michael

; APPLICANT: Ellis, Steven

; APPLICANT: Williams, Mark

; APPLICANT: Feldman, Daniel

; APPLICANT: McCue, Ann

; APPLICANT: Brenner, Robert

; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

; NUMBER OF SEQUENCES: 57

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Brown, Martin, Haller & McClain

; STREET: 1660 Union Street.

; City: San Diego

; STATE: California

; COUNTRY: USA

; ZIP: 92101-2926

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/455,543A

; FILING DATE: May 31, 1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/223,305

; FILING DATE: April 4, 1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/868,354

; FILING DATE: April 10, 1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/745,206

; FILING DATE: 15-AUG-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/620,250
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-52517
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1084 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-455-543A-56

Query Match 99.0%; Score 5691.5; DB 1; Length 1084;

Best Local Similarity 99.3%; Pred. No. 0;

Matches 1083; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY 1 MAAGCLLALTLTFLFOSLLIGSPSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
DB 1 MAAGCLLALTLTFLFOSLLIGSPSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
QY 61 YEKYQDLYTVEPNNAQOLVETAAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDFASN 120
DB 61 YEKYQDLYTVEPNNAQOLVETAAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDFASN 120
QY 121 EVVYNNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROIISYQHAHVHIPTDIYEGSTVL 180
DB 121 EVVYNNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROIISYQHAHVHIPTDIYEGSTVL 180
QY 181 NELNWTSAALDEVFKKKNREEDPSLLMQVFGSATGLARYYPASPWDNSRTPNKKIDLYDVR 240
DB 181 NELNWTSAALDEVFKKKNREEDPSLLMQVFGSATGLARYYPASPWDNSRTPNKKIDLYDVR 240
QY 241 RPWYIOGAASPKDMLILVDVSGSVSGLTLKLTIRTSVSEMLETSLDDDFNVASFNSNAQD 300
DB 241 RPWYIOGAASPKDMLILVDVSGSVSGLTLKLTIRTSVSEMLETSLDDDFNVASFNSNAQD 300
QY 301 VSCFOHLVQANVRNKKVLKDAVNNTAKGIDYKKGFSFAFEQLLNYSVRANCKIIML 360
DB 301 VSCFOHLVQANVRNKKVLKDAVNNTAKGIDYKKGFSFAFEQLLNYSVRANCKIIML 360
QY 361 FTDGGEERAQAEIFNKYNKDKKVRVFRFSVGQHNRYERGPQIOWMACENKGYEIPISGAIR 420
DB 361 FTDGGEERAQAEIFNKYNKDKKVRVFRFSVGQHNRYERGPQIOWMACENKGYEIPISGAIR 420
QY 421 INTQEYLDVLGRPMVLADGKAKQVQNTNYLDALBELGVITGTLVFNITGOFENKTNLK 480
DB 421 INTQEYLDVLGRPMVLADGKAKQVQNTNYLDALBELGVITGTLVFNITGOFENKTNLK 480
QY 481 NQLILGVNMGVDVSLIEDIKRLTPRFTLCPNGYFFADPNGYVLLHHPNLOPKPKPSQEPVTL 540
DB 481 NQLILGVNMGVDVSLIEDIKRLTPRFTLCPNGYFFADPNGYVLLHHPNLOPKPKPSQEPVTL 540
QY 541 DFLDAELENDIKVEIRNKKMIDGESGEKTFRTLVSQDERYIDKGNRTYTTWTPVNGTDYSL 600

Db 541 DFLDAELNDIKVEIRNKMIDGESGKTRTLVKSDERYIDKGNRTYTWTPVNGTDYSL 600
QY 601 ALVLPYTSYIIKAKLEETITQARKSKGKMDSETLKPNFESGYTFTAPRDYNDLKI 660
Db 601 ALVLPYTSYIIKAKLEETITQARY-----SETLKPNFESGYTFTAPRDYNDLKI 653
QY 661 SDNTEFLNNEFIDRKTPNPSCNADLINRVLLDAGFTNELVONYSKQNIKGVKAR 720
Db 654 SONTEFLNNEFIDRKTPNPSCNADLINRVLLDAGFTNELVONYSKQNIKGVKAR 713
QY 721 FVDTGGITRVYPKEAGENQENPETYEDSFYKRSIDNDNYYFTAPYFNKSGPGAYESGI 780
Db 714 FVDTGGITRVYPKEAGENQENPETYEDSFYKRSIDNDNYYFTAPYFNKSGPGAYESGI 773
QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTSIRDPCAGPVCCKRNSDVMDCVI 840
Db 774 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTSIRDPCAGPVCCKRNSDVMDCVI 833
QY 841 LDDGGFLMANHDDYTNOIGREFGEIDPSLMRHLVNSIVYAFNKSYDYQSVCEPGAAPKQ 900
Db 834 LDDGGFLMANHDDYTNOIGREFGEIDPSLMRHLVNSIVYAFNKSYDYQSVCEPGAAPKQ 893
QY 901 GAGHSAYVPSVADILIQGWATAAASILQOFLLSLPPRLLEAVEMDDDDFTASLSKQ 960
Db 894 GAGHSAYVPSVADILIQGWATAAASILQOFLLSLPPRLLEAVEMDDDDFTASLSKQ 953
QY 961 SCITQOTQFFNDKSPSGVLDGNCNCSIFHGEKLMNTNLFIMVESKGTGCPDTRLLI 1020
Db 954 SCITQOTQFFNDKSPSGVLDGNCNCSIFHGEKLMNTNLFIMVESKGTGCPDTRLLI 1013
QY 1021 QAEQTSQDGNPCDMQKPRYKGPVDFDNNVLEDYDTCGGVSGNLPSLWYIIGIQFLL 1080
Db 1014 QAEQTSQDGNPCDMQKPRYKGPVDFDNNVLEDYDTCGGVSGNLPSLWYIIGIQFLL 1073
QY 1081 WLVSSTHRL 1091
Db 1074 WLVSSTHRL 1084

RESULT 10

US-08-223-305C-56

; Sequence 56, Application US/08223305C

; Patent No. 5851824

; GENERAL INFORMATION:

; APPLICANT: Harpold, Michael

; APPLICANT: Ellis, Steven

; APPLICANT: Williams, Mark

; APPLICANT: Feldman, Daniel

; APPLICANT: McCue, Ann

; APPLICANT: Brenner, Robert

; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

; METHOD

; NUMBER OF SEQUENCES: 57

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Brown, Martin, Haller & McClain

; STREET: 1660 Union Street

; CITY: San Diego

; STATE: California

; COUNTRY: USA

; ZIP: 92101-2926

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/223.305C

; FILING DATE: April 4, 1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/868,354

; FILING DATE: April 10, 1992

; PRIOR APPLICATION DATA:

; APPLICATION DATA:

; APPLICATION DATA:

; APPLICATION DATA:

; APPLICATION DATA:

; APPLICATION DATA:

; APPLICATION DATA:

; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,250
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 52516 (P519739)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1084 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-223-305C-56

Query Match 99.0%; Score 5691.5; DB 2; Length 1084;

Best Local Similarity 99.3%; Pred. No. 0;

Matches 1083; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY 1 MAAGCLLALTTLFOSLLIGPSSEPPFSAVTKSWDKMQEDLVTLAKTAGSVNQLVDI 60
Db 1 MAAGCLLALTTLFOSLLIGPSSEPPFSAVTKSWDKMQEDLVTLAKTAGSVNQLVDI 60
QY 61 YEKYQDLYTVENPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDFASN 120
Db 61 YEKYQDLYTVENPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDFASN 120
QY 121 EVVYNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROISYQHAHVHPTDIYEGSTIVL 180
Db 121 EVVYNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROISYQHAHVHPTDIYEGSTIVL 180
QY 181 NELNWTSSALDEVYKKNREEDPSLLMQVFGSATGLARYYPASPWVDSNRTPNKNIDLYDVR 240
Db 181 NELNWTSSALDEVYKKNREEDPSLLMQVFGSATGLARYYPASPWVDSNRTPNKNIDLYDVR 240
QY 241 RPWYIQGAASPKDMLILVDVSGVSGSLTKLIRTSVSEMLETSDDDDFNVASFNSNAQD 300
Db 241 RPWYIQGAASPKDMLILVDVSGVSGSLTKLIRTSVSEMLETSDDDDFNVASFNSNAQD 300
QY 301 VSCFOHLVQANVRNKKVLKDAVNNTAKGIDTYKKGFSFAFQOLLNINVRANCKNIIML 360
Db 301 VSCFOHLVQANVRNKKVLKDAVNNTAKGIDTYKKGFSFAFQOLLNINVRANCKNIIML 360
QY 361 FTDGGEERAQEIFNKYNKDKKVRVFRFVSQGHNYERGPQIWMACENKGYEYIPSGAIR 420
Db 361 FTDGGEERAQEIFNKYNKDKKVRVFRFVSQGHNYERGPQIWMACENKGYEYIPSGAIR 420
QY 421 INTQBYLDVLRPMPVLADGKAKQVQWNTVYLDALGLVITGTLVPFNITGQFENKTNLK 480
Db 421 INTQBYLDVLRPMPVLADGKAKQVQWNTVYLDALGLVITGTLVPFNITGQFENKTNLK 480
QY 481 NOLILGVNGVDVSLDDIKRLTPRFTLCPNGYVFAIDPNGYVLLHLPNLPKPKSQEPVTL 540
Db 481 NOLILGVNGVDVSLDDIKRLTPRFTLCPNGYVFAIDPNGYVLLHLPNLPKPKSQEPVTL 540

Db 481 NQLILGVMDVDSLEDIKRLTPRFTLCNPGYFAIDPNGYVLLHPLQKPKSQEPVTL 540
Qy 541 DFLDAELNDIKVEIRNKMIDGESKEKTRTLVVKSQDERYIDKGNRTYTWTVPNGTDYSL 600
Db 541 DFLDAELNDIKVEIRNKMIDGESKEKTRTLVVKSQDERYIDKGNRTYTWTVPNGTDYSL 600
Qy 601 ALVLPYSFYIKAKLETTITQARSKKGMKDSFRLRPNDFEESGYTIAPRDYCNDLKI 660
Db 601 ALVLPYSFYIKAKLETTITQARY-----SEFLKPNDFEESGYTIAPRDYCNDLKI 653
Qy 661 SDNTEFLNNEFIDRTPNPNSCADLINRVLLDAGFTNELVONYSKOKNIKGVKAR 720
Db 654 SDNTEFLNNEFIDRTPNPNSCADLINRVLLDAGFTNELVONYSKOKNIKGVKAR 713
Qy 721 FVVDGGITRVYKPKAGNWOENPTYEDSFYKRLDNDNYYFTAPYFNKSGPGAYESGI 780
Db 714 FVVDGGITRVYKPKAGNWOENPTYEDSFYKRLDNDNYYFTAPYFNKSGPGAYESGI 773
Qy 781 MYKRAVEIYIOGKLLKPAVVGKIDVNSWIENTKTSIRDCAGPVCDCRNSDVMDCVI 840
Db 774 MYKRAVEIYIOGKLLKPAVVGKIDVNSWIENTKTSIRDCAGPVCDCRNSDVMDCVI 833
Qy 841 LDGGFLLMANHDDYTNOIGREFGIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGAAPKQ 900
Db 834 LDGGFLLMANHDDYTNOIGREFGIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGAAPKQ 893
Qy 901 GAGHSAYVPSVADILQGWATAAANSILOFLLSLFPRLLEAVEMDDDDFTASLSKQ 960
Db 894 GAGHSAYVPSVADILQGWATAAANSILOFLLSLFPRLLEAVEMDDDDFTASLSKQ 953
Qy 961 SCITBOTQYFFDNDKSGVGLDCGNCRIHFGKELMTNLIIFINVESKGTCCPCTRLLI 1020
Db 954 SCITBOTQYFFDNDKSGVGLDCGNCRIHFGKELMTNLIIFINVESKGTCCPCTRLLI 1013
Qy 1021 QAEQTSQDGNPNDVMKQPRYRKGPVDCFDNNVLEDYDCGGVSGNLNPSLIWYIIGIQFLLL 1080
Db 1014 QAEQTSQDGNPNDVMKQPRYRKGPVDCFDNNVLEDYDCGGVSGNLNPSLIWYIIGIQFLLL 1073
Qy 1081 WLVSQSTHRL 1091
Db 1074 WLVSQSTHRL 1084

RESULT 11

US-08-455-543A-53

; Sequence 53, Application US/08455543A

; Patent No. 5792846

; GENERAL INFORMATION:

; APPLICANT: Harpold, Michael

; APPLICANT: Ellis, Steven

; APPLICANT: Williams, Mark

; APPLICANT: Feldman, Daniel

; APPLICANT: McCue, Ann

; APPLICANT: Brenner, Robert

; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

; METHODS

; NUMBER OF SEQUENCES: 57

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Brown, Martin, Haller & McClain

; STREET: 1660 Union Street

; CITY: San Diego

; STATE: California

; COUNTRY: USA

; ZIP: 92101-2926

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/455,543A

; FILING DATE: May 31, 1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/223,305
; FILING DATE: April 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,250
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-52517
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1103 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-455-543A-53

Query Match

98.7%; Score 5672; DB 1; Length 1103;

Best Local Similarity 97.6%; Pred. No. 0;

Matches 1083; Conservative 0; Mismatches 1; Indels 26; Gaps 2;

Qy 1 MAAGCLLALTTLTFLQSLIGPSSEEPFPPSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60
Db 1 MAAGCLLALTTLTFLQSLIGPSSEEPFPPSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60
Qy 61 YEKYQDLYTVEPNNARQLVEITAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120
Db 61 YEKYQDLYTVEPNNARQLVEITAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120
Qy 121 EVVYNKADDDLDPEKNDSEPGSORIKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180
Db 121 EVVYNKADDDLDPEKNDSEPGSORIKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180
Qy 181 NELNWTSLDVEYFKKNREEDPSLLMQVFGSATGLARYYPASVPWVDSNRTPNKIDLYVRR 240
Db 181 NELNWTSLDVEYFKKNREEDPSLLMQVFGSATGLARYYPASVPWVDSNRTPNKIDLYVRR 240
Qy 241 RPWYIQTGAASPKDMLILVDVSGSVSGLTLKLTIRTSVSEMLETLSDDDFNVNVSFNSNAQD 300
Db 241 RPWYIQTGAASPKDMLILVDVSGSVSGLTLKLTIRTSVSEMLETLSDDDFNVNVSFNSNAQD 300
Qy 301 VSCFOHLVQANVRNKKVLKDAVNNTAKITDYKKGFSAFEQLLNYSRANCNKIIML 360
Db 301 VSCFOHLVQANVRNKKVLKDAVNNTAKITDYKKGFSAFEQLLNYSRANCNKIIML 360
Qy 361 FTDGGEERAQEIFNKYNDKKVVRVFRFVSGQHNVERGPIQWACENKGYVEIPSGAIR 420
Db 361 FTDGGEERAQEIFNKYNDKKVVRVFRFVSGQHNVERGPIQWACENKGYVEIPSGAIR 420

QY 421 INTQEXLDVLGRPMVLGADKAKOVQWNTNVYLDALGLVITGTLPVFNITGQFNKTNLK 480
Db 421 INTQEXLDVLGRPMVLGADKAKOVQWNTNVYLDALGLVITGTLPVFNITGQFNKTNLK 480
QY 481 NQLILGVMGVDSLEDIKRLTPFTLCPNGYYPFAIDPBGVLLHPNLPK-----530
Db 481 NQLILGVMGVDSLEDIKRLTPFTLCPNGYYPFAIDPBGVLLHPNLPKPIGVGPIPTIN 540
QY 531 -----NPKSQEPVTLDFDAELNDIKVEIRNMIDGESGKTFRLVKSQDERYI 581
Db 541 LKRRPNIQPKSQEPVTLDFDAELNDIKVEIRNMIDGESGKTFRLVKSQDERYI 600
QY 582 DKGRTYTTVPNGTDSLALVPTYSFYIKAKLEETITQARSKGKMKDSTLAPDNF 641
Db 601 DKGRTYTTVPNGTDSLALVPTYSFYIKAKLEETITQARSKGKMKDSTLAPDNF 653
QY 642 EESGYTFIAPRDCNDLKISDNTFELLNFEIDRKTNNPNSCNADLINRVLLDAGFTN 701
Db 654 EESGYTFIAPRDCNDLKISDNTFELLNFEIDRKTNNPNSCNADLINRVLLDAGFTN 713
QY 702 ELVQVWSKOKNIKGVKARFVTTDGGITRVYPKEAGENMQENPETYEDSFYKRSLDNDNY 761
Db 714 ELVQVWSKOKNIKGVKARFVTTDGGITRVYPKEAGENMQENPETYEDSFYKRSLDNDNY 773
QY 762 VFTAPYFNKSGPAGYSGINMVSXAVIYIYQKLLKPAVVGKIDVNSWIENFTKTSIRD 821
Db 774 VFTAPYFNKSGPAGYSGINMVSXAVIYIYQKLLKPAVVGKIDVNSWIENFTKTSIRD 833
QY 822 CAGPVCCKRNSDVCVILDDGGFLLMANHDDYTNOIGRFGCEIDPSLMRHLVNI SVYA 881
Db 834 CAGPVCCKRNSDVCVILDDGGFLLMANHDDYTNOIGRFGCEIDPSLMRHLVNI SVYA 893
QY 882 FNKSYDQVCEPAGAPKOGAGHRSAYVPSVADILQIGWATAAASIIQQFLLSITFPR 941
Db 894 FNKSYDQVCEPAGAPKOGAGHRSAYVPSVADILQIGWATAAASIIQQFLLSITFPR 953
QY 942 LLEAVEMEDDDFTASLSKSCITEQYQYFFDNDKSGFSGLDCGNSRIFHGKLMNTNL 1001
Db 954 LLEAVEMEDDDFTASLSKSCITEQYQYFFDNDKSGFSGLDCGNSRIFHGKLMNTNL 1013
QY 1002 IFTWESKGPCDCTRLLIQAQETSGPNPCDMVKOPRYRKGDPVCFDNNVLEDYDCGG 1061
Db 1014 IFTWESKGPCDCTRLLIQAQETSGPNPCDMVKOPRYRKGDPVCFDNNVLEDYDCGG 1073
QY 1062 VSGINPFLMWYIIQIFLLMLVSGSTHRL 1091
Db 1074 VSGINPFLMWYIIQIFLLMLVSGSTHRL 1103

RESULT 12

US-08-223-305C-53

Sequence 53, Application US/08223305C

Patent No. 5851824

GENERAL INFORMATION:

APPLICANT: Harpold, Michael

APPLICANT: Ellis, Steven

APPLICANT: Williams, Mark

APPLICANT: Feldman, Daniel

APPLICANT: McCue, Ann

APPLICANT: Brenner, Robert

TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

METHODS

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Martin, Haller & McClain

STREET: 1660 Union Street

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/223,305C
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
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PRIOR APPLICATION DATA:
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FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 52516 (P519739)
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1103 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-223-305C-53

Query Match

88.7%; Score 5672; DB 2; Length 1103;

Best Local Similarity 97.6%; Pred. No. 0;

Matches 1083; Conservative 0; Mismatcheq 1; Indels 26; Gaps 2;

QY 1 MAAGCLLALTILFQSLIGPSSEEPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
Db 1 MAAGCLLALTILFQSLIGPSSEEPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
QY 61 YEKYQDLYTVEPNNAARQLVEIAARDIEKLLSNRSKALVSLALEAEKVAQAAHWRDFASN 120
Db 61 YEKYQDLYTVEPNNAARQLVEIAARDIEKLLSNRSKALVSLALEAEKVAQAAHWRDFASN 120
QY 121 EVVYVNAKDDLDPEKNDSEPGSORIKPVEIDANFCRQISYQHAHVHIPTDIYEGSTIVL 180
Db 121 EVVYVNAKDDLDPEKNDSEPGSORIKPVEIDANFCRQISYQHAHVHIPTDIYEGSTIVL 180
QY 181 NELNMTSALDEVFKKNREEDPSLLMQVFGSGLTGLARYYPASPVWDSRTPNKIDLDYDVR 240
Db 181 NELNMTSALDEVFKKNREEDPSLLMQVFGSGLTGLARYYPASPVWDSRTPNKIDLDYDVR 240
QY 241 RPWYTOGAASPKDMLILVDVSGSVSGTLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300
Db 241 RPWYTOGAASPKDMLILVDVSGSVSGTLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300
QY 301 VSCFQHLVQANVRNKKVLKADVNNITAKGIDYKKGFSFAFQOLLNYSRANCNKIIML 360
Db 301 VSCFQHLVQANVRNKKVLKADVNNITAKGIDYKKGFSFAFQOLLNYSRANCNKIIML 360
QY 361 FTDGGEERAQEIFNKYNKDKKVRFRFVSQGHNYERGPQWMACENKNGYIYIPISGAIR 420

Db 361 FDGGEARAEINYNKDKKVRFRFVGQHNVERGPIQMACENKGYEIPISIGAIR 420
Qy 421 INTQYLDVLRPMVLGADKAKQVQWNTVNYLDALDELGLVITGTLVPFNITGQFENKTNL 480
Db 421 INTQYLDVLRPMVLGADKAKQVQWNTVNYLDALDELGLVITGTLVPFNITGQFENKTNL 480
Qy 481 NOLILGVMGVDSLEIDIKRLTPRFTLCPNGYFAIDPNGYVLLHHPNLPK----- 530
Db 481 NOLILGVMGVDSLEIDIKRLTPRFTLCPNGYFAIDPNGYVLLHHPNLPKPGIGVGIPTIN 540
Qy 531 -----NPKSQBPVTLDFDAELENDIKVEIRNKMGIDEGSEKTRTLVKSQDERYI 581
Db 541 LRKRPNTQPKSQBPVTLDFDAELENDIKVEIRNKMGIDEGSEKTRTLVKSQDERYI 600
Qy 582 DKGRTYTWTPVNGTDYSLALVLPYSYIYAKALEETITQARSKKGMKDSKSETLKPDPNF 641
Db 601 DKGRTYTWTPVNGTDYSLALVLPYSYIYAKALEETITQARY-----SETLKPDPNF 653
Qy 642 EESGYTFIAPRDYCNLDKISDNTEFLNFNEFIDRKTPNPNPSCNADLINRVLLDAGFTN 701
Db 654 EESGYTFIAPRDYCNLDKISDNTEFLNFNEFIDRKTPNPNPSCNADLINRVLLDAGFTN 713
Qy 702 ELVQYNSKQKNIKGVKARFVTTGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNY 761
Db 714 ELVQYNSKQKNIKGVKARFVTTGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNY 773
Qy 762 VFTAPYFNKSGPGAYESIMYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTKTSIRDP 821
Db 774 VFTAPYFNKSGPGAYESIMYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTKTSIRDP 833
Qy 822 CAGPVCCKRNSDMVDCVILDDGGFLLMANHDDYTNQIGRFFGETIDPSLMRHLNYSIYA 881
Db 834 CAGPVCCKRNSDMVDCVILDDGGFLLMANHDDYTNQIGRFFGETIDPSLMRHLNYSIYA 893
Qy 882 FNKSYDQSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAASWTLQOFLSLTPPR 941
Db 894 FNKSYDQSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAASWTLQOFLSLTPPR 953
Qy 942 LLEAVEMEDDFTASLSKQSCITQTOYFFDNDKSFSGVLDGNCGRIFHGEKLMNTNL 1001
Db 954 LLEAVEMEDDFTASLSKQSCITQTOYFFDNDKSFSGVLDGNCGRIFHGEKLMNTNL 1013
Qy 1002 IFIMVESKGTCPDTRLLIQAEQTSQGNPCDMYKQRYKGPDPVCFNNVLEDYTDGCG 1061
Db 1014 IFIMVESKGTCPDTRLLIQAEQTSQGNPCDMYKQRYKGPDPVCFNNVLEDYTDGCG 1073
Qy 1062 VSGLNPSLWYIIGIOFLLMLVSGSTHRL 1091
Db 1074 VSGLNPSLWYIIGIOFLLMLVSGSTHRL 1103

RESULT 13

US-08-455-543A-55
; Sequence 55, Application US/0845543A
; Patent No. 5792846
; GENERAL INFORMATION:

; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,543A
; FILING DATE: May 31, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/223,305
; FILING DATE: April 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,250
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
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; PRIOR APPLICATION DATA:
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-52517
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1079 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-455-543A-55

Query Match 98.3%; Score 5652; DB 1; Length 1079;

Best Local Similarity 98.8%; Pred. No. 0;

Matches 1078; Conservative 0; Mismatches 1; Indels 12; Gaps 2;

Qy 1 MAAGCLLATLTTLFQSLIGPSSEPPFSAVTIKSWDKMQEDLVTLAKTAGVGNOLVDI 60
Db 1 MAAGCLLATLTTLFQSLIGPSSEPPFSAVTIKSWDKMQEDLVTLAKTAGVGNOLVDI 60
Qy 61 YEKYODLYTVEPNNAQLVEITAARDIEKLLSNRSKALVSLALEAEKQAAHQRDEFASN 120
Db 61 YEKYODLYTVEPNNAQLVEITAARDIEKLLSNRSKALVSLALEAEKQAAHQRDEFASN 120
Qy 121 EVVYINAKDLDPEKNDSEPGSQRIKPVFIEDANFGROIYSQHAHVHTPIIYEGSTIVL 180
Db 121 EVVYINAKDLDPEKNDSEPGSQRIKPVFIEDANFGROIYSQHAHVHTPIIYEGSTIVL 180
Qy 181 NELNWTALDEVFKNREEDPSLLWVFGSATGLARYYPASFPWVDNSRTPNKIDLYDVR 240
Db 181 NELNWTALDEVFKNREEDPSLLWVFGSATGLARYYPASFPWVDNSRTPNKIDLYDVR 240
Qy 241 RPWYIOGAASPKDMLILVDVSGVSGLTCLKIRTSVSEMLETLSDDDDFVNVASFNSNAQ 300
Db 241 RPWYIOGAASPKDMLILVDVSGVSGLTCLKIRTSVSEMLETLSDDDDFVNVASFNSNAQ 300

301 VSCFQHLVQANVRNKKVLKDAVNNTAKGTDYKKGFSFAFEOALLNYSRANCKIIML 360
Db 301 VSCFQHLVQANVRNKKVLKDAVNNTAKGTDYKKGFSFAFEOALLNYSRANCKIIML 360
361 FTGGERAQEIPKNYKDKKVVFRFSVQGHNYERGIOMMACENKGYEIPSGAIR 420
Db 361 FTGGERAQEIPKNYKDKKVVFRFSVQGHNYERGIOMMACENKGYEIPSGAIR 420
421 INTQEVLDVLRPMVLGAKAKOVQNTVYLDALGLVITGTLPVFNITGOFENKTNLK 480
Db 421 INTQEVLDVLRPMVLGAKAKOVQNTVYLDALGLVITGTLPVFNITGOFENKTNLK 480
481 NQILGVMGVDSLEDIKRLTPFTLCPNGYFAIDPNGYVLLHLPNLPKQKSOBPVTL 540
Db 481 NQILGVMGVDSLEDIKRLTPFTLCPNGYFAIDPNGYVLLHLPNLPKQKSOBPVTL 540
541 DFLDAELNDIKVEIRNKMIDGESGKTRTLVKSDERYIDKGNRTYTWTPVNGTDYSL 600
Db 541 DFLDAELNDIKVEIRNKMIDGESGKTRTLVKSDERYIDKGNRTYTWTPVNGTDYSL 600
596 DFLDAELNDIKVEIRNKMIDGESGKTRTLVKSDERYIDKGNRTYTWTPVNGTDYSL 595
Db 596 DFLDAELNDIKVEIRNKMIDGESGKTRTLVKSDERYIDKGNRTYTWTPVNGTDYSL 595
601 ALVLPYSFYIKAKLEETITQARSKKMKDSETLKPDNFEESGYTFAPRDYCNLKI 660
Db 601 ALVLPYSFYIKAKLEETITQARSKKMKDSETLKPDNFEESGYTFAPRDYCNLKI 660
596 ALVLPYSFYIKAKLEETITQARY-----SETLKPDNFEESGYTFAPRDYCNLKI 648
Db 596 ALVLPYSFYIKAKLEETITQARY-----SETLKPDNFEESGYTFAPRDYCNLKI 648
661 SONTEFLNNEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQYNSKQKNIKGVKAR 720
Db 661 SONTEFLNNEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQYNSKQKNIKGVKAR 720
649 SONTEFLNNEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQYNSKQKNIKGVKAR 708
Db 649 SONTEFLNNEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQYNSKQKNIKGVKAR 708
721 FVTDGGITRVYPKEAGENWQENPEYEDSFYKRSLDNDNYFTAPYFNKSGPGAYESGI 780
Db 721 FVTDGGITRVYPKEAGENWQENPEYEDSFYKRSLDNDNYFTAPYFNKSGPGAYESGI 780
709 FVTDGGITRVYPKEAGENWQENPEYEDSFYKRSLDNDNYFTAPYFNKSGPGAYESGI 768
Db 709 FVTDGGITRVYPKEAGENWQENPEYEDSFYKRSLDNDNYFTAPYFNKSGPGAYESGI 768
781 MYSKAVEIYIOGKLKPAVVGKIDVNSWNIENFTKTSIRDPGAPVCDCKRNSDVMDCVI 840
Db 781 MYSKAVEIYIOGKLKPAVVGKIDVNSWNIENFTKTSIRDPGAPVCDCKRNSDVMDCVI 840
769 MYSKAVEIYIOGKLKPAVVGKIDVNSWNIENFTKTSIRDPGAPVCDCKRNSDVMDCVI 828
Db 769 MYSKAVEIYIOGKLKPAVVGKIDVNSWNIENFTKTSIRDPGAPVCDCKRNSDVMDCVI 828
841 LDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI SYAFNKSVDYOSVCEPGAAPQ 900
Db 841 LDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI SYAFNKSVDYOSVCEPGAAPQ 900
829 LDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI SYAFNKSVDYOSVCEPGAAPQ 888
Db 829 LDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI SYAFNKSVDYOSVCEPGAAPQ 888
901 GAGHRSAYVPSVADILQIGWATAAWSLIQOFLSLTLPRLLEAVEMEDDDFTASLSQ 960
Db 901 GAGHRSAYVPSVADILQIGWATAAWSLIQOFLSLTLPRLLEAVEMEDDDFTASLSQ 960
889 GAGHRSAYVPSVADILQIGWATAAWSLIQOFLSLTLPRLLEAVEMEDDDFTASLSQ 948
Db 889 GAGHRSAYVPSVADILQIGWATAAWSLIQOFLSLTLPRLLEAVEMEDDDFTASLSQ 948
961 SCITEQTYFFNDKSFSGVLDGNCGRIFHGEKLMNTNLIFIMVESKGTCTCDTRLII 1020
Db 961 SCITEQTYFFNDKSFSGVLDGNCGRIFHGEKLMNTNLIFIMVESKGTCTCDTRLII 1020
949 SCITEQTYFFNDKSFSGVLDGNCGRIFHGEKLMNTNLIFIMVESKGTCTCDTRLII 1008
Db 949 SCITEQTYFFNDKSFSGVLDGNCGRIFHGEKLMNTNLIFIMVESKGTCTCDTRLII 1008
1021 QAEQTSQSDGNPCDMVKQPRYRKGPVDFDNNVLEDYDCGGVSGLNPLSLWYIIGIQFLLL 1080
Db 1021 QAEQTSQSDGNPCDMVKQPRYRKGPVDFDNNVLEDYDCGGVSGLNPLSLWYIIGIQFLLL 1080
1009 QAEQTSQSDGNPCDMVKQPRYRKGPVDFDNNVLEDYDCGGVSGLNPLSLWYIIGIQFLLL 1068
Db 1009 QAEQTSQSDGNPCDMVKQPRYRKGPVDFDNNVLEDYDCGGVSGLNPLSLWYIIGIQFLLL 1068
1081 WLVSQSTHRL 1091
Db 1081 WLVSQSTHRL 1091
1069 WLVSQSTHRL 1079
Db 1069 WLVSQSTHRL 1079

RESULT 14

US-08-223-305C-55
; Sequence 55, Application US/08223305C
; Patent No. 5851824
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; NUMBER OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:

ADDRESSER: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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SOFTWARE: FastSeq Version 1.5
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REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 52516 (P519739)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 1079 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-223-305C-55

Query Match 98.3%; Score 5652; DB 2; Length 1079;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1078; Conservative 0; Mismatches 1; Indels 12; Gaps 2;

Qy 1 MAAGCLLALTTLFOSLLIGPSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNOLVDI 60
Db 1 MAAGCLLALTTLFOSLLIGPSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNOLVDI 60
Qy 61 YEKYQDLYTVEPNNAQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120
Db 61 YEKYQDLYTVEPNNAQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120
Qy 121 EVVYVNAKDDLPKNDSEPGSORIKPVFIEDANFGRQISYQHAHVHIPTDIYEGSTIVL 180
Db 121 EVVYVNAKDDLPKNDSEPGSORIKPVFIEDANFGRQISYQHAHVHIPTDIYEGSTIVL 180
Qy 181 NELNWTSLDVEYFKKNREDDPSLLMQVFGSATGLARYYPASPWNRSRTPNKIDLYDVR 240
Db 181 NELNWTSLDVEYFKKNREDDPSLLMQVFGSATGLARYYPASPWNRSRTPNKIDLYDVR 240

QY 241 RPYIOGAASPKDMLLVDSVSGSLTLKLRISVSEMLETLSDDDFVNVSFNSNAQD 300
Db 241 RPYIOGAASPKDMLLVDSVSGSLTLKLRISVSEMLETLSDDDFVNVSFNSNAQD 300
QY 301 VSCFQHLVQANVRNKKVLDKDAVNNITAKGIDYKGFSAFQQLLNNVSRANCNKIIML 360
Db 301 VSCFQHLVQANVRNKKVLDKDAVNNITAKGIDYKGFSAFQQLLNNVSRANCNKIIML 360
QY 361 FTDGGEERAQEIFNKNKDKKVRVRFSGQHNVERGPIQWACENKGYIIPISGAIR 420
Db 361 FTDGGEERAQEIFNKNKDKKVRVRFSGQHNVERGPIQWACENKGYIIPISGAIR 420
QY 421 INTQEVLDVLRPMVLGDKAKQVQNTNVLDAELGLVITGLPVFNITGOFENKTNLK 480
Db 421 INTQEVLDVLRPMVLGDKAKQVQNTNVLDAELGLVITGLPVFNITGOFENKTNLK 480
QY 481 NQILIGVMGVDSLEIDIKRLTPFRFLCPNGYFAIDPNGYVLLHPLNLPKPKSOEPTVL 540
Db 481 NQILIGVMGVDSLEIDIKRLTPFRFLCPNGYFAIDPNGYVLLHPLNLPKPKSOEPTVL 540
QY 541 DFLDAELENDIKVEIRNKMIDGSEKFTRTLUVKSODERYIDKGNRTYTWTPVNGTDYSL 600
Db 541 DFLDAELENDIKVEIRNKMIDGSEKFTRTLUVKSODERYIDKGNRTYTWTPVNGTDYSL 600
QY 601 ALVLPITYFYIYKALEETITQARSKKGKMDSETLKPDPFESGYTTPADRYCNDLKI 660
Db 601 ALVLPITYFYIYKALEETITQARSKKGKMDSETLKPDPFESGYTTPADRYCNDLKI 660
QY 661 SDNNTFELLNFEFIDRTPNPNPCNADLINRVLLDAGFTNELVQYNSKQKNIKGVKAR 720
Db 661 SDNNTFELLNFEFIDRTPNPNPCNADLINRVLLDAGFTNELVQYNSKQKNIKGVKAR 720
QY 721 FVVDGGITRVYKPEAGENWQENPETYEDSFYKRSNDNDNYVFTAPYFNKSGPGAYESGI 780
Db 721 FVVDGGITRVYKPEAGENWQENPETYEDSFYKRSNDNDNYVFTAPYFNKSGPGAYESGI 780
QY 781 MYSKAVEIYIQGLKLPVAVGKIDVNSWENFTKTSIRDPGAGVPCCKRNSDYMDCVI 840
Db 781 MYSKAVEIYIQGLKLPVAVGKIDVNSWENFTKTSIRDPGAGVPCCKRNSDYMDCVI 840
QY 841 LDGCGFLLMANHDDYTNQIGRFEGIDPSLRHLNYSVIAFNKSYDYOSVCEPGAAPKQ 900
Db 841 LDGCGFLLMANHDDYTNQIGRFEGIDPSLRHLNYSVIAFNKSYDYOSVCEPGAAPKQ 900
QY 901 GAGHSAYVPSVADILQIGWATAAWSILOQLSLTFPRLLLEAVEMEDDDFTASLSKQ 960
Db 901 GAGHSAYVPSVADILQIGWATAAWSILOQLSLTFPRLLLEAVEMEDDDFTASLSKQ 960
QY 961 SCITQOTQYFFDNDKSFSGVLDGNCGRIFRFGKLMNTNLFIMVESKGTGCPDTRLLI 1020
Db 961 SCITQOTQYFFDNDKSFSGVLDGNCGRIFRFGKLMNTNLFIMVESKGTGCPDTRLLI 1020
QY 1021 QAEQTSQDGNPCDMVKQRYRKGPDVCFDNNVLEDYTDGCGVSGLNPSLWYIIGIQFLL 1080
Db 1021 QAEQTSQDGNPCDMVKQRYRKGPDVCFDNNVLEDYTDGCGVSGLNPSLWYIIGIQFLL 1080
QY 1081 WLVSQSTHLL 1091
Db 1081 WLVSQSTHLL 1091
QY 1091 WLVSQSTHLL 1091
Db 1091 WLVSQSTHLL 1091

RESULT 15

US-08-435-675B-5
; Sequence 5, Application US/08435675B
; Patent No. 5710250
; GENERAL INFORMATION:
; APPLICANT: Ellis, Steven Bradley
; APPLICANT: Williams, Mark E.
; APPLICANT: Harpold, Michael Miller
; APPLICANT: Schwartz, Arnold
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,675B
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,083
; FILING DATE: 28-SEP-1994
; APPLICATION NUMBER: US 07/914,231
; FILING DATE: 13-JUL-1992
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 08-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-53193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1106 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-435-675B-5

Query Match 95.8%; Score 5508.5; DB 1; Length 1106;
Best Local Similarity 94.7%; Pred. No. 0;
Matches 1054; Conservative 15; Mismatches 15; Indels 29; Gaps 4;

QY 1 MAAGCLLALTTLFOS--LLIGPSSEEPFPPSAVTITKSWDKMQEDLVTLAKTASGVNQLV 58
Db 1 MAAGPLAWTLTQAWLILIGPSSEEPFPPSAVTITKSWDKMQEDLVTLAKTASGVNQLV 60
QY 59 DIYKYQDLYTVEPNNAQQLVEIAARDIEKLSNRSKALVSLALEAEKVQAHAHWRDFA 118
Db 61 DIYKYQDLYTVEPNNAQQLVEIAARDIEKLSNRSKALVRLALEAEKVQAHAHWRDFA 120
QY 119 SNEVYVYNAKDDLDPEKNDSEPGSORIKPVFTEDANFRQSYQHAHVHPTDIYEGSTI 178
Db 121 SNEVYVYNAKDDLDPEKNDSEPGSORIKPVFTEDANFRQSYQHAHVHPTDIYEGSTI 180
QY 179 VLNELNWTSLADVEPKKNREEDPSLLWQVFGSATGLARYYPASPVNDNSRTNPKIDLVDV 238
Db 181 VLNELNWTSLADVEPKKNREEDPSLLWQVFGSATGLARYYPASPVNDNSRTNPKIDLVDV 240
QY 239 RRRPWYIOGAASPKDMLILVDVSGSVGLTLKLRISVSEMLETLSDDDFVNVSFNSNA 298
Db 241 RRRPWYIOGAASPKDMLILVDVSGSVGLTLKLRISVSEMLETLSDDDFVNVSFNSNA 300
QY 299 QDVSCFQHLVQANVRNKKVLDKDAVNNITAKGIDYKGFSAFQQLLNNVSRANCNKII 358
Db 301 QDVSCFQHLVQANVRNKKVLDKDAVNNITAKGIDYKGFSAFQQLLNNVSRANCNKII 360
QY 359 MLFTDGGGEERAQEIFNKNKDKKVRVRFSGQHNVERGPIQWACENKGYIIPISGA 418
Db 361 MLFTDGGGEERAQEIFNKNKDKKVRVRFSGQHNVERGPIQWACENKGYIIPISGA 420

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QY 419 IRIHQEYLDVLRPMVLGDKAKOVQNTNYYLDALBELGLVITGTLPVFNITGOFENKTN 478
Db 421 IRIHQEYLDVLRPMVLGDKAKOVQNTNYYLDALBELGLVITGTLPVFNITGOFENKTN 480
QY 479 LKNQILGVMGVDVSDLEDIKRLTFRFTLCPNGYYFAIDPNGYVLLHNPLOPK----- 530
Db 481 LKNQILGVMGVDVSDLEDIKRLTFRFTLCPNGYYFAIDPNGYVLLHNPLOPKPIGVGIPT 540
QY 531 -----NPKSQEPVTLDFDAELENDIKVEIRNKMIDGESGEKTFRTLVKSQDER 579
Db 541 INLRKRRPNVQNPQSQEPVTLDFDAELENDIKVEIRNKMIDGESGEKTFRTLVKSQDER 600
QY 580 YIDKGNRTYTWTPVNGDY-SLAVLPTYSPYIKAKLEETITQARSKKMKMDSETLKP 638
Db 601 YIDKGNRTYTWTPVNGDYSSLAVLPTYSPYIKAKIEETITQARY-----SETLKP 653
QY 639 DNFEESGYTFIAPRDYCNLDKISDNTEFFLNFEFIDRKTPNPNPCNADLINRVLLDAG 698
Db 654 DNFEESGYTFIAPRDYCNLDKPSDNTEFFLNFEFIDRKTPNPNPCNADLINRVLLDAG 713
QY 699 FTNELVQNYNSKQNIKGVKARFVTTGGITRVYPKEAGENWQENPETYEDSFYKRSLDN 758
Db 714 FTNELVQNYNSKQNIKGVKARFVTTGGITRVYPKEAGENWQENPETYEDSFYKRSLDN 773
QY 759 DNYVFTAPYFNKSGPGAYESGIMYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSI 818
Db 774 DNYVFTAPYFNKSGPGAYESGIMYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSI 833
QY 819 RDPGAGPVCDCCKRNSDVMDCVILDDGGFLLMANHDDYTNOIGRFFGEIDPMSLMRHLVNI 878
Db 834 RDPGAGPVCDCCKRNSDVMDCVILDDGGFLLMANHDDYTNOIGRFFGEIDPMSLMRHLVNI 893
QY 879 YAFNKSVDYOSVCEPGAAPKQAGAGHRSAYVPSVADILQIGWATAAAWSTLQOFLLSLT 938
Db 894 YAFNKSVDYOSVCEPGAAPKQAGAGHRSAYVPSIADILQIGWATAAAWSTLQOFLLSLT 953
QY 939 FPRLEAVEMEDDDFTASLSKSCITOTQYFFONDSPKSFSGVLDGCGNCSRIHFGEKLMN 998
Db 954 FPRLEAVEMEDDDFTASLSKSCITOTQYFFONDSPKSFSGVLDGCGNCSRIHFGEKLMN 1013
QY 999 TNLIFIMVESKGTCPDTRLLIQAQETSDGPNPCDMVKQPRYKGPDPVCFDNNVLEDTYD 1058
Db 1014 TNLIFIMVESKGTCPDTRLLIQAQETSDGPNPCDMVKQPRYKGPDPVCFDNNVLEDTYD 1073
QY 1059 CGGVSGLNPLSLWYIIGIQLLWLVSGSTRLL 1091
Db 1074 CGGVSGLNPLSLWYIIGIQLLWLVSGSTRHCLL 1106

```

Search completed: July 23, 2001, 07:38:26
Job time: 493 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 23, 2001, 07:29:43 ; Search time 84.28 Seconds
(without alignments)
986.075 Million cell updates/sec

Title: US-09-397-548-14
Perfect score: 5748
Sequence: 1 MAAGCLLATLTFLQSLIG.....IIGIQFLLWLWVGSTHRL 1091

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5748	100.0	1091	2 JH0565	calcium channel al
2	5505	95.8	1091	2 A4147	calcium channel pr
3	5503.5	95.7	1106	1 CHRBA2	calcium channel al
4	1127.5	19.6	1091	2 T30256	calcium channel al
5	607	10.6	734	2 S44617	C50C3.11 protein -
6	580.5	10.1	1148	2 T18770	probable calcium c
7	198	3.4	1450	2 C86880	hypothetical prote
8	194.5	3.4	886	2 S54355	inter-alpha-trypsi
9	185	3.2	885	2 S30350	inter-alpha-trypsi
10	164.5	2.9	889	2 JC5576	inter-alpha-trypsi
11	161	2.8	2706	2 T28155	variant-specific s
12	159	2.8	1984	2 A44396	p-type cation tran
13	157.5	2.7	575	2 D64998	hypothetical prote
14	155	2.7	1516	2 E71619	RAD2 endonuclease
15	155	2.7	2364	2 I40884	cytotoxin L - Clos
16	154.5	2.7	946	1 IYH02	inter-alpha-trypsi
17	154.5	2.7	1315	2 T28679	fibrinogen-binding
18	153	2.7	932	2 JC5953	inter-alpha-inhibi
19	152	2.6	1291	2 S46431	botulinum neurotox
20	152	2.6	1291	2 A49777	botulinum neurotox
21	151.5	2.6	420	2 S76691	hypothetical prote
22	150.5	2.6	921	2 JC4625	inter-alpha-trypsi
23	150	2.6	654	2 A69656	methyl-accepting c
24	149	2.6	459	2 F64688	proteinase (EC 3.4
25	149	2.6	930	2 JX0368	inter-alpha-trypsi
26	148.5	2.6	2401	2 T28676	rhodopy protein -
27	148	2.6	964	2 S25855	DNA-directed DNA p
28	146.5	2.5	1285	2 B72420	hypothetical prote
29	146	2.5	4688	2 F82885	hypothetical prote

30	145.5	2.5	576	2 T47637	hypothetical prote
31	145.5	2.5	589	2 F84811	probable retroelem
32	145.5	2.5	5005	2 F82884	hypothetical prote
33	144	2.5	1087	1 S41797	cellulose 1,4-beta
34	144	2.5	1091	2 J33850	fibronectin-binding
35	143	2.5	946	2 JC5575	inter-alpha-trypsi
36	143	2.5	1864	2 T18485	hypothetical prote
37	142.5	2.5	382	2 S44618	C50C3.10 protein -
38	142	2.5	1169	2 A64505	PII5 homolog - Met
39	142	2.5	1599	2 S22737	glucosyltransferas
40	141	2.5	1252	2 B42771	reticulocyte-bind
41	140.5	2.4	2269	2 T28677	rhodopy protein -
42	140	2.4	1180	2 A28858	parapsoral crystal
43	140	2.4	2710	2 A37052	toxin A - Clostrid
44	140	2.4	3305	2 T18358	apolipoprotein prec
45	139.5	2.4	764	2 I39934	protective antigen

ALIGNMENTS

RESULT 1
JH0565
calcium channel alpha-2b chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug-1999
C:Accession: JH0565
R:Williams, M.E.; Feldman, D.H.; McCue, A.F.; Brenner, R.; Velicelebi, G.; Ellis, S.B
Neuron 8, 71-84, 1992
A:Title: Structure and functional expression of alpha1, alpha2, and beta subunits of
A:Reference number: JH0564; MUID:92110010
A:Accession: JH0565
A:Molecule type: mRNA
A:Residues: 1-1091 <WIL>
A:Cross-references: GB:M6559; NID:gl79761; PIDN:AAA51903.1; PID:gl79762
A:Experimental source: basal ganglia
A:Note: Several conflicts are found between GenBank submission, authors' translation
C:Comment: This protein is a subunit of the voltage dependent calcium channel.
C:Superfamily: calcium channel alpha-2 chain
C:Keywords: glycoprotein; phosphoprotein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-1067/Product: calcium channel alpha-2b chain #status predicted <CAL>
F:32,268,326,539,635,1087/Binding site: phosphate (Thr) (covalent) (by protein kinase
F:91,142,250,625,817/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #
F:92,136,184,324,348,468,475,585,594,663,682,769,812,876,883,973,986/Binding site: ca
F:501/Binding site: phosphate (Thr) (covalent) #status predicted
F:833/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status pre

Query Match	100.0%	Score 5748;	DB 2;	Length 1091;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1091;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	1	MAAGCLLATLTFLQSLIGPSEEPFPPSAVTIKSWDKMQEDLVTLAKTAGVQNLVDI	60	
QY	61	YKQYDLYTVEPNNAQOLVEIAARDTEKLLSNRSKALVSLAEKVAQAQHWREDFASN	120	
Db	61	YKQYDLYTVEPNNAQOLVEIAARDTEKLLSNRSKALVSLAEKVAQAQHWREDFASN	120	
QY	121	EVVYNAKDDLPKNDSEPGSQRIKPVFIEDANFGRIQISYQAAHVHIPTDIYEGSTIVL	180	
Db	121	EVVYNAKDDLPKNDSEPGSQRIKPVFIEDANFGRIQISYQAAHVHIPTDIYEGSTIVL	180	
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Db	181	NEUNWTSALDEVPKKNREEDPSLLQVFGSATGLARYYPASPWWDSRTNPKIDLYDVR	240	
QY	241	RPVYIOGAASPKDMLIIVDVGSGVGLTLKIRTSVSEMLETLSDDDFVNVSFNSNAQD	300	
Db	241	RPVYIOGAASPKDMLIIVDVGSGVGLTLKIRTSVSEMLETLSDDDFVNVSFNSNAQD	300	

QY 301 VSCFOHLVQANVRNKKVLKDAVNNTAKGIDYKKGFSFAFEOLLNLYNVRANCNKIIML 360
DB 301 VSCFOHLVQANVRNKKVLKDAVNNTAKGIDYKKGFSFAFEOLLNLYNVRANCNKIIML 360
QY 361 FTDGGEERAQEIFNKYNKDKKVRVFRFSGVGHNYERGPQIOWMACENKGYEYIPEISGAIR 420
DB 361 FTDGGEERAQEIFNKYNKDKKVRVFRFSGVGHNYERGPQIOWMACENKGYEYIPEISGAIR 420
QY 421 INTQEYLDVLRGPRVLAGDKAKQVQWNTNYLDALBELGLVITGTLVPFNITGOFENKTNLK 480
DB 421 INTQEYLDVLRGPRVLAGDKAKQVQWNTNYLDALBELGLVITGTLVPFNITGOFENKTNLK 480
QY 481 NOLLILGVMDVDSLEIDIKRLTPRFTLCPNGYFAIDPNGYVLLHHPNLOPKNPKSOEPTVL 540
DB 481 NOLLILGVMDVDSLEIDIKRLTPRFTLCPNGYFAIDPNGYVLLHHPNLOPKNPKSOEPTVL 540
QY 541 DFLDAELENDIKVEIRNKMIDGESGKFTLTVKSDERYIDKGNRTYTWTPVNGTDYSL 600
DB 541 DFLDAELENDIKVEIRNKMIDGESGKFTLTVKSDERYIDKGNRTYTWTPVNGTDYSL 600
QY 601 ALVLPITYFYIYKAKLEETITQARSKGKMKDSETLKPDNFEESGYTFTAPRDXCNDLKI 660
DB 601 ALVLPITYFYIYKAKLEETITQARSKGKMKDSETLKPDNFEESGYTFTAPRDXCNDLKI 660
QY 661 SDNNTFELNFEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVQYNSKQNIKGVRAR 720
DB 661 SDNNTFELNFEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVQYNSKQNIKGVRAR 720
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QY 781 MYSKAVEIYIQGLKLPVAVGKIDVNSHIEFTKTSIRDPCAGPVCDCRNSDVMDCVI 840
DB 781 MYSKAVEIYIQGLKLPVAVGKIDVNSHIEFTKTSIRDPCAGPVCDCRNSDVMDCVI 840
QY 841 LDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLNYSIYAFNKSVDYQSVCEPGAAPQ 900
DB 841 LDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLNYSIYAFNKSVDYQSVCEPGAAPQ 900
QY 901 GAGHSAYVPSVADILQIGWATAAASWILQOFLSLTFRLLLEAVEMEDDDFTASLSKQ 960
DB 901 GAGHSAYVPSVADILQIGWATAAASWILQOFLSLTFRLLLEAVEMEDDDFTASLSKQ 960
QY 961 SCITEQTOYFFDNDKSFSGVLDGNCGRIFHGEKLMNTNLIPIWVESKGTCPDTRLLI 1020
DB 961 SCITEQTOYFFDNDKSFSGVLDGNCGRIFHGEKLMNTNLIPIWVESKGTCPDTRLLI 1020
QY 1021 QABQTSQGNPCDMVKQPRYKGPVDFVCFNNVLEDYTDGGSVSLNPLSLWYIIGIOFLLL 1080
DB 1021 QABQTSQGNPCDMVKQPRYKGPVDFVCFNNVLEDYTDGGSVSLNPLSLWYIIGIOFLLL 1080
QY 1081 WLVSQSGTHRELL 1091
DB 1081 WLVSQSGTHRELL 1091

RESULT 2
A44147
calcium channel protein alpha-2 chain precursor - rat
N;Alternate names: dihydropyridine-sensitive L-type
N;Contains: calcium channel alpha-2 chain
C;Species: Rattus norvegicus (Norway rat)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 20-Aug-1999
C;Accession: A44147
R;Kim, H.L.; Kim, H.; Lee, P.; King, R.G.; Chin, H.
Proc. Natl. Acad. Sci. U.S.A. 89, 3251-3255, 1992
A;Title: Rat brain expresses an alternatively spliced form of the dihydropyridine-sensitive
A;Reference number: A44147
A;Accession: A44147
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1091 <KIM>

A;Cross-references: GB:M86621; NID:g203954; PIDN:AAA41088.1; PID:g203955
C;Superfamily: calcium channel alpha-2 chain
C;Keywords: calcium; glycoprotein; ion channel; transmembrane protein

Query Match 95.8%; Score 5505; DB 2; Length 1091;
Best Local Similarity 95.3%; Pred. No. 0;
Matches 1040; Conservative 26; Mismatches 23; Indels 2; Gaps 2;

QY 1. MAAGCLLALTTLFOSLLIGPSSSEPPFSAVTIKSWDKMQEDLVTLAKTAGVGNQLVDI 60
DB 1. MAAGCLLALTTLFOSLLIGPSSSEPPFSAVTIKSWDKMQEDLVTLAKTAGVGNQLVDI 60
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DB 61 YEKYQDLTYVEPNNAQOLVEIAARDIEKLLSNRSLVLALEAEKVQAAHQRDEFASN 120
QY 121 EVVYNAKDDLPENDSPGSRQIKPVIEDANFGROIYSQHAHVHITDIEGSTIVL 180
DB 121 EVVYNAKDDLPENDSPGSRQIKPVIEDANFGROIYSQHAHVHITDIEGSTIVL 180
QY 181 NELNWTSSALDEVFKNRREDPSLLMQVFGSATGLARYYPASPWVDNSRTPNKIDLYDVR 240
DB 181 NELNWTSSALDEVFKNRREDPSLLMQVFGSATGLARYYPASPWVDNSRTPNKIDLYDVR 240
QY 241 RPWYIQAASPKDMLILVDVSGVSGTLTKLIRTSYSEMLETSLDDDFVNFASFNSAO 300
DB 241 RPWYIQAASPKDMLILVDVSGVSGTLTKLIRTSYSEMLETSLDDDFVNFASFNSAO 300
QY 301 VSCFOHLVQANVRNKKVLKDAVNNTAKGIDYKKGFSFAFEOLLNLYNVRANCNKIIML 360
DB 301 VSCFOHLVQANVRNKKVLKDAVNNTAKGIDYKKGFSFAFEOLLNLYNVRANCNKIIML 360
QY 361 FTDGGEERAQEIFNKYNKDKKVRVFRFSGVGHNYERGPQIOWMACENKGYEYIPEISGAIR 420
DB 361 FTDGGEERAQEIFNKYNKDKKVRVFRFSGVGHNYERGPQIOWMACENKGYEYIPEISGAIR 420
QY 421 INTQEYLDVLRGPRVLAGDKAKQVQWNTNYLDALBELGLVITGTLVPFNITGOFENKTNLK 480
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DB 481 NOLLILGVMDVDSLEIDIKRLTPRFTLCPNGYFAIDPNGYVLLHHPNLOPKNPKSOEPTVL 540
QY 541 DFLDAELENDIKVEIRNKMIDGESGKFTLTVKSDERYIDKGNRTYTWTPVNGTDY 599
DB 541 DFLDAELENDIKVEIRNKMIDGESGKFTLTVKSDERYIDKGNRTYTWTPVNGTDY 599
QY 600 LALVLPITYFYIYKAKLEETITQARSKGKMKDSETLKPDNFEESGYTFTAPRDXCNDL 659
DB 600 LALVLPITYFYIYKAKLEETITQARSKGKMKDSETLKPDNFEESGYTFTAPRDXCNDL 659
QY 660 ISDNTEFLNFEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVQYNSKQNIKGVRAR 719
DB 660 ISDNTEFLNFEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVQYNSKQNIKGVRAR 719
QY 720 RFVYTDGGITRVYPKEAGENQWNPETIEDSFYKRSLDNDNYVFTAPYFNKSGFGAYES 779
DB 720 RFVYTDGGITRVYPKEAGENQWNPETIEDSFYKRSLDNDNYVFTAPYFNKSGFGAYES 779
QY 780 IMYSKAVEIYIQGLKLPVAVGKIDVNSHIEFTKTSIRDPCAGPVCDCRNSDVMDCV 839
DB 780 IMYSKAVEIYIQGLKLPVAVGKIDVNSHIEFTKTSIRDPCAGPVCDCRNSDVMDCV 839
QY 840 ILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLNYSIYAFNKSVDYQSVCEPGAAPK 899
DB 840 ILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLNYSIYAFNKSVDYQSVCEPGAAPK 899
QY 900 QGAGHSAYVPSVADILQIGWATAAASWILQOFLSLTFRLLLEAVEMEDDDFTASLSK 959
DB 900 QGAGHSAYVPSVADILQIGWATAAASWILQOFLSLTFRLLLEAVEMEDDDFTASLSK 959

```
QY 960 QSCITEQYQYFPDNDKSFSGVLDGCGNSRPHGKLMNTNLIFIMVSKGTCPCDTRLL 1019
Db 960 QSCITEQYQYFPKNTKSFGLDGCNGSRIPHVKLMNTNLVFIWVSKGTCPCDTRLL 1019
QY 1020 IQAEOISDGNPCDMVKQPRYRKGPVDFDNNVLEDDYDTCGGVSLNPSLWIIIGIQFLL 1079
Db 1020 MQAEOISDGNPCDMVKQPRYRKGPVDFDNNVLEDDYDTCGGVSLNPSLWIIIGIQFLL 1079
QY 1080 LMLVSGSTHRL 1090
Db 1080 LMLVSGSRHYL 1090

RESULT 3
CHRB2
N:Alternate names: dihydropyridine-binding protein, 140K
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 22-Jun-1999
C:Accession: S10579; A39518; A33409
R:Ellis, S.B.; Williams, M.E.; Ways, N.R.; Brenner, R.; Sharp, A.T.; Campbell, K.P.
A>Title: Sequence and expression of mRNAs encoding the alpha(1) and alpha(2) subunits of
A:Reference number: S10579; MUID:88336904
A:Accession: S10579
A:Molecule type: mRNA
A:Residues: 1-1106 <ELL>
A:Cross-references: EMBL:M21948; NID:g164762; PID:AAA81562.1; PID:g164763
R:Jay, S.D.; Sharp, A.H.; Kahl, S.D.; Vedvick, T.S.; Harpold, M.M.; Campbell, K.P.
J.Biol. Chem. 266, 3287-3293, 1991
A>Title: Structural characterization of the dihydropyridine-sensitive calcium channel al
A:Reference number: A39518; MUID:91131638
A:Accession: A39518
A:Molecule type: Protein
A:Residues: 961-973 <AY>
A>Note: this sequence represents the amino end of a glycosylated peptide that appears af
e at the amino end and identical molecular weights (17K) following deglycosylation
R:Hamilton, S.L.; Hawkes, M.J.; Brush, K.; Cook, R.
Biochemistry 28, 7820-7828, 1989
A>Title: Subunit composition of the purified dihydropyridine binding protein from skelet
A:Reference number: A33409; MUID:90122765
A:Accession: A33409
A>Status: preliminary
A:Molecule type: protein
A:Residues: 27-44, 'S', 46-47 <HAM>
C:Superfamily: calcium channel alpha-2 chain
C:Keywords: calcium; disulfide bond; glycoprotein; ion channel; membrane protein; phosph
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-1106/Product: calcium channel alpha-2 chain #status predicted <MAT>
F:94,138,186,326,350,470,477,606,615,678,697,784,827,891,898,988,1001,1081/Binding site:

Query Match 95.7%; Score 5503.5; DB 1; Length 1106;
Best Local Similarity 94.68; Pred. No. 0;
Matches 1053; Conservative 16; Mismatches 15; Indels 29; Gaps 4;

QY 1 MAAGCLLALTTLFQS--LLIGPSSEEPFSAVTTKSWDKMQEDLVLIATASGVNQIV 58
Db 1 MAAGRPLAWTLTLQAWLLIGPSSEEPFSAVTTKSWDKMQEDLVLIATASGVHQLV 60

QY 59 DIYKYQDLYTEPNNAQLVEIARDEKLSNRKALVSLALEAEKVAQAAHQWREDA 118
Db 61 DIYKYQDLYTEPNNAQLVEIARDEKLSNRKALVSLALEAEKVAQAAHQWREDA 120

QY 119 SNEVYYNAKDDLEPKNDSEPGSORIKFPVIEDANFRQISYQAAHYIPTDIYEGSTI 178
Db 121 SNEVYYNAKDDLEPKNDSEPGSORIKFPVIEDANFRQISYQAAHYIPTDIYEGSTI 180

QY 179 VLNELNWTSAIDVEPKKREEDPSLLWQVFGSATGLARYYPASPMWDSRTPNPKIDLDYV 238
Db 181 VLNELNWTSAIDVEPKKREEDPSLLWQVFGSATGLARYYPASPMWDSRTPNPKIDLDYV 240
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QY 239 RRRPHYIOGAASPDKMLILVDYSGSVSGITLKLIRTSVSEMLETISDDDFVNVASENSA 298
Db 241 RRRPHYIOGAASPDKMLILVDYSGSVSGITLKLIRTSVSEMLETISDDDFVNVASENSA 300
QY 299 QDVSCFOHLVQAVNRNKKVLDVANNITAKGTDYDKKGFSAFEQLLNLYNVRANCNKII 358
Db 301 QDVSCFOHLVQAVNRNKKVLDVANNITAKGTDYDKKGFSAFEQLLNLYNVRANCNKII 360
QY 359 MLFTDGGEEAQAEIFKNYKNDKKVRFRFSGQHNYERGPQIOMMACENKGYEYIIPSIGA 418
Db 361 MLFTDGGEEAQAEIFAKYNKDKKVRVFTFSGQHNYDRGPQIOMMACENKGYEYIIPSIGA 420
QY 419 IRIHQEYLDVLGRPMVLADGKAKQVQWNTNYLDALGLVITGLTPVNTIQTGFENKTN 478
Db 421 IRIHQEYLDVLGRPMVLADGKAKQVQWNTNYLDALGLVITGLTPVNTIQTGFENKTN 480
QY 479 LKNQLILGVMGVDVSLIEDIKRLTPRFTLPCNGYVPAIDPNGVLLHPNLQPK----- 530
Db 481 LKNQLILGVMGVDVSLIEDIKRLTPRFTLPCNGYVPAIDPNGVLLHPNLQPKIGVIGIPT 540
QY 531 -----NPKSQEPVTLDFDALENDIKVEIRNMKIDGESGEKTFRTLVKSQDER 579
Db 541 INLRKRRPNVQPKSQEPVTLDFDALENDIKVEIRNMKIDGESGEKTFRTLVKSQDER 600
QY 580 YIDKGNRTYTPVNGTDY-SIALVLPYTSFYIRAKLEETITQARSKKGGKMKDSETLKP 638
Db 601 YIDKGNRTYTPVNGTDYSSIALVLPYTSFYIRAKLEETITQARY-----SETLKP 653
QY 639 DNFEESGTYFIAPROYCDNCLKTSDNTELLNFNFIIDRKTNPNSCNADLNRVLDDAG 698
Db 654 DNFEESGTYFIAPROYCDNCLKTSDNTELLNFNFIIDRKTNPNSCNADLNRVLDDAG 713
QY 699 FTNELVQNTWSKQNKIKGVKARFVVTGGITRVYKPEAGENQENPETYEDSFYKRSLDN 758
Db 714 FTNELVQNTWSKQNKIKGVKARFVVTGGITRVYKPEAGENQENPETYEDSFYKRSLDN 773
QY 759 DNYVTAPYFNKSGGAYESGIMVSKAVIYIQGLLKLPVAVGIKIDVNSWIENFTKTSI 818
Db 774 DNYVTAPYFNKSGGAYESGIMVSKAVIYIQGLLKLPVAVGIKIDVNSWIENFTKTSI 833
QY 819 RPPCAGPVCDCKRNSDMVDCVILDGGLMANHDDYTNQIGRFFGEIDPDLMLRHVLNIS 878
Db 834 RPPCAGPVCDCKRNSDMVDCVILDGGLMANHDDYTNQIGRFFGEIDPDLMLRHVLNIS 893
QY 879 VYAFNKSYDYQSVCEPAGAPKOGAGHRSAYVPSVADILQIGWATAAASIIQQFLLSLT 938
Db 894 VYAFNKSYDYQSVCEPAGAPKOGAGHRSAYVPSIADILQIGWATAAASIIQQFLLSLT 953
QY 939 FPRLEAVEMEDDDFTASLSKSCITEQYQYFDDNDSKFSGLDGCNGSRIPHGKLMN 998
Db 954 FPRLEAVEMEDDDFTASLSKSCITEQYQYFDDNDSKFSGLDGCNGSRIPHGKLMN 1013
QY 999 TNLITIMVESKGTCPDTRLLIQAEQTSQPNPCDMVKQPRYRKGPVDFDNNVLEDDYTD 1058
Db 1014 TNLITIMVESKGTCPDTRLLIQAEQTSQPNPCDMVKQPRYRKGPVDFDNNVLEDDYTD 1073
QY 1059 CGGVSGLNPSLWIIIGIQFLLMLVSGSTHRL 1091
Db 1074 CGGVSGLNPSLWIIIGIQFLLMLVSGSTHRL 1106
```

RESULT 4

```
T30256
calcium channel alpha-2-delta-C chain - mouse
C:Species: Mus musculus (house mouse)
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 20-Jun-2000
C:Accession: T30256
R:Klugbauer, N.; Lacinova, L.; Marais, E.; Hobom, M.; Hofmann, F.
J. Neurosci. 19, 648-691, 1999
A>Title: Molecular diversity of the calcium channel alpha2delta subunit.
A:Reference number: Z20794
A:Accession: T30256
A>Status: preliminary; translated from GB/EMBL/DBJ
```


A:Molecule type: mRNA
A:Residues: 1-1091 <KLU>
A:Cross-references: EMBL:AJ010949; PIDN:CAA09423.1
A:Experimental source: brain
C:Superfamily: calcium channel alpha-2 chain

Query Match 19.6%; Score 1127.5; DB 2; Length 1091;
Best Local Similarity 28.6%; Pred. No. 4.9e-60;
Matches 328; Conservative 230; Mismatches 451; Indels 137; Gaps 42;

QY 3 AGCLLALTLFOSLLIGSPSEPPSAVTKSVKMDQEDLVTLAKTASGVNQLDYIE 62
DB 14 ASALLA-TALLYAALGDVVRSEQQIPLSV-VKLWASAFGEIGKSAIAKYSQSLLQKKYK 71

QY 63 KYQDLTYVPPNNAROLYEIARIEKLLNRSKALYSIALALEAEKVQAHOHREDFASNEV 122
DB 72 EYKDAVAIEIDGLQVLKLAKEEMFHKSEAVRRLVEAAEAHLKHEFDADL---QY 128

QY 123 VYNAK--DLDPEKNDSEPSQRIKPVFTEDANFGR-QISYQAAVHIPTDIYEGSTIV 179
DB 129 EYFNVLINERDKGNFLELGKEFI---LAPNDFNNLPVNISLSDVOVPTNMYNKDPAI 185

QY 180 LNEUNWTSALDEVFKNREEDPSLLMQVFGSATGLARYYPASVPWDSNRPKNIDLYVR 239
DB 186 VNGVWSESLNKVFVDFNDRDPSLIWYFGSAKGFQYPGIKWEPDE---NGVIAFDCR 242

QY 240 RRPYIOGAASPRDMLTLVDVSGVSLGLTKLRTSVSEMLETLSDDDFVNVASFNSNAQ 299
DB 243 NRKWIQAATSPKDWLVLDVSGSMGLRUTIAKQTVSSILDTLGDODFFNIITYNEELH 302

QY 300 DVS-CFO-HLVQAVNRNKKVLDKAVNNITAKITDYKKGFSFAFQOLLNVSRAN--CN 355
DB 303 YVEPLNGTLVQADRTNKEFREHLDKLPAKGIGMLDIALNEAFNLISDNFHHQGSICS 362

QY 356 KIIMFTDGGEEAQAEIFNKYN-KDKRVRFVSQGHYNERGPIOMMACENKGYIYEP 414
DB 363 QAIMLITDGAVDVDTIFAKYNNPDRKVRIFTYLGREAAFAADNLKWMCAKNGFFQIS 422

QY 415 SIGAIRNTQYLDVGRPMVLADGAKAQVQWNTNYLD-----ALBELGLVI--TGT 463
DB 423 TLADVQENVMYELHLVSRPKVI--DQPHDVVMTYAYIDSTLPOAKLADQGLVMTVA 480

QY 464 LPVFNITQGENKTLNKLQILGVMGVDSLEDIKRLTPRTLCPCNGYYPADIPNGVLL 523
DB 481 MPVFS---KONETRSK--ILDGVGVDVDPKELLTPKIKLIGIHAFATINNGTILT 535

QY 524 HPNLQP---KNPKSQEP--VTLDFDLAELENDIKVEIRNMIDGESGKTRTLVKSQDE 578
DB 536 HPELRPLYEEGKKRRKPNYSVDLSEVWEDEDRODV-LRNAVNRKTGK--FSMEVK--- 588

QY 579 RYDKGNRT-----YTWTPVNGTDYSALVLPY-YSFYTIKAKLEETITQARKKKGKMK 631
DB 589 KTVDKGRKRLVMTNDYTYTDIKGTPEFSLGVALSRGHGKYFF-----RGNVT 634

QY 632 DSEPLKPDNPEESGYTFIADRYCN-DLKISDNNTPELLNFNEFIDRKTNNPSCNADLI 690
DB 635 IEELG--HDLHPDVSUADSEWSTNDLDPHEHLSOLEAIKILKLGKEP-LLOCDKELI 691

QY 691 NRVLDAAGTNELVQNTWS-----KOKNIKGVKAREVWTDGGITRYYP----- 733
DB 692 QEVLEDA-VVSAPIEAVTSLANKSENSDKGEVAFGLTRTGLSLNLFVGAQLTNQD 750

QY 734 -KEAGENWQENPEYEDSFYKRSLDN--DNYVTFAPY-----FNKSGPAGESIMVSKAV 786
DB 751 FLKAGDENIFNADHFLWYRAAEQIAGSFYSIPSTGTGVNKS-----NVVTASTSI 804

QY 787 EIIYQGLLKPAPVGVIKIDVNSWIENTKTSIRDPACAGPVCDCKRNSDVMDCVILLDDGGF 846
DB 805 QLLDERKSPVVAAGIQMKLEFFQKFWTASROQASLDGKSCSDDETNYCLIDNNGF 864

QY 847 LLMAHDDYTNQIGRFFGEIDPSLMRHLNIVSVAFNKSVDYQSVCEPAGPAKQAGHR\$ 906
DB 906

DB 865 ILVS--EDYT-QTGDFFEVEGAVMNKLLTMGSKRITLYDYQAMCR---ANKESSDAH 918
QY 907 AVYPSVADILQIGWATAAAWSILQOFLLSLTPRLLEAVEMEDDDFTASLSK-----QS 961
DB 919 GLDDPYKAFI-----SAKWIMTELVLFLVEF---NLCSWHSMTAKAQKLKQTLPEP 968

QY 962 CITEQTYQFFDNDKSKFSVGLDCGNSRIFHGKLMNTNLIIFINVESKGTCPDTRLLIQ 1021
DB 969 CDTEYPAFVSERTIKETGTGNIACEDCSKSPVIOQIPSSNLFMVVDS--SCLCESVAPIT 1026

QY 1022 AEQTSQGN---PCDMVKQPRYRKGPVDFDNNVLEDYDCGGVSGLNPLSLWTIIGIQFL 1078
DB 1027 MAPTEIRYNESLACERLKAQKIRRPESCHGFHPEENARECGASSLQAQ-----AALL 1080

QY 1079 LLWLVS 1084
DB 1081 LPLVLS 1086

RESULT 5
S44617
C50C3.11 protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C:Accession: S44617
R:Pavello, A.D.
submitted to the EMBL Data Library, May 1993
A:Description: Sequence of the C. elegans cosmid C50C3.
A:Reference number: S44618
A:Accession: S44617
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-734 <PAV>
A:Cross-references: EMBL:L14433; NID:g289649; PID:g289650
C:Genetics:
A:Introns: 24/2; 87/3; 175/1; 259/1; 290/3; 346/3; 460/3; 538/3

Query Match 10.6%; Score 607; DB 2; Length 734;
Best Local Similarity 26.6%; Pred. No. 7.7e-29;
Matches 180; Conservative 127; Mismatches 258; Indels 112; Gaps 20;

QY 47 LAKTASGVNLDIYKQYQDLYTVPEPNARQLVEIAARDIEKLLSNRS-----KALVSLAL 102
DB 36 MKETFSKISHETILKQYKLVVEEQDPAELKKSKHRIEDYLVRSQFAYKAKIS--L 93

QY 103 EAEKQAAHQRWEDFASNEVYVYNKADDDLDPEK-NQSEPGSRIKP-----VFIEDANF 155
DB 94 EARSVRNDSTVNDPQSKSFIREMSAKQGNQDGTITYESNHLGKRLKVNKTSFNLQANF 153

QY 156 -GRQISYQHAHVHPTDIYEGSTIVLNELNWTALDEVFKNREEDPSLLWQVFGSATGL 214
DB 154 YTLPTSVSSAVHIPTLYDRNEDLLRKIDW-SDIDAVYETNREETKDLAFOLFCEAGY 212

QY 215 ARYPASPWY-DNSRTPNKIDLYDVRPPWYIQGAAPKDMILILVDVSGVSGVGLTLKLIR 273
DB 213 MRYPPAASFWDNQ--DEHLDLDFDCRNTWYINSATNSKNVILMDMSGMLGQRYEVAK 270

QY 274 TSYSEMLETLSDDDFVNVASFNSNA-----QDVSCFQHLVQANRNKKVYLDVANNITAKGI 330
DB 271 QTTEAILETLSHNDYENIMTFKNTFLDCCNGTNGLLQATMRNKKALRRKMDTYQSEK 330

QY 331 TDYKKGFSFAFQELLNPN-----VSRANCNKIIMLTFDGGEEAQAEIFNKYNDKKVRF 385
DB 331 AEYEKALPLAFVLLDINNGGDNRRGACENVIMLITDGPANAYKIKFIDMADKKVRF 390

QY 386 RFSVGOHNTYERGIQWACENKGYIYEPISGAIRINTQYEL-----DVLGRPWVLAGDKA 441
DB 391 TFLVGEADIDFNEVREMACNRRGYMWHVANADYDEKIHYYIRMSRVGGRHYESQLS 450

QY 442 KOVQWNTVYLDALDELGL--VITGLPVPNTIGTFENKTN----- 478
DB 451 ---WTVGVYRERLYLPRPEIFAPVPITNQSFVAMNKMARRKIRLQKSEARSRMFVTV 507

QY 479 -----LKNQLILGVGVDSLEDIKRLTPFTLCPNGYYFAIDPBGVYLLHPNLPKPNP-- 532
Db 508 SYPVIYNETFMGVAAYNIPLEVAQKSHPANIGSKSYFFMLDQNGFVMTHPOLRPIDPET 567
QY 533 --KSQEPVTLDFLD-----AELENDIKVEIRKNMID 561
Db 568 KYHKQYNMMDLLELVGQNGQNVRSQKSAVSDLVCEGSAVAECVDDLRKAVRKMID 627
QY 562 GESGEKTFRLTKSODERY----IDK---GNRTYTPVNGTDYSLALVLPYTFYFIKA 614
Db 628 CDNSD-----VQOLDVLYATELLDRVYPTNTYYAEACINHANFVLGLAVAKGDDYRVVK 681
QY 615 KLEETITQARSKKGMK 631
Db 682 K-----QKDYDFGRVK 692

RESULT 6
probable calcium channel protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C:Accession: T18770; T25249
R:Sulston, J.
submitted to the EMBL Data Library, June 1995
A:Reference number: 219019
A:Accession: T18770
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1148 <W14>
A:Cross-references: EMBL:Z49907; PIDN:CAA90091.1; GSPDB:GN000020; CESP:T24F1.6
A:Experimental source: clone B0491
R:Chui, C.
submitted to the EMBL Data Library, June 1995
A:Reference number: 220004
A:Accession: T25249
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1148 <W2>
A:Cross-references: EMBL:Z49912; PIDN:CAA90141.1; GSPDB:GN000020; CESP:T24F1.6
A:Experimental source: clone T24F1
C:Genetics:
A:Gene: CESP:T24F1.6
A:Map position: 2
A:Introns: 91/2; 131/3; 170/3; 283/1; 322/2; 410/3; 487/1; 563/1; 602/3; 654/3; 683/3; 7

Query Match 10.1%; Score 580.5; DB 2; Length 1148;
Best Local Similarity 21.2%; Pred No. 6.3e-27;
Matches 244; Conservative 217; Mismatches 437; Indels 251; Gaps 43;
QY 37 VDKMQEDLVTLA-----KTASGVNQLVDIYEKYQDLYTFVPPNNARQLVETAAARDI 86
Db 99 VDTIEAPASIAQFSANILRDPETQSRFSLVQEEFEKLPDIKSKKEDAAKLVRATEHL 158
QY 87 EKLNSRSLVSLALEAKVQAQHWREDFASNEVYVYNAKDDLDPERNDSEPGSQR-- 144
Db 159 DRLVTRVDAKLLASSAASAFAV-----DEYDDQAYAVPQADKRCE 201
QY 145 --IKPVFIEDANFGRIQISQVH--AAVHTPTDIYEGSTIVLNLNWTSA--LDEVFKNR 197
Db 202 AYMKKNESDMHFVSNM--VEHNSKSGIHTVSYQCDPRVRMRDFTDWTGKHLKETSMSDNK 260
QY 198 EEDPSLLMWQFSGATGLARYIPASPVVDNSRTPNKIDLYDVRRRRWYIOGAASPDMLIL 257
Db 261 ERAPENGHOYICTYSLTRMYPRRW-KVEPTITIDLPDRFPWFVNAESVPKDIVL 319
QY 258 VDYSVSGSLTKLINTSVSEMLETSLDDDFVNVASFNSAOD-VSCFOH-LVQANVRNK 315
Db 320 LDYSGSVKPTMHLIKITMYYTLSTLSPNDYFEGVYFNHFNPIISCANRTEPATTNSK 379
QY 316 KYLKDANNITAKGTDYKKGSFAFEQL--LNNVNS-----RANCNKIIMLFTDGGEE 367

Db 380 KYFEFELGMLLEKQDQAHFATPLKFSLDVLRGNLDSNQSOLFADYRSEGHKLILIFTDGVDE 439
QY 368 RAQEIEFN--KYNKDKVRVRFESVQGHNYRERPIQWACENKGYEYIPISGAIRINTQ 424
Db 440 WPHQIILDEEFQTRSELIRIFGSMGYGSLPLQOYMACKSHGGYSEIDSIWDRPQSR 499
QY 425 EYLDVLRPMVLADGKAK-----QVQNTNYYLDALGLGLVITGLTPVFNITQGEENKT 477
Db 500 TIONVLSQ---VRGDELKGTNAEKREPSWTQLYMETQGTGPIVTLSPILT-----SEQR 551
QY 478 NLKNQILGVMGVDVLEDIKRLTPFTLCPNGYYFAIDPBGVYLLHPNLPKPNP-- 533
Db 552 IWRDQKLAGVVAIDISIKETKHL--TSSEQMGIYVNNGMILYHPQIQIPTEVHCV 609
QY 534 -----SQEPV-----TLDFLDAELENDIKVEIRN 557
Db 610 RRSACYDAQVQKQKAGSLRVHYGFSDEVYRLVGLIDSIPTLDMYDLEGDSFAIRDLRR 669
QY 558 KMIDGESSEKTFRLTKSODERYIDKGNRTYTPVNGTDYSLALV--LPTFYFYIKAK 615
Db 670 -----RITTKCYEEAIDKNSKEYHCHSHKIDSPFTLVIVNNIOLKTVYDDSV 717
QY 616 LEETITQ-----ARSKKGMKDETLKPDNFEESGYTFIAPRDY--NDLKISDNNT 665
Db 718 QELGLTDNKLVTFFYPRDVCQWKLDEYAAHDFRV--WSDISEKEICAQDMLRPRAFT 775
QY 666 EFLNFEETDRKTPNPNPCNADLINRVLIDAGFTNELQVNYWSKOKNIKGVKARFVTD 725
Db 776 KGLGWTQSWPKSDIEHTTC-----LLAQYPENASVPHYVNS-----FVHTR 817
QY 726 GGITRVYPRKEAGNWOENPETEDSYKRLSDNDNVYTFAPYENKSGPGAYESGIMVSKA 785
Db 818 SKLTAFYPTCSSHDMKAVNKKFDEEI--KLTDNDFV---QFSMR-----SESLIYRT 866
QY 786 VEYIOGKLLKPAVGIKIDVN--SWIENFTKTSIRDCAGPVCCKRNSD-----VMD 837
Db 867 IADYDNRL---AVGTQWKENFFDYFDNFT-----RQPDWKICKRQE 908
QY 838 CVILDDGGFLLMANHDDYTNQIGRFEIGEDPSLMRHLNIVSYAFNKSVDYQSVCEPGAA 897
Db 909 CSIITRNHGVIIASSAHRAPAHAKF---DPQLFESLVKNVLVSTNSWTEVQSECK--- 960
QY 898 PKGAGHRSAYVPSVADIQIGWATAA--AWSILOQFLLSLTFPRLLEAVEHEDDDFTA 955
Db 961 -----AKRVAPWSSAAPGSSSILRYFTSI-----FKLAKTSFWR 995
QY 956 SLSKQSCITEQYQYFFDNDKSKSPGLDCGNC--SRIFHGKELMNTNLIIFIMVSKGTC-- 1012
Db 996 NLLESALTLDVAQPSMTGNTCTFKIKPFCPCPKFHYRMTLNITK-QLQLTGMSTCSR 1054
QY 1013 -----PCDTRLLIOAEGTSDGNP-----CDMYKQPRYKGPVDFD--N 1050
Db 1055 YAKLYVPVHTLTLIADACSOYRPRKIFSEPRKLEKCDVY-HSHARRRPPALNDWKI 1113
QY 1051 NVLEDYDTC 1059
Db 1114 DLQNKHVDC 1122

RESULT 7
C86880
hypothetical protein yvcC [imported] - Lactococcus lactis subsp. lactis (strain IL140)
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
C:Accession: C86880
R:Botolin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Eh
Genome Res. in press, 2001
A:Title: The complete genome sequence of the lactic acid bacterium.
A:Reference number: A86625
A:Accession: C86880
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-1450 <STO>
A:Cross-references: GB:AE005176; NID:gl2725093; PIDN:AAK06141.1; GSPDB:GN001446
A:Experimental source: strain II1403
C:Genetics:
A:Gene: yvcC

Query Match 3.4%, Score 198; DB 2; Length 1450;
Best Local Similarity 21.0%; Pred. No. 0.0012;
Matches 242; Conservative 149; Mismatches 439; Indels 322; Gaps 56

QY	37	VDKQEDVLTAKASGVNQLVDIYEKQDLYTVEPNNAOLVEIAARDTEK-----L 89
DB	69	INTKNDKELKLFSPGNQPIEEE--NESWTLKERKT-----IISDFEKENEGKIVL 120
QY	90	LSNRKALYSALAEAKVQAAHWR---EDFA-----SNEVVIYNA 127
DB	121	RANNSISLNLLEQADAKLIENDQEVISEDILAKKESTIFSLYIPENNAKDSREKDNKT 180
QY	128	KDLDPEKNDSEPGSORIKP---VFIEDANFGROIYSOHAAVH----- 167
DB	181	EEVLNNSEOEETVSQKKDSQLAFSYPSNFCIKASFNDLAQNYENISPEYRQDETGISP 240
QY	168	----IPTDIYEGSTIVYLNELNWTLSALDFEYKKNREEDPSLWQVGSATGLARYYPASPW 223
DB	241	NHSWIPT---GNTTVYNHOGWNSF-----SSQWDGVNSWN--GEATNLSENSIYIYAG 287
QY	224	VDN-----SRTPNKIDLY-DYRRRPWYIQAASPKDMLILVDVSGSVSGLTLK 270
DB	288	VNPVDFAIRKAKYAKETETGLDYVLNVRGN--VQNPiKVPDIVLVDMSGSGQAKET 344
QY	271	LIRTSVSEMLETISDD---DFNVV--ASFNSNAQDVSCFQHLVQANVRNKKVLKD----A 321
DB	345	AVRGVSDFLTSTIONTAYADYVNVGIVGYSSPGNVYTGASGYITVPI--DKVSSESHVKS 402
QY	322	VNNITA---KGIDYKKGSPAFQELLNWNYSRANCKNIIMLFTDGGERAQEIFNKYNK 378
DB	403	INOALAPQFGGGYFTGLGRUKGTEML---EODSSNQKMMILMTDG---VPTFSYKVS 455
QY	379	DKVR--VFRFSYQGHNYERG---PIQ---WMACENKGYVEI-----PSIGAIRINTQE 425
DB	456	ASKVDNVYIQCSFAESRDEPGNTSKIQSPYYVKDINGSNIEIRDTWAATLGEAEISKQE 515
QY	426	YLDVLRPMWLAGD-----KAKOVQWNTYILDALGLVITGTLPVFNITQOFE 474
DB	516	ISEHTLGIQLGNDGYSVLSQEEVKRSRTSLIATTGLYQDANSAN-----DITDYLK 565
QY	475	NKTN-----LKNOLILGVMGDVVSLEDIKRLPRTFLCPNGYYFAIDPNGVYLLHPN 526
DB	566	NOANVLSRENTINGLILDPLGAOFYKDKT-----FEITSVG----- 604
QY	527	LQPNKRSQEPVTLDFDLAELENDIKVEIRNMKDGESEKTFRTLKYSQODERYIDKGNR 586
DB	605	-----EDSIDMLPTGKKINEKLEISNLNI--GKNQEVQIHYQVRLNLTETDFTTNY 653
QY	587	TY-----TWTPTYNGT--DYSLALVLPYTSFYIIKAKLE-----ETIQARSKK 627
DB	654	WYQMNGETTLTP--NGSNPDKNVFGVPSAKSSGINLTLEKQWLANSENIPENVELLIGRR 712
QY	628	GKKKDS-----TLKPDNTEESGYTFIAPRDCYNDLKTSDNNTEPLNPNFEIDRKPNN 682
DB	713	SAQISSDWTKTVTLKEDDEWRSQLENPLKYSITLGEFYEIKDEIVLN--SBIYDOWITGE 771
QY	683	PSCNADLINRVLVD---AGFTNELVQYWSKQKIKGVKARFVVTDCGITRVYPKAGE 738
DB	772	DKTTIANIEFRQLKITSNHDNEPUSVEFVLKNSQGEEDKAVTN-----EKGE 822
QY	739	NWQENPETYEDSFYKRSLDNDNVFTAPYFNKSGPGAYESIMYSK-----AVEYIQ 791
DB	823	ILFDKTRLNGEYQVQLHEIKSPGHSLEGPWKTKT---EFENGQPIIKYVDGSQLALDEHYN 879
QY	792	GKLLKPAVGIGIKIDVNSWIENFTKTSIRDPACGPVCDCKRNSDVMDCVILD-----DG-- 844

QY 467 ENITGFENKTNLKNOLLIVGVMDVSLSDIKRLTPRFTLCPNGYFAIDPNCYVLLHPN 526
Db 492 F-----YDG-----SIIVAGRLVDRMDN-----FKADVKGHGALN--- 523
QY 527 LOPKPKSQEPVTLDFDLAELENDIKVEIRNKMIDGESGEK--TFRTLVKSODERYIDRG 584
Db 524 ---DLTFEEVDMEBDAALK-----EQGVIFGDYIERLWAYLTIQELLEKKRNGK 572
QY 585 NRTYTWTPVNGTDYSLA--LVLPYTSFYIKAKLETTIQARSKKGMKMDSET-----LK 637
Db 573 DEKENIT-AEALDLSLKYHFVPLTSMVYTPEDNEDOTSADNAGEEAFATETMTSFLT 631
QY 638 PNFESGVTFTAPRDYCNLDKISDNNTFELNFEIDRKPNNPCSNADLINRVLLDA 697
Db 632 TQOSSSPYIV-----DGDPHFIQI-----PGKNDSCFNIDEKP 668
QY 698 GFTNELVQYWSQKNIKGVARFVVDGTRVYPKEAGENQWENPETYDSFYKRSLD 757
Db 669 GTVLRLIQD-----PVT--GIT-VTQIIIGD-----KRS-- 694
QY 758 NDNYFTAPYFNKSGPAYESGIMWSKAVEITIQGLLPAPVGVKIDVNSWIENETKTS 817
Db 695 NASSRTGRTYFGKLTGNAMDFRVEVTEKILG-----TGAELETSFSLDVTVTQ 747
QY 818 IRDPCAGPVCDCKRNSDVMDCVILDDG--GFLLMAN-----HDDYTNQIGRFGGEIDP 868
Db 748 -----TGLSVTNRKKNMV--VSFGDGISFVILHGWKKHPVHQDFLG-----FVVDVS 795
QY 869 SLMRHLNVSIVAFNKSQYQSV-CEPGAAP 898
Db 796 HRMSAQTHGLLGQFTQFPDFKVGIRPGSDP 826
RESULT 9
S30350
Inter-alpha-trypsin inhibitor heavy chain 3 precursor - human
N:Alternate names: HC3; Inter-alpha-trypsin inhibitor chain H3; pre-alpha-inhibitor heavy
C:Species: Homo sapiens (man)
C:Date: 03-May-1994; sequence_revision 20-Feb-1995 text_change 04-Feb-2000
C:Accession: S30350; S34123; S02141; D34245; A39079; S50133; B53642; A59167
R:Bourguignon, J.; Diarra-Mehrpour, M.; Thiberville, L.; Bost, F.; Sesbouee, R.; Martin,
Eur. J. Biochem. 212, 771-776, 1993
A:Title: Human pre-alpha-trypsin inhibitor-precursor heavy chain cDNA and deduced amino-
A:Reference number: S30350; MUID:93215566
A:Accession: S30350
A:Molecule type: mRNA
A:Residues: 1-885 <BOU1>
A:Cross-references: EMBL:X67055; NID:g288562
R:Bourguignon, J.
submitted to the EMBL Data Library, June 1992
A:Reference number: S34123
A:Accession: S34123
A:Molecule type: mRNA
A:Residues: 1-310, 'K', 312-343, 'R', 345-885 <BOU2>
A:Cross-references: EMBL:X67055; NID:g288562; PIDN:CAA47439, 1; PID:g288563
R:Diarra-Mehrpour, M.; Bourguignon, J.; Sesbouee, R.; Mattai, M.G.; Passage, E.; Sallier,
Eur. J. Biochem. 179, 147-154, 1989
A:Title: Human plasma inter-alpha-trypsin inhibitor is encoded by four genes on three ch
A:Reference number: S02141; MUID:89137072
A:Accession: S02141
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 341-356, 'G', 358-845, 'H', 847-885 <DIAL>
A:Cross-references: EMBL:X14690; NID:g35464; PIDN:CAA32821, 1; PID:g35465
R:Englund, J.J.; Thogersen, I.B.; Pizzo, S.V.; Salvesen, G.
J. Biol. Chem. 264, 15975-15981, 1989
A:Title: Analysis of inter-alpha-trypsin inhibitor and a novel trypsin inhibitor, pre-al
A:Reference number: A92736; MUID:89380192
A:Accession: D34245
A:Molecule type: protein
A:Residues: 30-49 <ENGI>
R:Englund, J.J.; Salvesen, G.; Hefta, S.A.; Thogersen, I.B.; Rutherford, S.; Pizzo, S.V.
J. Biol. Chem. 266, 747-751, 1991

A:Title: Chondroitin 4-sulfate covalently cross-links the chains of the human blood p
A:Reference number: A39079; MUID:91093267
A:Accession: A39079
A:Molecule type: protein
A:Residues: 631-647 <ENG2>
R:Diarra-Mehrpour, M.; Bourguignon, J.; Sarafan, N.; Bost, F.; Sesbouee, R.; Muschio-
Blochim. Biophys. Acta 1219, 551-554, 1994
A:Title: Tandem orientation of the inter-alpha-trypsin inhibitor heavy chain H1 and H
A:Reference number: S50132; MUID:95002176
A:Accession: S50133
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-27 <DIA2>
A:Cross-references: EMBL:X75318
R:Wisniewski, H.G.; Burgess, W.H.; Oppenheim, J.D.; Vilcek, J.
Biochemistry 33, 7423-7429, 1994
A:Title: TSG-6, an arthritis-associated hyaluronan binding protein, forms a stable co
A:Reference number: A53642; MUID:94271799
A:Accession: B53642
A:Molecule type: protein
A:Residues: 30-34, 'X' <WIS>
R:Jessen, T.E.; Faarvang, K.L.; Ploug, M.
FEBS Lett. 230, 195-200, 1988
A:Title: Carbohydrate as covalent crosslink in human inter-alpha-trypsin inhibitor: a
A:Reference number: S02431; MUID:88167187
A:Accession: A59167
A:Molecule type: protein
A:Residues: 30-32, 'GERBQAVDT' <JES>
C:Comment: As pre-alpha-inhibitor, this protein is covalently cross-linked by chondro
C:Genetics:
A:Gene: GDB:ITIH3
A:Cross-references: GDB:120109; OMIM:146650
A:Map position: 3p13-3p12
C:Superfamily: Inter-alpha-trypsin inhibitor complex component II
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-29/Domain: propeptide #status predicted <PRO>
F:30-647/Product: inter-alpha-trypsin inhibitor heavy chain 3 #status experimental <M
F:648-885/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:87-576/Binding site: carboxylate (Asn) (covalent) #status predicted
F:647/Modified site: chondroitin sulfate ester carboxyl end (Asp) (in mature form) #s
Query Match 3.2%; Score 185; DB 2; Length 885;
Best Local Similarity 20.9%; Pred. No. 0.0034;
Matches 137; Conservative 101; Mismatches 239; Indels 180; Gaps 34;
QY 27 FPSAVTIKSWDKMOEDLVTLAKTASGVNLVDIYEKYQDLYTVEPNARQLVEIAARDI 86
Db 97 YGNVKEVAKQYKAVSQGTAG-----LVKASGRKL 131
QY 87 EKLLSNRSKAL---VSLALEAEKVQAAHQWREDFASNEVVYNAKDDLDPEKNDSEPGSQ 143
Db 132 EKFTSVNVAAGSKVTFELTYELLKRHKGK-----YEMYLKVQPK-----Q 173
QY 144 RKPVFIEDANFGROIQSYOAAVHIPTDIYEGSTIVLNELNWTSAIDVEFKKNEEDPSL 203
Db 174 LYKHFEIE-----VDIFEPOGI-----SMLD-----AEASFI 200
QY 204 LMQVFGSA-----TGLARYVPASPVDNSRT-PNKID-----LYDVRRRP----- 242
Db 201 TNDLLGSALTAKSFSGKKGHVSFKPSLDQORSCTCTDLSLLNGDFTTYDVNRSPGNVQI 260
QY 243 ---WYI-----QG-AAASPKDMLILVDVSGVSLGTLKLIRTSVSEMLETSLDSDDFVNVAS 293
Db 261 VNGYFVHFPAQGLPVVPKNVAFVIDISGMAGRKLEQTKAALLRILEDMQEEEDYLNFL 320
QY 294 FNSNAQDVSCF-QHLVQANVRNKKVLKDAVNNTAKITDYDKGFSFAEQLLNYSVR- 351
Db 321 FSG-----DVSTWKEHLVQATPENLQEAQTFVKSMEDKGMTNINDGLLRGISML---NKARE 374
QY 352 ----ANCKIIMLFTDG---GEEAQAQEFNKYNK--DKKRVFRFVSVOHNERGPQ 400

Db 375 EHRIPERSTSVIMLTGDGADVNGESRPEKIQENVRNAIGGRFPLYNLGFQ-NLNYNFLE 433
Qy 401 WMACENKGYVEISIGAIRINTQYLDVLRPMVLADGAKQVQWNTVNYDALE----- 455
Db 434 NMALENHGFARIEDSDADLOQGFVEEVANPL-LTGVEMEYPE--NAILDLTQNTYQH 490
Qy 456 ---LGLVITGTLFVNITGOFENKTNLK-----NOLILGVMGVDVSLDEDIKRLTPRFTL 506
Db 491 FIDSEIVVAGRL-VDEDMNSF--KADVKHGATNDL---TFTTEVDMKENEK-----AL 539
Qy 507 CPNGYFAIDPN-----GYVLLHPNLPK---NPKSQEPVTLDFDAELNDIKVEIRN 557
Db 540 QERDYIFG---NYIERLWAYLTLEQLLEKRNKHAKEENLTAARALDLSKYHFVTPUTS 596
Qy 558 KMGIDSEKTRILVKSQDRYI-DKGNRTYITTPVN-GTDYSALVLPYISFYI 612
Db 597 MVVTKPE-----DNEDEIRAIDKPGDAEATPVSPAMSYLTSTYQPPQNPYYV 644

RESULT 10

JC5576
Inter-alpha-trypsin inhibitor heavy chain 3 - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 17-Mar-1999
C:Accession: JC5576; PC4486
R:Nakatani, T.; Suzuki, Y.; Yamamoto, T.; Sinohara, H.
J. Biochem. 122, 71-82, 1997
A:Title: Molecular cloning and sequencing of cDNAs encoding three heavy-chain precursors in inhibitor heavy chain family.
A:Reference number: JC5574; MUID:97420688
A:Accession: JC5576
A:Molecule type: mRNA
A:Residues: 1-889 <NA>
A:Cross-references: DBJ:D89287
A:Experimental source: liver
A:Accession: PC4486
A:Molecule type: protein
A:Residues: 34-53; 449-475; 509-526 <NA>
C:Comment: In the plasma three inter-alpha-trypsin inhibitor heavy chains 1, 2 and 3 were that the complexes play important role for pancreatic cancer.
C:Superfamily: inter-alpha-trypsin inhibitor complex component II
F:236-239,664-865/Disulfide bonds: #status predicted

Query Match 2.9%; Score 164.5; DB 2; Length 889;
Best Local Similarity 23.2%; Pred. No. 0.059;
Matches 66; Conservative 56; Mismatches 112; Indels 51; Gaps 11;

Qy 202 SLLQVFGSATGLARYYPASPPVNSRT-PNKID-----LYDVRRL-PWYIQA-- 248
Db 211 SALTQSFSGKGVHVFKPS---LQQRSCPTCTDLSLLNGDFTIVYDVARESPGVVNG 267
Qy 249 -----ASPKMLILVDVSGVSGLTKLIRTSVSEMLETLSDDDDFNVASFNS 296
Db 268 YVHFPAQGLPVVPKNIVFVIDISGSAGRIQOTRALLKILDDMKODDVLNILEST 327
Qy 297 NAQDVSCFOHLVQAVNRKVKLKDANNITAKITDYDKGFSFAPEQLN-----YVNSRA 352
Db 328 GV--TTWKDSLQVATPANLEEARTEVRSISDOGTNINDGLLRIGRMLTDAREQHTVPER 385
Qy 353 NCNKKIIMLFTDG----GEERAQEIFNKYKDKKRVFRFVSG-QHNYERGPQWACENK 407
Db 386 STSIIML-TDGDANTGSRPEKIQENVRNAIGGRFPLYNLGFNGNLNINFLTMALENH 444
Qy 408 GYVEIPTSIGAIRINTQYLDVLRPMVLADGAKQVQWNTVNYLD 452
Db 445 GVARRIYSDANLQLOGFVEEVANPL-----TNVEVE 478

RESULT 11

T28155
variant-specific surface protein 1 - malaria parasite (Plasmodium falciparum) (fragments)
N:Alternate names: erythrocyte membrane binding protein 1 (EMPI)

C:Species: Plasmodium falciparum

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C:Accession: T28155
R:Rowe, J.A.; Moulds, J.M.; Newbold, C.I.; Miller, L.H.
Nature 388, 292-295, 1997
A:Title: Plasmodium falciparum rosetting is mediated by PfEMP1 and requires complement
A:Reference number: 220477; MUID:97373957
A:Accession: T28155
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2706 <ROW>
A:Cross-references: EMBL:Y13402; PIDN:CAA73831.1
A:Experimental source: strain IT 4/25/5
C:Genetics:
A:Introns: 2493/3
A:Note: R29R+var1

Query Match 2.8%; Score 161; DB 2; Length 2706;
Best Local Similarity 18.2%; Pred. No. 0.56;
Matches 183; Conservative 137; Mismatches 345; Indels 338; Gaps 46;

Qy 36 WDKMQEDLVTLAKTASGVNQLVDIYEKQDLYTVEPNNA-----RQL 78
Db 308 WFEWAEEFCIRIKI-----KLENYKKECRD---EPNNKYCSGDGCHCKRYLKDNTIF 358
Qy 79 VEAARDTEKLSNRSKALVSLALEAEKVQAAHQWREDFASNEVYVYNAKDDLPKNDL 138
Db 359 IDLNCPCENACSNYTK-----WIEIQKQFDKQK--YNNEL---KIKTNISNNNDK 408
Qy 139 E-----PGSORIKPVFIEDANFGRIQISYHAAVHIPTDIYEGSTIVLNELNWTSALE 191
Db 409 EYENLDKKGYSTIN-TFLESNLHGKQCQ-----DN 438
Qy 192 VFKNREEDPSLLQVFGSATGLARYYPASP-----WDNSRTPNKI 233
Db 439 IDKKNKTNFKNNL-ETFGP---SGYCEACPIYKVCSEKCTPVTEENWNSNNRLPTDT 493
Qy 234 DLYDVRRLPWIQGAASPKDMLILVDVSGVSGLTKLIRTSVSEMLETLSDDDDFNVAS 293
Db 494 STKNL-----ATNIDMLVNDGIGNAI----- 515
Qy 294 FNSNAQDVSCFOHLVQAVNRK-----VLKDAVNNTAKITDYKKGFSFAPEQL 345
Db 516 ---DNELEKNCIKYGLKGGKQKQWQCYLLNIDOCKINNVMNSGYFDNKIAFNVLFORWL 573
Qy 346 NYNVSRAKNIIMLFTDGGEEPAQEIFNKYKDKKRVFRFVSGQHNHYERGPQWMAE 405
Db 574 RYFVRDHRNLK-----EKIDVCIKKENINENICIKRCKTN-----CE 610
Qy 406 NKGYIYEIPTSIGAIRI---NTQEVLDVLRPMVLADGAKQVQWNTVNYDALEGLVIT 461
Db 611 CVGKLEKEAEAWDKNHYNOKNHIMFLIPYITWTFYK--ITFPNDFKALE-----DV 665
Qy 462 GTLPVNTIGQPKNTNLKNQLILGVMGVDVSLDEDIKRLTPRFTLCPNGYIFAIDPNGV 521
Db 666 DTINVLDLTKECQD--THCKIEKIRSI-DVDLKEILSWLONKIEVCKS--HDEDKHEYC 721
Qy 522 LHLPLQPKNPKSQBPVTLDFDAELNDIKVEIRNKTMDGSEGET-----FRT 571
Db 722 C---DILPKSVDDDEDD--EEVDEEKESSQTKRN--ISQKGGTKSASCVGACAIKVG 775
Qy 572 LVKSQDERYID---KGNRTYTW-----TPVNGTD-----YSLALVLPYISF 609
Db 776 VLQQKNSGSDNCNAKRNKKNEMQCDKNTFVDGNEGVCMPPRRKSCICIHNLTEEGTKNK 835
Qy 610 Y-----YIKAKLEET--ITOARSKGKMKDSEITLK-----PDNFEE--SGYTFIAPRDYC--N 656
Db 836 YOLREAFIKCAAKETNLLWDKYNDKNEAEELLKKGKIPEDFMRIMFYTFGDFRDFCLEN 895
Qy 657 DL-----KISDNNTEFLNFFIDRK-----TPNPNPSC--NADLNVLINVLADAGTNEL 703
Db 896 DMGKDVKYKKNINKYVFNNSKRGFKKIDPENWNNENGPOIWNGLCALIHADTKDSIKN 955

Db	765	KNTKIDNNKKYIYNLELBQEBINEKKYNNKND-----SNKTF-----LKINEF	812
QY	426	YLDVLRPMVLADK-----AKQVMT-----NVYLDALGLVITGTLVPFNIT	470
Db	813	KKDLDDSQITGDSLLADIKEYNTADLNNNNENKSLYEDGENF---ITRNP---IT	866
QY	471	GQFENTNL-----KNOLLIGVMGVDSLEDIRKLTPRFLCPN---G	510
Db	867	NEYEEKNNIIYISDEQYNEEDIIPDKIKKEKKNNDTSSDDFENCVQEKIYVNEKIEE	926
QY	511	YFPAID---PNGVYLLHPLQPKNKSPPVT-----LDFLD---AELEN-----DI	551
Db	927	YNNKNDKSSSSSIILEIKYKKEKDELSPNLCVLLDFEHSNDLENNYISVSSDDM	986
QY	552	KVEIRNMIDGSGEKTFTFLVKQODERYDKGNRTYTWTPVNGTDYSALVLPTYSFY	611
Db	987	KTNVSKNNITG-----VK---ENKVDKTNVEY-----	1010
QY	612	IKAKLEETIQARSKG-----KMKDSETLKPDNEESGYTF-----IAPRDYCN	656
Db	1011	-----DKKGDDGVIEISFEDSHKLEESKFDDNNNIYDNDDELEKNLSKYIIS	1057
QY	657	DLKISDNNTEFLNF-----NBFIDRKTNNPS-----CNADL	689
Db	1058	D--VDKNHVNINNIERGEDENEFENKIQSTESHKSNEEICTENKSLRQKYSKEDI	1115
QY	690	IN--RVLLDAGFTNELVQNYWSKQKNIKGVKARFVYTDGGITRVYPKEAGENQENP	748
Db	1116	SNVRILKSDDDINNLSKQNYFE-----ILLD-----KKQVMDNFQMNIEQNN	1156
QY	749	DSFYKSLNDNVTFTAPYFNKSGPGCVGESGIMVSKAVEIYI-----QGKLLK	796
Db	1157	DKLKEKDLDE-----GAFYELEDNKIIDSITIKETNKENEBELIEYKKLK	1201
QY	797	PAYVGKIDVNSWIE---NFTKTS--IRDFC--AGPYCDCCKRNSDVMDCVILDDGGFL	851
Db	1202	KNNIEINDEMDDIKLLNFFGPIYQSPCEAAQCSYLNKNKNCYDAIISDSDVLVFSG	1261
QY	852	HDYTNQIGRFFGE-----IDPSL---MRHLVNIISV	879
Db	1262	-----KTVIKNFFNKKTVYVEKKAIEEKLGLYQBELINISL	1299
RESULT	15		
I40884			
cytotoxin L - Clostridium sordellii			
C:Species: Clostridium sordellii			
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 15-Oct-1999			
A:Accession: I40884			
R:Greep, G.A.; Schue, V.; Montell, H.			
Gene 161, 57-61, 1995			
A:Title: Cloning and characterization of the cytotoxin L-encoding gene of C			
A:Reference number: I40884; MUID:95369733			
A:Accession: I40884			
A:Status: preliminary; translated from GB/EMBL/DBJ			
A:molecule type: DNA			
A:Residues: 1-2364 <RES>			
A:Cross-references: EMBL:X82638; NID:g1000694; PIDN:CAA57959.1; PID:g1000694			
C:Superfamily: cpl repeat homology			
C:Keywords: cytotoxin			

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C;Species: Clostridium Sordellii
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 15-Oct-1999
C;Accession: I40884
R;Green, G.A.; Schue, V.; Montell, H.
Gene 161, 57-61, 1995
A;Title: Cloning and characterization of the cytotoxin L-encoding gene of Clost
A;Reference number: I40884; MUID:95369733
A;Accession: I40884
A;Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A;Residues: 1-2364 <RES>
A;Cross-references: EMBL:X82638; NID:g1000694; PIDN:CAA57959.1; PID:g1000695
C;Superfamily: cpl repeat homology
C;Keywords: cytotoxin

Query Match          2.7%; Score 155; DB 2; Length 2364;
Best Local Similarity 18.7%; Pred.No.1;
Matches 21; Conservative 13; Mismatches 342; Indels 468; Gaps 57;

QY   12 TLFOSLLIGPSSEPFPSAVTIKSWDKMQEDLVTLAKTAGVNLVDIYEKYQDLTYVE 71
    || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|
Db   1137 TLLDDKIIMPODD-----LVLSRID-FNNNSITLGKC-----EIWRAE 1173

QY   72 PNNARQLVFETIARDIEKLILSNRS----KALYS----LALEAEKVQAHHOWREDPASNEVV 123
    || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|
Db   1174 GGSGHTLTU-----DIDHFFGSPSTYRKPLWISYDVNLKKIKEKI-----DFSKOLMW 1221
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Search completed: July 23, 2001, 07:37:40
Job time: 477 sec

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QY 124 YNABD-----DLDPEKNDSEPGSQRIKP-----VFIEDANFGR- 157
D 1222 LPNAPNRVFGYEMWTGPGFSLD---NDGTLKLDRIHRYEGQFYWRYEAFIADALITKL 1278
QY 158 QISYQHAHVHPTDIVEGSTIVLNLNWTLSALDEYFKKNREEDPSLLQWQVFGSATGLARY 217
D 1279 KRYEDTNRINLDGNTRFIV-----PVIITEQIRKN-----LSYSFYGS--GGSYS 1324
QY 218 YPASPVWDSRTPNKIDLYDVRRRPWYIQGAASPKDMLILVDVSGVSLTKLIRTSVS 277
D 1325 LSLSPVNMN-----IDLNLVENDIW-----VIDVNVKNITIESDEIQKG 1365
QY 278 EMLETLSDDDFVNVSFNSNAODVCFQHLVQAVNRKVKLDAVNNTAK---GITDYK 334
D 1366 ELIENI-----LSKLNIEDNKII---LNNHTINFYGDINESN 1399
QY 335 KGFSFAFEOLLNAN-----VSRA-----NCNKIIMLFTD-----GGEERAQ 370
D 1400 RFISTFSLIEDINIIIEIDLVSRYKILLSGNCKMLIENSDDIOCKIDHIGFNGEHQY 1459
QY 371 EIFN-----KYN-----KDKYRVFRFVSQGHYERGPQIMACENKGYEYIPISGAIR 420
D 1460 IPYSVIDNETKNGFIDYSKKEGLTAEFESNIIIRN--IYMPDSNNLFYSSKDLKDIR 1517
QY 421 INTQEYLDVLRPWLAGDKAQ-----VQWNTNVDLALEGLVITGILP 465
D 1518 IINK-----GDVKLLIGNFYKDDMKVLSFTIEDTNTIKLNGVYLDE-----NGVAQ 1564
QY 466 VFNITQPKENTLNKQLILGVMGVDSLEDIKRLTPRETLCPNGYFFAIDPNGYVLLHP 525
D 1565 ILKFMNNAKSALNTSLSNLFLESNIK-----NIFYNNLDPNIEFILD 1609
QY 526 NLQPKNPKSQEPVTLDFDLAELENDIKVEIRNMIDGSEKFTFTLVKSODERYIDKGN 585
D 1610 NF-----IISGNSIQOFE-LICDKDN-----1631
QY 586 RRYTWTVPNGTDYSALVLPYTSFYIIRAKLEETTOARSKKGMKDSSETLKPDPNFESG 645
D 1632 -----IQP-----YFINFKIKET-----SYTLVVGNRQN-- 1655
QY 646 YTFIAPROYCNDLKISDNTTEFLAFNE---FIDR---KTPNPNFSCHADLIN-----691
D 1656 -LIVEPSTHLDD---SGNISSTVINFSOKYLYGIDRYVKNVILAPNLYTDEINITPVYKP 1711
QY 692 -----RVLLDAGFTNE-----LVQNYW-----SKQKNIKGVKARFVVT 724
D 1712 NYICEVILIDANYINEKINYNININDLSIRYVWDNDGSDLLILIANSEEDNQPOVKIRFV-- 1769
QY 725 DGGITRVYPKEAGE-----NMOENPE-----TYEDSFYKR-----SLDNDNY 761
D 1770 -----NVFKSDTAADKLSFNFSKODSVSKIIISFSLAAYSDFGFEYFGLVSLDND-- 1822
QY 762 VFTAPYFNKSGPGAYESGIMYSKAVEIYIOGKL--LKPAVVGIKIDVNSWIENFTKTSIR 819
D 1823 -----YFYNIFSGNMVSGL-----IYINDSLYTFKP-----PKNNLITGFTTI--- 1860
QY 820 DPCAGPVCDCKRNSDVMCDVILDDGGLFLMANHDDYTNOIGRFFGEIDPISLMRHLWNISV 879
D 1861 -----DGN-----KYFPDPTKSGAASIGEI-----TIDGKD 1886
QY 880 YAFNKSIDYQSVCEPGAAPKOGAGHRSAYVPSVADILOIGMWATAAAMSILQQFLLSLTF 939
D 1887 YFYN-----KOG-----ILOQGVINTSDG---LKYFAPAGTL 1915
QY 940 PRLLAEVEME-----DDDFASLSKSCITEQTOYFFDNDSDKSFSGVLDCG 985
D 1916 DENLEGESVNFIGNIDGKYIYFEDNRYAAV-EWKLDDDETYTFNPKTGEALGLHQIG 1974
QY 986 NCSRIHFHGEKLMNTNLIFI 1004
D 1975 DNKYFFDDNGIMQTGFTTI 1993
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 23, 2001, 07:38:39 ; Search time 66.28 seconds
(without alignments)
563.861 Million cell updates/sec

Title: us-09-397-548-14
Perfect score: 5748
Sequence: 1 MAGCLLTLTLFQSLIG.....IIGIQLLLWLVSSTHRL 1091

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5748	100.0	1091	1	CIC2_HUMAN
2	5505	95.8	1091	1	P54289 rattus norv
3	5503.5	95.7	1106	1	P34290 rattus norv
4	607	10.6	734	1	P3806 oryctolagus
5	194.5	3.4	886	1	P34374 caenorhabdi
6	182	3.2	885	1	Q61704 mus musculu
7	180.5	3.1	887	1	Q06033 homo sapien
8	164.5	2.9	886	1	Q63416 rattus norv
9	161	2.8	1829	1	P37280 mesocricetu
10	159	2.8	1956	1	Q3845 thermococcu
11	157.5	2.7	575	1	Q04956 plasmodium
12	154.5	2.7	946	1	P76481 escherichia
13	152	2.6	1290	1	P19823 homo sapien
14	151.5	2.6	420	1	P18640 clostridium
15	150.5	2.6	921	1	Q5874 synechocyst
16	150	2.6	654	1	P79263 sus scrofa
17	149	2.6	930	1	P34576 bacillus su
18	148	2.6	964	1	Q14624 h interalp
19	144	2.5	1087	1	P30319 choristoneu
20	143	2.5	946	1	P38535 clostridium
21	142.5	2.5	382	1	P97279 mesocricetu
22	141	2.5	1251	1	P34373 caenorhabdi
23	140.5	2.4	935	1	Q00799 plasmodium
24	140	2.4	2710	1	O02668 sus scrofa
25	140	2.4	3305	1	P16154 clostridium
26	139.5	2.4	764	1	Q25490 manduca sex
27	139	2.4	1180	1	P13423 bacillus an
28	139	2.4	1513	1	P16480 bacillus th
29	137	2.4	984	1	P38198 saccharomyc
30	136.5	2.4	3063	1	Q53591 streptococc
31	135.5	2.4	946	1	Q99715 homo sapien
32	134.5	2.3	2077	1	Q61703 mus musculu
33	133	2.3	862	1	P52340 human herpe
					O51737 borrelia bu

34	133	2.3	1323	1	ADRL_YEAST	P07248 saccharomyc
35	132.5	2.3	547	1	SYM_BUCAI	P57210 buchnera ap
36	132.5	2.3	929	1	CAIC_NOTVI	Q91145 notophthalm
37	132.5	2.3	1679	1	Y109_YEAST	P40457 saccharomyc
38	132	2.3	697	1	YE9C_SCHPO	O13773 schizosacch
39	131.5	2.3	1018	1	YC14_METJA	Q58611 methanococc
40	131	2.3	1634	1	DPOL_METJA	Q58295 methanococc
41	131	2.3	1658	1	Y167_YEAST	Q03661 saccharomyc
42	130.5	2.3	987	1	YD94_METJA	Q58789 methanococc
43	129	2.2	1244	1	Y307_MYCPN	P75342 mycoplasma
44	128.5	2.2	1254	1	UBPC_YEAST	P39538 saccharomyc
45	128	2.2	1113	1	Y140_MYCPN	P75033 mycoplasma

ALIGNMENTS

RESULT 1						
CIC2_HUMAN						
ID	CIC2_HUMAN	STANDARD;	PRT;	1091 AA.		
AC	P54289;					
DT	01-OCT-1996 (Rel. 34, Created)					
DT	01-OCT-1996 (Rel. 34, Last sequence update)					
DT	01-OCT-2000 (Rel. 40, Last annotation update)					
DE	DIHYDROXYRIBINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-2/DELTA					
DE	SUBUNIT PRECURSOR.					
GN	CACNA2D1 OR CACNL2A OR CCHL2A.					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=92110010; PubMed=1309651;					
RA	Williams M.E., Feldman D.H., McCue A.F., Brenner R.,					
RA	Velicelebi G., Ellis S.B., Harpold M.M.;					
RT	"Structure and functional expression of alpha 1, alpha 2, and beta					
RT	subunits of a novel human neuronal calcium channel subtype.";					
RL	Neuron 8:71-84(1992).					
CC	- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN					
CC	EXCITATION-CONTRACTION COUPLING					
CC	- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:					
CC	ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS					
CC	HETERODIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).					
CC	- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.					
CC	- TISSUE SPECIFICITY: CENTRAL NERVOUS SYSTEM, SKELETAL MUSCLE AND					
CC	AORTA TISSUES					
CC	- PFM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM					
CC	A PRECURSOR FORM (BY SIMILARITY).					
CC	- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.					
CC	-----					
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration					
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -					
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CC	or send an email to license@isb-sib.ch).					
CC	-----					
DR	EMBL; M76559; AAA51903.1; -					
DR	MIM; 114204; -					
DR	InterPro; IPR002035; -					
DR	Pfam; PF00092; vwa; 1.					
DR	PROSITE; PS50234; VWFA_DOMAIN; 1.					
KW	Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;					
KW	Calcium channel; Glycoprotein; Phosphorylation; Signal.					
FT	SIGNAL	1	24	POTENTIAL.		
FT	CHAIN	25	944	(BY SIMILARITY).		
FT	CHAIN	945	1091	L-TYPE CALCIUM CHANNEL ALPHA-2 SUBUNIT		
FT	TRANSMEM	446	469	L-TYPE CALCIUM CHANNEL DELTA SUBUNIT (BY		
FT	TRANSMEM	906	930	POTENTIAL.		

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FT TRANSMEM 1067 1086 POTENTIAL.
FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 324 324 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 348 348 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 475 475 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 585 585 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 594 594 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 663 663 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 769 769 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 876 876 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 883 883 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 973 973 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 986 986 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 501 501 PHOSPHORYLATION (BY CAPK)
FT MOD_RES 833 833 PHOSPHORYLATION (BY CAPK)
FT MOD_RES 1091 AA; 123183 MW; 2E4E13EE29A47837 CRC64;
FT SEQUENCE 1091 AA; 123183 MW; 2E4E13EE29A47837 CRC64;

Query Match 100.0%; Score 5748; DB 1; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1091; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLTFLQSLIGSPSEPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
DB 1 MAAGCLLALTLTFLQSLIGSPSEPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
QY 61 YEKVODLYTEPNNAROLVETARDIEKLNSRSKALVSLALEAEKVORAAHOREDPASN 120
DB 61 YEKVODLYTEPNNAROLVETARDIEKLNSRSKALVSLALEAEKVORAAHOREDPASN 120
QY 121 EVVYNKADLDPEKNDSEPGSORIKPFVIEDANFGRQISYQAAHVHPIDYEGSTIVL 180
DB 121 EVVYNKADLDPEKNDSEPGSORIKPFVIEDANFGRQISYQAAHVHPIDYEGSTIVL 180
QY 181 NELNWTSALEDEPKKNEEDPSLLQVFGSATGLARYYPASPWWDSNRTNPKIDLYDVR 240
DB 181 NELNWTSALEDEPKKNEEDPSLLQVFGSATGLARYYPASPWWDSNRTNPKIDLYDVR 240
QY 241 RPWYIQGAASPDKMLILVDYVSGVSGTGLKIRTSVSEMLETSDDDFVNVSFNSNAQD 300
DB 241 RPWYIQGAASPDKMLILVDYVSGVSGTGLKIRTSVSEMLETSDDDFVNVSFNSNAQD 300
QY 301 VSCFQHLVQAVNRKKVLDKAVNNITAKGITYDKKGSFAFEQQLNLYNVRANCKITIML 360
DB 301 VSCFQHLVQAVNRKKVLDKAVNNITAKGITYDKKGSFAFEQQLNLYNVRANCKITIML 360
QY 361 FTDGGERAQEIPFNKKNKRVFRFSGOHNVYERGPIONMACENKGYEYIPIGAI 420
DB 361 FTDGGERAQEIPFNKKNKRVFRFSGOHNVYERGPIONMACENKGYEYIPIGAI 420
QY 421 INTQEYLDVLRPMVLAGDRAKQVQWNTNVYLDALGLVITGTLPVNTGQENKTNL 480
DB 421 INTQEYLDVLRPMVLAGDRAKQVQWNTNVYLDALGLVITGTLPVNTGQENKTNL 480
QY 481 NQLILGVMDVDSLEDIKRLTPFTLCPNGYIFAIDPNGVYLLHPNLPKNPKSQEPVTL 540
DB 481 NQLILGVMDVDSLEDIKRLTPFTLCPNGYIFAIDPNGVYLLHPNLPKNPKSQEPVTL 540
QY 541 DFLDAELNDIKVEIRKNMIDGSGEKFTFLVKQSDERYIDKGNRTYTTPVNGTDYSL 600
DB 541 DFLDAELNDIKVEIRKNMIDGSGEKFTFLVKQSDERYIDKGNRTYTTPVNGTDYSL 600
QY 601 ALVLPYTFYIYKAKLEETITQARSKGKMDSETLKPDPNFESGYTFIAPROYCNDLKI 660
DB 601 ALVLPYTFYIYKAKLEETITQARSKGKMDSETLKPDPNFESGYTFIAPROYCNDLKI 660
QY 661 SDNTEFLNFEIDRKTNNPNSCNADLNRLVLLDAGFTNELVQVWSKQNIKGVKAR 720
DB 661 SDNTEFLNFEIDRKTNNPNSCNADLNRLVLLDAGFTNELVQVWSKQNIKGVKAR 720
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DB 661 SDNTEFLNFEIDRKTNNPNSCNADLNRLVLLDAGFTNELVQVWSKQNIKGVKAR 720
QY 721 FVYTDGGITRVYKPEAGENQWENPETYEDSFYKRSLDNDNYVTAPYFNKSGPGAYESGI 780
DB 721 FVYTDGGITRVYKPEAGENQWENPETYEDSFYKRSLDNDNYVTAPYFNKSGPGAYESGI 780
QY 781 MVSKAVEIYIQGLKLLPAPVVGIVGIDVNSWIENFTKTSIRDPACGVPDCCKRNSDVMDCVI 840
DB 781 MVSKAVEIYIQGLKLLPAPVVGIVGIDVNSWIENFTKTSIRDPACGVPDCCKRNSDVMDCVI 840
QY 841 LDGSGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI SVYAFNKSIDYQSVCEPGAAPKQ 900
DB 841 LDGSGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI SVYAFNKSIDYQSVCEPGAAPKQ 900
QY 901 GAGHRSAYVPSVADIIQIGWATAAASIIQQFLLSLTFPRLLAEVEMEDDDFTASLSKQ 960
DB 901 GAGHRSAYVPSVADIIQIGWATAAASIIQQFLLSLTFPRLLAEVEMEDDDFTASLSKQ 960
QY 961 SCITEQTOYFFDNDKSFSGVLDGCGNSRIFHGKELMNTNLI FIMVESKGTCPCDTRLLI 1020
DB 961 SCITEQTOYFFDNDKSFSGVLDGCGNSRIFHGKELMNTNLI FIMVESKGTCPCDTRLLI 1020
QY 1021 QAEQTSQSDGNPCDMVKQPRYKGPVDFVCFDNNVLEDYTDGCGVSGLNPSLMWYIIGIQFLL 1080
DB 1021 QAEQTSQSDGNPCDMVKQPRYKGPVDFVCFDNNVLEDYTDGCGVSGLNPSLMWYIIGIQFLL 1080
QY 1081 WLVSQSGSTHRL 1091
DB 1081 WLVSQSGSTHRL 1091

RESULT 2
CIC2_RAT ID CIC2_RAT STANDARD; PRT; 1091 AA.
AC P54290;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE DIHYDROXYRINDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-2/DELTA
DE SUBUNITS PRECURSOR.
GN CACNA2D1 OR CACNA2A OR CCHL2A.
OC Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92228762; PubMed=1314383;
RA Kim H.L., Kim H., Lee P., King R.G., Chin H.;
RT "Rat brain expresses an alternatively spliced form of the
dihydropyridine-sensitive L-type calcium channel alpha 2 subunit.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:3251-3253(1992).
CC -1- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN
EXCITATION-CONTRACTION COUPLING.
CC -1- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:
ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS
HETERODIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE
SPLICING.
CC -1- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM
A PRECURSOR FORM (BY SIMILARITY).
CC -1- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.
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EMBL; M86621; AAA1088.1; -.
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DR InterPro: IPR002035;
DR Pfam: PF00092; wva; 1.
DR PROSITE: PS0234; WVA_DOMAIN; 1.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Calcium channel; Glycoprotein; Phosphorylation; Signal;
KW Alternative splicing.
FT SIGNAL 1 24
FT CHAIN 25 944
FT CHAIN 945 1091
FT CHAIN 945 1091
FT TRANSMEM 445 468
FT TRANSMEM 906 930
FT TRANSMEM 1067 1086
FT CARBOHYD 92 92
FT CARBOHYD 136 136
FT CARBOHYD 184 184
FT CARBOHYD 323 323
FT CARBOHYD 347 347
FT CARBOHYD 474 474
FT CARBOHYD 584 584
FT CARBOHYD 593 593
FT CARBOHYD 663 663
FT CARBOHYD 769 769
FT CARBOHYD 812 812
FT CARBOHYD 876 876
FT CARBOHYD 883 883
FT CARBOHYD 973 973
FT CARBOHYD 986 986
FT MOD_RES 500 500
FT MOD_RES 833 833
FT SEQUENCE 1091 AA; 123822 MW; 7054907D9D343B34 CRC64;

Query Match 95.8%; Score 5505; DB 1; Length 1091;
Best Local Similarity 95.3%; Pred. No. 0;
Matches 1040; Conservative 26; Mismatches 23; Indels 2; Gaps 2;

Qy 1 MAAGCLLATLTLSQSLIGSPSEPPSPVYIKSWDKMQEDLVTLAKTASGVNQLVDI 60
Db 1 MAAGCLLATLTLSQSLIGSPSEPPSPVYIKSWDKMQEDLVTLAKTASGVYQLADI 60

Qy 61 YEKQDLYTVEPNARQLVETAEARDIEKLLNSRKALVSLALEAEKVAQAQHWREDFASN 120
Db 61 YEKQDLYTVEPNARQLVETAEARDIEKLLNSRKALVRLAMEAEKVAQAQHWREDFASN 120

Qy 121 EWYVYNAKDDLDPEKNDSEPGSQRIKPVIEDANFGROIYSQHAHVHTPTDIYEGSTIVL 180
Db 121 EWYVYNAKDDLDPEKNDSEPGSQRIKPVIEDANFGROIYSQHAHVHTPTDIYEGSTIVL 180

Qy 181 NELNWTALDEVFVKKNREDEPDLWQVFGSATGLARYYPASFWVDNSRTPNKIDLYDVR 240
Db 181 NELNWTALDEVFVKKNREDEPDLWQVFGSATGLARYYPASFWVDNSRTPNKIDLYDVR 240

Qy 241 RPWTIOGAASPKMILVDSVSGSLTKLIRTSVSEMLETSDDDFVNVAASNQAQ 300
Db 241 RPWTIOGAASPKMILVDSVSGSLTKLIRTSVSEMLETSDDDFVNVAASNQAQ 300

Qy 301 VSCFQHLVQANRKNVVKLVKDAVNITAKGIDYKKGFSFAEQLLNYSRANCKIIML 360
Db 301 VSCFQHLVQANRKNVVKLVKDAVNITAKGIDYKKGFSFAEQLLNYSRANCKIIML 360

Qy 361 FTDGEERAQEIFKNKDKKVRFRFSVQGHNYERGPQIOWACENKGYEIPISGAIR 420
Db 361 FTDGEERAQEIFKNKDKKVRFRFSVQGHNYERGPQIOWACENKGYEIPISGAIR 420

Qy 421 INTQEYLDVLRPMVLADGKAKQVQWNTNVLDALEGLVITGTLPTFNITQGFENKTNLK 480
Db 421 INTQEYLDVLRPMVLADGKAKQVQWNTNVLDALEGLVITGTLPTFNITQGFENKTNLK 480

Qy 481 NQLILGVMGVDVSLIEDIKRLTPRTLCPNGYIFAIDPNGYVLLHPNLQPKPKSQEPVTL 540

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Db 480 NQLILGVMGVDVSLIEDIKRLTPRTLCPNGYIFAIDPNGYVLLHPNLQPKPKSQEPVTL 539
Qy 541 DFLDAELENIDKVEIRNKMIDGESGEKTRTLVKQSDERYIDKGNRTYTWTPVNGTDS- 599
Db 540 DFLDAELENIDKVEIRNKMIDGESGEKTRTLVKQSDERYIDKGNRTYTWTPVNGTDS- 599
Qy 600 LALVLPYTSFYIYKAKLETTQARSKKGMKDSSETLPDNPFEESGYTFIAPRDYCNLJK 659
Db 600 LALVLPYTSFYIYKAKLETTQARSKKGMKDSSETLPDNPFEESGYTFIAPRDYCNLJK 659
Qy 660 LSNNTTEFLANFNERIDRKTNNPCNADLNRLVLLDAGFTNELVQNTWSKOKNKGKVA 719
Db 660 LSNNTTEFLANFNERIDRKTNNPCNADLNRLVLLDAGFTNELVQNTWSKOKNKGKVA 719
Qy 720 RFVVTDDGTRVYPKEAGENQENPETYEDSFYKRSNDNDNTVFTAPYFNKSGPGAYESG 779
Db 720 RFVVTDDGTRVYPKEAGENQENPETYEDSFYKRSNDNDNTVFTAPYFNKSGPGAYESG 779
Qy 780 IMVSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPCAGPVCDCRNSDVMDCV 839
Db 780 IMVSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPCAGPVCDCRNSDVMDCV 839
Qy 840 ILDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNSVYAFNKSIDYQSVCEPGAAPK 899
Db 840 ILDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNSVYAFNKSIDYQSVCEPGAAPK 899
Qy 900 QGAGHRSAYVPSVADILQIGWATAAASIIQQFLLSTFPRLLEAVEMEDDDFTASLSK 959
Db 900 QGAGHRSAYVPSVADILQIGWATAAASIIQQFLLSTFPRLLEAVEMEDDDFTASLSK 959
Qy 960 QSCITEQTYQYFFDNDKSFSGVLDGCGNSRIFPHGKLMNTNLIFIMWESKGCPCDTRL 1019
Db 960 QSCITEQTYQYFFDNDKSFSGVLDGCGNSRIFPHGKLMNTNLIFIMWESKGCPCDTRL 1019
Qy 1020 IOAETSQDPNPNQKVPYKRGPDVCFDNNVLDYTDGCGVSGLNPSLWYIIGIQFL 1079
Db 1020 IOAETSQDPNPNQKVPYKRGPDVCFDNNVLDYTDGCGVSGLNPSLWYIIGIQFL 1079
Qy 1080 LWLVSQSGTHRL 1090
Db 1080 LWLVSQSGTHRL 1090

RESULT 3
CIC2_RABIT STANDARD; PRT; 1106 AA.
AC P13806;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-2/DELTA
DE SUBUNITS PRECURSOR.
GN CACNA2D1 OR CACNL2A OR CCHL2A.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88336904; PubMed=2458626;
RA Ellis S.B., Williams M.E., Ways N.R., Brenner R., Sharp A.H.,
RA Leung A.T., Campbell K.P., McKenna E., Koch W.J., Hui A.,
RA Schwartz A., Harpold M.M.;
RT "Sequence and expression of mRNAs encoding the alpha 1 and alpha 2
RL subunits of a DHP-sensitive calcium channel.";
RL Science 241:1661-1664(1988).
RN [2]
RP SEQUENCE OF 961-973.
RX MEDLINE=91131638; PubMed=1847144;
RA Jay S.D., Sharp A.H., Kahl S.D., Vedvick T.S., Harpold M.M.,
RA Campbell K.P.;
RT "Structural characterization of the dihydropyridine-sensitive calcium

```


154 YTLPTSSVSAVIHPIPLDRNEDLLRKIDW--SDIDAVYTNREETKDLAQFLFCSEAGY 213
 QY ARYPASPWW-DNSRTPNKIDLYDVRRRPWPYIOGAASPKDMLILVDVSGSLGTLKLIR 273
 Db :
 213 MRYVPAAASFWDNQ--DEHLDFDCRNTEWYINSATSKNVYLIMLDSMGSMIGORVEAK 270
 QY TSVSEMLETLSDDDFVNVAFSFNSA---QDVSCFOHLVQANWNKKVLKDVAVNNTAKGI 330
 Db :
 271 QTTEALLETLSHDNYFNIMTFSKNTETLLDGCNGTGLLOATMNRKALKRMKMDTYOSEG 330
 QY TDYKKGFSFAFEOLLNVN-----VSFRANCNKIITMLFTDGGEERAQEIFKNYNKDKKRVVF 385
 Db :
 331 AEYEKALPAFVSLLDINNGGDNNGRGACENVITMLITDGNAPYAKKIFDMYNADKKRVVF 390
 QY RFSVGQHNYERGPDIOMMACENKGYEIPSIIGAIRINTOEYL-----DVLGRPMVLADKA 441
 Db :
 391 TFLVGDEAIDEFNEVREMCAANNRCMYHVHANMAADVDEKIHHYIRMSRVVGRHYKESGQLS 450
 QY KQOWTNVYLDLELGL--VITGTLPVNITGTFENKTN-----DVLGRPMVLADKA 478
 Db :
 451 --WTGVYRERYLPRPEIFAEPVPIQTQSFAVMNKMARRIRLQKSEARSMEFVTIV 507
 QY ---LNKOLLISGMVGVDVSLIEDIKRLTPRTCLPCNGYYEFAIDPNGVYLLHPNLQPNP-- 532
 Db :
 508 SYPVIVNETFMGVAANIPLUTEVAQKSHPANIGSKSYFFMLDQNGFVTHPQRDPDPFT 567
 QY --KSQBPVTLDFLD-----AELENDIKVIERINKMID 561
 Db :
 568 KYHKQNVNNMDLLELVGQONVRSQKSQAVSDLVCESGANVAECVDDLRAKAVRKMID 627
 QY GESGEKFTRLVKSQDERY----IDK---GNRIYTTPVNGTDYSIALVLPPTYSFYYIKA 614
 Db :
 628 CDNSD-----VOOLDVLVATELLDRVYPTQNTYYAACINHANFVLGLAVAKGGDDYRVVK 681
 QY KLEETITQARSKKKGMMK 631
 Db :
 682 K-----QKYDFGRVK 692

RESULT 5
 ITH3_MOUSE STANDARD; PRT; 886 AA.

ID	ITH3_MOUSE	STANDARD;	PRT;	886 AA.
AC	Q61704;			
AD	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3).			
GN	ITI H3.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-C57BL/6N; TISSUE=Liver;			
RA	MEDLINE=95194326; PubMed=7534067;			
RX	Chan P., Risler J.-L., Raguenez G., Salier J.-P.;			
RT	"The three heavy-chain precursors for the inter-alpha-inhibitor family in mouse: new members of the multicopper oxidase protein group with differential transcription in liver and brain."			
RL	Biochem. J. 306:505-512(1995).			
CC	- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,			
CC	INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY SIMILARITY).			
CC	- SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN.			
CC	BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2 AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.			

CC -1- TISSUE SPECIFICITY: EXPRESSED IN BOTH LIVER AND BRAIN.
CC -1- PPM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
CC 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ITIH FAMILY.
CC -1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
CC
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CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X70393; CAA49843.1; -
DR MGD; MGI:96620; Itih3.
DR InterPro: IPR002035; -
DR Pfam: PF00092; vwa; 1.
DR PROSITE: PS0234; VWFA_DOMAIN; 1.
KW Serine protease inhibitor; Repeat; Signal; Multigene family;
KW Glycoprotein. 1 18
FT SIGNAL 19 30
FT PROPEP 19 30
FT CHAIN 31 646
FT
FT PROPEP 647 886
FT DOMAIN 279 439
FT CARBOHYD 88 88
FT CARBOHYD 577 577
FT BINDING 646 646
FT
FT SEQUENCE 886 AA: 98977 MW: 159553087 P5030A CRC64;
SQ
Query Match 3.4%; Score 194.5; DB 1; Length 886;
Best Local Similarity 19.9%; Pred. No. 0.00081;
Matches 185; Conservative 138; Mismatches 347; Indels 261; Gaps 44;
QY 27 FPSAVTIKSWDKMDELVTIAKTASGVNQLVDIYEKQDLYTVPEPNARQLVETAAARDI 86
DB 98 YPGNKEREVAQKQYKAVSOCKTAG----LVKASGRKLEKFTVSVNVAAGSKVTFELTY 153
QY 87 EKLNSRKALVSLAEAFKQAAHQWREDFASNEVYVNAKDDLDPEKNDSEPGSORIK 146
DB 154 EELL-KRNGKYMELTKVQKOLVRHEID-----AHIFEP-----Q 189
QY 147 PVFIEDANFGQISYQAAHVIPTDIYEGSTIVLNELNWTSALEDEVFKKNREEDPSLLWQ 206
DB 190 GISMLDAE-----ASFITNDL-LGSALTFSF----- 214
QY 207 VEGSATGLARYYPASPWDNSFT-PNKKID-----LYDVRRRP-----WYI-- 245
DB 215 -----SGKKGHVSFRPSLDQQRSCPTCTDLSLLGDFITVDVNRSPGNVQIVNGYFVHF 269
QY 246 ---QG-AASPKDMLILDVSGSVGLTKLRTSVSEMLETSLDDDFYNVASFNSNAODV 301
DB 270 FAPQGLVPVPRKIVFIDVSGSGSRKKIQOTREALTKLDDVKEDDYLNFLFST-----DV 326
QY 302 SCFQ-HLVQANRNKKVLKDAYNNITAKGIDYKKGFSFAFQQLLNYNVSRAN-----C 354
DB 327 TTKDKHLVQATPANLKEAKTFVKNIDHOSMTNINDGLKGIEML---NKAREDHVTPERS 383
QY 355 NKIIMFLTDG-----GEERAQEIFNKYNK--DKKVRVFRFSVQGHNYERGPQIMACENKG 408
DB 384 TSIITMLTDGDANTGESRPEKIQENVRNAIGKFFLYNLGFG-NNLNLYNFLTLELHNG 442
QY 409 YVEPSPGAINIQEYLDVLRGPNVLGAKQVQWNTVYLDALGLL--VITGTLPV 466
DB 443 LARRIYEDSANLQOGFYEEVANELL-----TNVEVEYPENALDLTRNSYPH 491
QY 467 FNIITQGFENKTNLKNQLIILGVNGVDSVLEDIKRLTPRTLCPNGYFFAIDPNGYVLLHPN 526

DB 492 F-----YDG-----SEIVVAGRLVDRNMDN-----FKADYKVGHGALN-- 523
QY 527 LQPNPKSQEPVTLDFDAELNDIKVEIRNKNMIDGESGEK--TERTLVKSODERYIDKG 584
DB 524 ----DLTFTEEDVMEEMDAALK-----EQYIFGDYIERLWALYLTIOLEKRNKAG 572
QY 585 NRTYTWTPVNGTDSLAL--LVLPYTSFYIYIAKLSETITQARSKKGMKDSSET-----LK 637
DB 573 DEKENIT-AEALDLSLKYHFVTPLTSMVTKPEDNEDQTSIADNAGEEAFATTTMSFLT 631
QY 638 PDNTEESGYTIAPRDYCNLDKISDNTEFLNFEFIDRKTPNPNPSCNADLINVLDA 697
DB 632 TQSSQSPYYV-----DGDPHFIIQI-----PGKNDSCICFVDEKRP 668
QY 698 GFTNELVQYNSKQKNGKARFVVTDGRTVRYPKAGENNQENPENIYEDSFYKRSID 757
DB 669 GTVLRLLIQD-----PVT--GIT-VTQIIIGD-----KRS-- 694
QY 758 NDNYVFTAPYFNKSGPGAYESGIMYSKAVEIYIOGKLLKPAVVGKIDVNSWIEFTKTS 817
DB 695 NASSRTGKTYFGKLGITNAWMDFRVEVTEKIILG-----TGAELSTFSWLDFTVVTQ 747
QY 818 IRDPCAGPVCDCKRNSDVMDVILDDG-GFLLMAN-----HDDYTNQICGRFGEIDP 868
DB 748 ----TGLSVTINRKNMV--VSFGDGISFVILHQVWKKHPVHQDFLG-----FYWDS 795
QY 869 SLMRHLVNISYAFNKSVDYQSV-CEPGAAP 898
DB 796 HRMSAQTHGLLGQFFQFDFKVGIRPGSDP 826
RESULT 6
ITIH3_HUMAN
ID ITIH3_HUMAN STANDARD; PRT; 885 AA.
AC Q06033; Q99085;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY
DE CHAIN H3) (SERUM-DERIVED HYALURONAN-ASSOCIATED PROTEIN) (SHAP).
GN ITIH3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC TISSUE=Liver;
RX MEDLINE=93215656; PubMed=7681778;
RA Bourguignon J., Diarra-Mehrpour M., Thiberville L., Bost F.,
RA Sesboue R., Martin J.P.;
RT "Human pre-alpha-trypsin inhibitor-precursor heavy chain. cDNA and
RT deduced amino-acid sequence."
RL Eur. J. Biochem. 212:771-776(1993).
RN [2]
RC TISSUE=Liver;
RX MEDLINE=89137072; PubMed=2465147;
RA Diarra-Mehrpour M., Bourguignon J., Sesboue R., Mattei M.-G.,
RA Passage E., Sallier J.P., Martin J.P.;
RT "Human plasma inter-alpha-trypsin inhibitor is encoded by four genes
RT on three chromosomes."
RL Eur. J. Biochem. 179:147-154(1989).
RN [3]
RC TISSUE=Liver;
RX MEDLINE=89380192; PubMed=2476436;
RA Enghild J.J., Thøgersen I.B., Pizzo S.V., Salvesen G.;
RT "Analysis of inter-alpha-trypsin inhibitor and a novel trypsin
RT inhibitor, pre-alpha-trypsin inhibitor, from human plasma."
RL J. Biol. Chem. 264:15975-15981(1989).
RN [4]
RC TISSUE=Liver;
RX MEDLINE=91093267; PubMed=1898736;

DR Pfam: PF00092; vwa: 1.
DR PROSITE: PS50234; VWFA_DOMAIN: 1.
KW Serine protease inhibitor; Repeat; Signal; Multigene family;
KW Glycoprotein.
FT SIGNAL 1 21 POTENTIAL.
FT PROPEP 22 33 BY SIMILARITY.
FT CHAIN 34 647 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN
FT FT
FT FT
FT PROPEP 648 887 BY SIMILARITY.
FT DOMAIN 282 442 VWFA.
FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 580 580 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT BINDING 647 647 CHONDROITIN 4-SULFATE, CROSS-LINK SITE
FT (BY SIMILARITY).
SQ SEQUENCE 887 AA; 99097 MW; 389F0FF96D514096 CRC64;

Query Match 3.1%; Score 180.5; DB 1; Length 887;
Best Local Similarity 18.5%; Pred. No. 0.0052;
Matches 173; Conservative 139; Mismatches 350; Indels 275; Gaps 39;

QY 27 FPSAVTIKSWDKQEDLVTLAKTAGSNVQLVDIYEKQDLYTVEPNARQVLEAARDI 86
DB 101 YPGSVKEEVAQKQYKAVSQGKTAG---LVKASGRKLEKFTSVNVAAGSKVIFELTY 156
QY 87 EKLNSRKALYSALAEKVAQAAHQRD---FASNEVVYVNAKDDLDPEKNDSEPGSQ 143
DB 157 EELL-KRNGKYEYKQPKQVLPKQVLPKQVLPKQVLPKQVLPKQVLPKQVLPKQVLP 199
QY 144 RIKPFIEDANFGROISYOHAAVHIPTDIYEGSTIVLNELNWTLSALDEVFKKNREEDPSL 203
DB 200 -----DASE-----ITNDL-LGSALTKSF----- 217
QY 204 LKQVFGSATGLARYPASVWNSRT-PNKID-----LYDVRRP-----WY 244
DB 218 -----SGKKGHSFVPSLQDQSCPTCTDSLLNGDFTIYDVNRESPGNVQVNGYF 269
QY 245 I-----QG-AASPDKMLIYDVGSGVGLTLRTSVSEMETLSDDDFVNVAFSNSA 298
DB 270 VHFAPQGLPVVPKNIAFVIDVSGMSGKRIQOTREALKILDDMKEDYLFILFSTGV 329
QY 299 QDVSCFQHLVQANRNVKYLKDAVNITAKGTIDYKKGFSAFEOELNLYNVRAN----- 353
DB 330 --TWKDLHLVKATPANLEEARAFVKNIRDSNTNINDGLLRIEML--NKAREHLVPE 384
QY 354 -CNKIIMLTG-----GEERAQEIFKNKKVRFPSVG-QHNYERGPQWACENK 407
DB 385 RSTSLVMTLDGANTGESRPEKIOENVRNAIRGKFPYLNGLFGNNLNFLESALENH 444
QY 408 GYVEIPTSIGAIRINTQVLDVLRPMVLGAKQVQVNTVYLDLLEGL--VITGTLPL 465
DB 445 GFARRIYEDSASLOQGYEEVAPLL-----TNELEYEPENAILDTRNSYP 493
QY 466 VFNITQFENKTNKQLILYGVGVDSLEDIKRLTPRTCPNGYFAIDPNGYVLLHP 525
DB 494 HP-----YGV-----SEIVVAGRLVDRVND-----FRADYKVGHCALN- 526
QY 526 NLOPKNPKSQEPVTLFDLAELENDIKVEIRNMIDGESGKTF-----RTLVKSQDER 579
DB 527 -----DLTTEEDVMKEMDAALK-----EQGYIFGDYIRLWAYLTIEQLLEKRNAR 574
QY 580 YIDKGNRTVTPVNGTDSL--LVLPYSFYIKAKLEETITQARSKGKMKSET-- 635
DB 575 GDEKENIT-----AEALESLKSYHFVTLPTLSMVTVPEDNEQDTAIDRPGEAISASTA 629
QY 636 -LAKPDNFEESGTFIAPRCDNKLKSDNNTPELLNF---NEFIDRKTNPNSCADNLLN 691
DB 630 YLTSQOSSHSPIYIY-----DGDHPFTIQVPGKNDITICNIDEKPGCTVLUSLIQ 677
QY 692 RVLIDAGFTNELQVYWSKQKNIKGVKARFVVDGGITRVYKRAENQENPETYEDSF 751
DB 678 DPTGIATVQII-----GEKGNASSTRCKT----- 704

QY 752 YKRLDNDNVFTAPYFNKSGPGAYESIMVSKAVEIYIOGKLLKPAVVGIKIDVNSWIE 811
DB 705 -----YFGKLGIANAWMDFRIVETEKILGN-----GDALSTFSWLD 742
QY 812 NFTKYSIRDCAGPVCDCRNSDVMDCVILDDG-GFLMAN-----HDDYTNQIGRF 862
DB 743 TTVTVTQ-----TGLSVTINRKNMV--VSFEDGISFVILVHQVWKKHVPVHQDFLG----- 790
QY 863 FGEIDPSLMRHLNLSVYAFNKSVDYQSV-CEPGAAP 898
DB 791 FYVDVSHRMSAQTHGLLGQFFQFPDFKVDVVRPGSDP 827

RESULT 8
ITH3_MESAU STANDARD; PRT; 886 AA.
ID ITH3_MESAU
AC P97280;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3) (HC3).
GN ITH3.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=97420688; PubMed=9276673;
RA Nakatani T., Suzuki Y., Yamamoto T., Sinohara H.;
RT "Molecular cloning and sequencing of cDNAs encoding three heavy-chain precursors of the inter-alpha-trypsin inhibitor in Syrian hamster: implications for the evolution of the inter-alpha-trypsin inhibitor heavy chain family";
RT J. Biochem. 122:71-82(1997).
RL -I- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY SIMILARITY).
CC -I- SUBUNIT: I-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN, BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2 AND BIKUNIN. INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.
CC -I- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN 4-SULFATE BRIDGE TO THEIR C-TERMINAL ASPARTATE (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE ITH FAMILY.
CC -I- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
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CC EMBL: D89287; BAA13940.1; -
CC InterPro: IPR002035; -
DR Pfam: PF00092; vwa: 1.
DR PROSITE: PS50234; VWFA_DOMAIN: 1.
KW Serine protease inhibitor; Repeat; Signal; Multigene family;
KW Glycoprotein.
FT SIGNAL 1 18 POTENTIAL.
FT PROPEP 19 30 BY SIMILARITY.
FT CHAIN 31 646 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3.

Db 867 NGEVFKVIGETIDRYMEQKDKVTDVNTDTEVLEVDNIFAFSLNKESSKSEIKVKAL-- 924

QY 723 VTDGGITRYPKPEAGE 738

Db 925 -----IRHKYGEAYE 935

RESULT 10

ATX1_PLAFA STANDARD; PRT; 1956 AA.

AC Q04956;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE PROBABLE CATION-TRANSPORTING ATPASE 1 (EC 3.6.1.-).

OS Plasmodium falciparum.

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

OX NCBI_TaxID=5833;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=T9/96;

RX MEDLINE=93132070; PubMed=8421054;

RA Krishna S., Cowan G., Meade J.C., Wells R.A., Stringer J.R.,

RA Robson K.J.;

RT "A family of cation ATPase-like molecules from Plasmodium falciparum";

RL J. Cell Biol. 120:385-398(1993).

CC -/- CATALYTIC ACTIVITY: ATP + H₂O -> ADP + ORTHOPHOSPHATE.

CC -/- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

CC -/- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2 ATPASES). SUBFAMILY V.

CC -----

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CC -----

DR EMBL: X65738; CA446646.1; -

DR InterPro: IPR001757; -

DR Pfam: PF00122; E1-E2_ATPase; 4.

DR PROSITE: PS00154; ATPASE_E1_E2; 1.

KW Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding.

FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 36 58 POTENTIAL.

FT DOMAIN 59 61 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 62 80 POTENTIAL.

FT DOMAIN 81 407 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 408 427 POTENTIAL.

FT DOMAIN 428 440 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 441 462 POTENTIAL.

FT DOMAIN 463 1818 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 1819 1837 POTENTIAL.

FT DOMAIN 1838 1845 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 1846 1863 POTENTIAL.

FT DOMAIN 1864 1881 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 1882 1905 POTENTIAL.

FT DOMAIN 1906 1928 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 1929 1952 POTENTIAL.

FT DOMAIN 1953 1956 CYTOPLASMIC (POTENTIAL).

FT MOD_RES 496 496 PHOSPHORYLATION (PROBABLE).

FT METAL 1760 1760 MAGNESIUM (BY SIMILARITY).

FT METAL 1764 1764 MAGNESIUM (BY SIMILARITY).

FT DOMAIN 246 251 POLY-ASN.

FT DOMAIN 252 256 POLY-LYS.

FT DOMAIN 937 941 POLY-ASN.

FT DOMAIN 1344 1347 POLY-LYS.

FT DOMAIN 1363 1372 POLY-ASN.

FT DOMAIN 1680 1684 POLY-ASN.

SEQUENCE 1956 AA; 230285 MW; AE708AAE99009335 CRC64;

Query Match 2.8%; Score 159; DB 1; Length 1956;

Best Local Similarity 17.1%; Pred. No. 0.29;

Matches 179; Conservative 144; Mismatches 359; Indels 366; Gaps 45;

QY 58 VDIYEKYQDLYTVEPNNAQVLEIAARDIEKLKLSNR-----SKALVSLALEAEK 106

DB 100 INVY-RYNTSYIISSS-----ELVPGDIYEIKNNMTIPCDTIILSGSVTMEHMLTGES 152

QY 107 VQAQHQRWEDFASNEVYVNAKDDLDPEKD-----SEPGSORIKPVFIEDANFGROIS 160

DB 153 V-PIHKERLPFEGNAIINKNNKYSNDEKDDYLRYYNNHASINMIKRNHILIEETLCKKDR 211

QY 161 YQHAHVHIPTDIYEGSTIVLNELNW-TSALDEVFKNREEDPSLLMQVFGSATGLARYTP 219

DB 212 EYKSNTH-----DLCSMNLKYINNTYDDVHKNNKMD-----244

QY 220 ASPWVDNSTPNKIDLYVRRRPWTIQGA-ASPKOMLILVDVSGSVGLTKLIRTSVSE 278

DB 245 ---YNNNNNNKKKKINLN---FVKGTIINSNLLY-----275

QY 279 MLETISDDDFVNVASFNSNAQDVSCFOHLVQANVRNKKVLDKAVNNITAKGITDYKKGFS 338

DB 276 -----DDKIGVNIPE---DDVNNMKH---KFNQRNINYNKDTNNL-----EYNNKIR 317

QY 339 FAFEOQLLYNVSRANCKIIMLTGDEGERAOFIFKNYKNKDKKRVRFVSQGHNYERG 398

DB 318 YIYDCLLKKEVAISQKNKIY-----SNEDINKY-----346

QY 399 IOWMACENKGYEYIETPSIGAIRNQYLDVIGRPVLAG-----DRAKQV 444

DB 347 ----MLYGGTYVLSYLNKINKNKKEENRIIGL-VIKTGFITTKGIVNNILYHKKEL 401

QY 445 QWTVYVLDALGLVLTGTLVPFNTIGQFENKTLNKLILG-----V 487

DB 402 NLINDSYKELII-LIYALFVSFVILYILSNNETNHHIIKCLDIITDAIPALPTILT 460

QY 488 MGVDSLEDKRLTPRTICPGNYIFA-----IDPNGYVLLHPNLQ-----PKMKPSQ 535

DB 461 VGISAISSLKKKFSICSLCPHKINAGIINTWVFDKGT-TLTENNLFQIGIITQNKKN 519

QY 536 EPVTLDFDAELENDIKVEIRKNKIDGESGEKTFRLVLVSQDERYIDKGNRYTWTVPNG 595

DB 520 NMLS-DFIHIK-----EMNTESIYHSKDDNNIHNKN-----549

QY 596 TDSLALVLTPTSYFYIKAKLEETITQARSKGKMKD-----SETLKPDPNEESG 645

DB 550 -----SIIEYIKDNMKNLHTSSK-KKSITKERSNFLVQTIKSCLLKDHYIKEKK 599

QY 646 YTFIAPRDYCNLKIISDNN-TEFLN-----FNEF--IDRKTNNPNSCNADILNVLVD 696

DB 600 KEYTNTNTYCNLHINDSTCSSYLLNSETKDAYCEYINIDH-----LCD---INKNMD 650

QY 697 AGFTNELVQYWSKQKNIGKVARFVVTGGITRVYPKAGENQWQENPETEYDSFKRSL 756

DB 651 INSKNELMGKYSKNELMGTKITNELM-----GKYSKNEL 684

QY 757 DNDNYVFTAPYFNKSGPAYESIMVSKAVEIYIOGKLLKPAVVG-----IKIDVNSWI 810

DB 685 -----MGKYSKNELMGKYSKNELMGKYSKNELMGKYSKNELMGKYSKNELMGKYSKNEL 737

QY 811 ENFTKTSIRD-PCAGPVCDCKRNSDYMDCV-----ILDDGGFLMANHDDYTNIGRF--- 862

DB 738 MNCNDNYNDYPCD---YNNCNCNDYTHRLEYHNINKDSNFSNIPPEKNKSYNNISEHIKI 794

QY 863 -----FGEIDPSLMRHLNIVSVAF-----NKSIDYQ 889

DB 795 NYPLLEALACCHTILSKVNNKIMGDVLEILMFNTNCDMLNNNSFIIEKKKNCSDYEQ 854

QY 890 SVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAANSILOQFLSLTFLPRLEAVE 949

DB 855 KI---DGDKNIGANDERCHLNN-----NLSYNNILKRF-----884

ID AC BXCL_CLOBO STANDARD; PRT; 1290 AA.
DT P18640;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE BOTULINUM NEUROTOXIN TYPE C1 PRECURSOR (EC 3.4.24.69) (BONT/C1)
DE (BONTXILYSIN C1).
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1491;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90370487; PubMed=2204031;
RA Hauser D., Eklund M.W., Kurazona H., Binz T., Niemann H., Gill D.M.,
RA Boquet P., Popoff M.R.;
RA "Nucleotide sequence of Clostridium botulinum C1 neurotoxin.";
RL Nucleic Acids Res. 18:4924-4924(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=TYPE C STOCKHOLM / C-ST;
RX MEDLINE=91024998; PubMed=2222445;
RA Kimura K., Fujii N., Tsuzuki K., Murakami T., Indoh T.,
RA Yokosawa N., Takeshi K., Syuto B., Oguma K.;
RA "The complete nucleotide sequence of the gene coding for botulinum
RT type C1 toxin in the C-ST phage genome.";
RL Biochem. Biophys. Res. Commun. 171:1304-1311(1990).
RN [3]
RP SEQUENCE OF 2-25.
RC STRAIN=TYPE C STOCKHOLM / C-ST;
RX MEDLINE=88153072; PubMed=2450068;
RA Tsuzuki K., Yokosawa N., Syuto B., Ohishi I., Fujii N., Kimura K.,
RA Oguma K.;
RA "Establishment of a monoclonal antibody recognizing an antigenic site
RT common to Clostridium botulinum type B, C1, D, and E toxins and
RT tetanus toxin.";
RL Infect. Immun. 56:898-902(1988).
RN [4]
RP IDENTIFICATION OF SUBSTRATE.
RX MEDLINE=94038966; PubMed=7901002;
RA Blas J., Chapman E.R., Yanasaki S., Binz T., Niemann H., Jahn R.;
RA "Botulinum neurotoxin C1 blocks neurotransmitter release by means of
RT cleaving HPC-1/syntaxin.";
RL EMBO J. 12:4821-4828(1993).
CC -|- FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER
CC RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED
CC AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD
CC WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT
CC INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
CC ENDOPEPTIDASE THAT CLEAVES SYNTAXIN.
CC -|- SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAIN (L) AND A
CC HEAVY CHAIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL ACTIVITY,
CC WHILE THE N- AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE CHANNEL
CC FORMATION AND TOXIN BINDING, RESPECTIVELY.
CC -|- SUBCELLULAR LOCATION: SECRETED.
CC -|- MISCELLANEOUS: THERE ARE SEVEN ANTIGENICALLY DISTINCT FORMS OF
CC BOTULINUM NEUROTOXIN: TYPES A, B, C1, D, E, F, AND G.
CC -|- MISCELLANEOUS: BOTULINUM TYPE C1 NEUROTOXIN IS SYNTHESIZED BY C
CC STRAIN OF CLOSTRIDIUM BOTULINUM WHICH CARRY THE APPROPRIATE
CC BACTERIOPHAGE.
CC -|- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27 (ZINC
CC METALLOPROTEASE); ALSO KNOWN AS THE TETANUS/BOTULINUM NEUROTOXIN
CC SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X66433; CAA47060.1; -

DR EMBL; X72793; CAA51313.1; -
DR EMBL; X53751; CAA37780.1; -
DR EMBL; D90210; BAA14203.1; -
DR EMBL; X62389; CAA44263.1; -
DR PIR; S11291; S11291.
DR PIR; A35396; A35396.
DR PIR; A43503; A43503.
DR MEROPS; M27.002; -
DR InterPro; IPR000130; -
DR InterPro; IPR000395; -
DR Pfam; PF01742; Peptidase_M27; 1.
DR PRINTS; PR00760; BONTXILYSIN.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc.
FT INIT_MET 0
FT CHAIN 1 448 BOTULINUM NEUROTOXIN C1, LIGHT-CHAIN.
FT METAL 449 1290 BOTULINUM NEUROTOXIN C1, HEAVY-CHAIN.
FT METAL 228 228 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 229 229 BY SIMILARITY.
FT METAL 232 232 ZINC (CATALYTIC) (BY SIMILARITY).
FT DISULFID 436 452 INTERCHAIN (PROBABLE).
FT CONFLICT 84 84 P -> T (IN REF. 2).
SQ SEQUENCE 1290 AA; 148734 MW; 71FBE379F97129E8 CRC64;

Query Match 2.6%; Score 152; DB 1; Length 1290;
Best Local Similarity 20.3%; Pred. No. 0.4;
Matches 205; Conservative 125; Mismatches 346; Indels 334; Gaps 54;

QY 106 KVOAAHQWREDFASNEVYVYNAKDDLDPEKNDSEPGSQRK---PVFIEDANFGR----- 157
DB 138 KTRQNNVWKGSIINPSVIITG-----PRENIIDETSTFKLTNTTFAAQEGFGALSIIS 192
QY 158 -----QISYQHAAVAHIPTDIYEGS-----TIVLNELNMTSALDEVFK---KNRE 198
DB 193 ISPREMLYSNAT---NDVGEGRFSKSEFCMDPILILMHELN--HAMHNLGYAIPNDQ 246
QY 199 EDPSSLQWFGSATGLARYP-----ASPVDNSTPKKIDLYVRRRPWYTOGAASPKD 253
DB 247 TTSSTVTSNIFYSQYNVWLEYAEIYAFGGPTID--LIPKSARKYFEKALDYRSKRLN 304
QY 254 MLILVDVSG---SVSGSLTLKLIR-----TSVSEMLETLSDDDFYNVASFNADVSCF 304
DB 305 SITTANPSFNKYIGEYKOKLIRKYRFVVESSGEV--TVNRKRFVEL--YNELTOIFTEF 360
QY 305 QHLVQAQYRNKKV-LKDAVNNTAK---GITDYKKGFSFAFEQL---LNTNVSR----- 351
DB 361 NYAKIYVQNRKIYLSNVYTPVTANILDDNVYDIQNGFNIPKSNLNVLFMGQNLSPAL 420
QY 352 --ANCKMIPLT-----DGGEERAQEIFNK-----YNKD-----KKVVRP 386
DB 421 RKNVPENMLYLFKFKCHAIDG-----RSLYNKTLDRELLYKNTDLPFIGDISVKTDI 475
QY 387 FSVGQHNYERGPIONMACENKGYVEIPEISGAIRI--NFOEY--LDVL----- 430
DB 476 FURKINETEVI-----YYPDNVSDQVILSKNTSEHGQDLDPSTDSSEILP 526
QY 431 GRPMVLADGKAKQOVMTN--VYLDALGLVITGTLGVFNITGQFNKTN----- 478
DB 527 GENQVYDNRNTQNDVLSNYYSLEOKL-----SDNVDEFTFTRSTEEALDNSAKVYVFP 582
QY 479 -LKNOLLIGVMG-----VDVSLIEDIKRLTRPFLPCPNGYFAIDPNQYVLLHNPLOPK 530
DB 583 TLANKVNAVQVGGFLMWANDVVEFTTNILRKDTLDKISDVSAIIP-----YIGPALNIS 638
QY 531 NPKSPEPTVLDL-----LDAELENDI-----KVEIRNKMDGESGEKTERFL 572
DB 639 NSVRGNFTFAVGTGVTILLAEAFPEFTIPALGAFVYSKVQVERNEII-----KTIDNC 692
QY 573 QKSDQERYDKGNRTYTW-----TPVNGTQYSLALVLPYTSFYVYKAKLEETITQ 622
DB 693 LQRIKRWKD-----SYENMMGTWLSRIITQFNNSIQMYDSL-NYQAGAIAKAKID----- 742

QY 623 ARSKGKMKDSELPK--DNFESGYTFIAPRDYCNLDKISDNNTTEFLNNEFI----- 675
DB 743 LEYKYSKSGDENIKSOVENLKN-----LDVKIS-----EAMNNINKFIRECSV 787
QY 676 -----DRKTPNPNPCNADLINRVLLDA----- 697
DB 788 TYLFKNMLPKVIDELNEFORNT-----KAKLIN--LIDSHNIIIVGEVDKILKAKVNNFSF 839
QY 698 -----GFTN-----ELVQNYW-----SKOKNIKGVKARFVYTDGITRYVYKPEACE 738
DB 840 QNTIPNFISYTNNSLLKDIINEYFNINDSKILSLQNRKNTLVDTS-----YNAEVSE 894
QY 739 --NQENPERYEDSFYKRSILDNDVYFTAPYFNKSPGAYESGIMVSKAVEIYIOGKLLK 796
DB 895 EGDVQLNP-----IP--PFDFKLGSSGDEGRKVIIVTQENIYVNSWYE 935
QY 797 PAVVGKIDVNSWIENTKTSIRDCAGPVCDCRNSDVMDCVILDGDFLLMANHD----- 853
DB 936 SFSISFIRIKVNSVLPVYTIID-----SVKNNSGWSIGIISNLFVTLKQNEDESEQ 988
QY 854 -----DYTNQIGR-----PFGEIDPSLMRLHVLNIVSYAFNKSVDYQSVCE 893
DB 989 SINFSDISNNAFGYNKWFVVTNNMVG---NMKIYINGKLIDITIKVKE 1035

RESULT 14

Y103_SINY3
ID Y103_SINY3 STANDARD; PRT; 420 AA.
AC Q55874;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL 45.8 KDA PROTEIN SLL0103.
GN SLL0103.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96127529; PubMed=8590279;
RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA Sugita M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT region from map positions 64% to 92% of the genome.";
RL DNA Res. 2:153-166(1995).
CC -1- SIMILARITY: TO E.COLI YF8K.
CC
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CC
CC EMBL; D64004; BAA10635.1; -
DR InterPro; IPR002035; -
DR Pfam; PF00092; vwa; 1.
DR PROSITE; PS50234; VWFA_DOMAIN; 1.
KW Hypothetical protein.
SQ SEQUENCE 420 AA; 45849 MW; E7111B51478E74F3 CRC64;

Query Match 2.6%; Score 151.5; DB 1; Length 420;
Best Local Similarity 20.8%; Pred. No. 0.085;
Matches 85; Conservative 85; Mismatches 183; Indels 55; Gaps 16;
QY 251 PKDMLIVDVGSGVSGTGLKIRTSVEMLETLSDDDFVNVASFNSNAQDVSCFQHLVQA 310
DB 41 PLNCLVLDHSGMDGQPLETVKSAALGLDRLEEDDLRLSVAFDRRAKIV-----IENQ 95
QY 311 NVNRKKVLKDAVNITAKGITDYKKGFSFAFEQLLNIVNSRANCKIIMLFTDGGERAQ 370

DB 96 QVRNGAATAKATERLAKEGGTAIDEGKLGIAQAAKREDRVs---HIFLLTDGENEHGD 152
QY 371 E-----IFKNYKDKKVRVFRFSGVQHNYPGPIOWMACENKG--YYEIPSGAIRINTO 424
DB 153 NDRCKLKTVASDYKLTVHTLGFGDH-WNQDVLAEIAASAQSLSYIENPS-EALHTFRQ 210
QY 425 EYLDVLRPMVLGDKAKQVQVNTVYLDALGLG-----LVITGTLPVFNITGFENKTNLK 480
DB 211 LF-----QRMSNVGLTNAHL-LLELAPOHAI--VKPVAQVSPETMDLT-VQ 254
QY 481 NOLILGVGVDSLEDIKRLTPRFTLPCPNGYFAIDPNGYVLLHNPLOPKNKSOE----- 536
DB 255 NQGAITEEVRGLDMLTDQERV-----LLNLNLYDQLLPQGHVIGQVQIRYDDPASGOTNLL 309
QY 537 -----PVTLDLDALENDIKVEIRKNMIDGESGKT--PRTLVKSODERYIDKGNRTYTW 590
DB 310 SDPLPLTIQ-VOTQYQSPDVQVQESILTLAKYRQTIAETKLKAGDRGGAATMLQTAAK 368
QY 591 TPVNGTDYSLALVLTYSFYIKALEETITQARSKKGMKDSITLKP 638
DB 369 TALQMGDKNGATILQTN-----TRLQSGEDLSEGDRLKTRMVKSTLIQ 413

RESULT 15

ITH4_PIG
ID ITH4_PIG STANDARD; PRT; 921 AA.
AC P79263;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H4 PRECURSOR (ITI HEAVY
DE CHAIN H4) (INTER-ALPHA-TRYPsin INHIBITOR FAMILY HEAVY CHAIN-RELATED
DE PROTEIN) (IHRP) (MAJOR ACUTE PHASE PROTEIN) (MAP).
GN ITI4 OR IHRP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-36; 695-703 AND 710-722.
RX TISSUE=Liver;
RX MEDLINE=96271024; PubMed=8830057;
RA Hashimoto K., Tohe T., Sumiya J.-I., Sano Y., Choi-Miura N.-H.,
RA Ozawa A., Yasue H., Tomita M.;
RT "Primary structure of the pig homologue of human IHRP: inter-alpha-
RT trypsin inhibitor family heavy chain-related protein.";
RL J. Biochem. 119:577-584(1996).
RN [2]
RP PRELIMINARY SEQUENCE OF 267-556 FROM N.A.
RX TISSUE=Liver;
RX MEDLINE=90371455; PubMed=1697703;
RA Buchman T.G., Cabin D.E., Vickers S., Deutschman C.S., Delgado E.,
RA Sussman M.M., Bulkeley G.B.;
RT "Molecular biology of circulatory shock. Part II. Expression of four
RT groups of hepatic genes is enhanced after resuscitation from
RT cardiogenic shock.";
RL Surgery 108:559-566(1990).
RN [3]
RP SEQUENCE OF 28-54 AND 223-240.
RX TISSUE=Serum;
RX MEDLINE=96013138; PubMed=7556597;
RA Gonzalez-Ramon N., Alava M.A., Sarsa J.A., Pineiro M., Escartin A.,
RA Garcia-Gil A., Lampreave F., Pineiro A.;
RT "The major acute phase serum protein in pigs is homologous to human
RT plasma kallikrein sensitive PK-120.";
RL FEBS Lett. 371:227-230(1995).
CC -1- FUNCTION: MAY BE INVOLVED IN ACUTE PHASE REACTIONS.
CC -1- TISSUE SPECIFICITY: LIVER-SPECIFIC.
CC -1- INDUCTION: LEVELS INCREASE SIGNIFICANTLY AFTER CARDIOGENIC
CC SHOCK.
CC -1- PTM: APPEARS TO BE BOTH N- AND O-GLYCOSYLATED (BY SIMILARITY).
CC -1- PTM: CLEAVED BY PLASMA KALLIKREIN TO YIELD 55- AND 25-KDA

CC FRAGMENTS.
CC -!- SIMILARITY: BELONGS TO THE ITH FAMILY.
CC -!- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
CC -!- CAUTION: REF.2 SEQUENCE IS INCORRECT DUE TO FRAMESHIFTS AND OTHER
CC SEQUENCING ERRORS.
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CC -----
CC EMBL: U43164; AD00024.1; -;
CC EMBL: S82800; AAB46821.1; -;
CC EMBL: M29507; -; NOT_ANNOTATED_CDS.
CC InterPro: IPR002035; -;
CC Pfam: PF00092; vwa; 1.
CC PROSITE: PS0234; VWFA_DOMAIN; 1.
CC Serine protease inhibitor; Repeat; Signal; Multigene family;
KW Glycoprotein.
FT SIGNAL 1 27
FT CHAIN 28 921 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN
FT H4.
FT DOMAIN 270 428 VWFA.
FT CARBOHYD 80 80 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 513 513 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 577 577 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 49 50 HT -> SK (IN REF. 3).
FT CONFLICT 703 703 D -> H (IN REF. 1; AA SEQUENCE).
SQ SEQUENCE 921 AA; 102146 MW; E2BF9525DE8D07C CRC64;

Query Match 2.68; Score 150.5; DB 1; Length 921;
Best Local Similarity 19.9%; Pred. No. 0.3;
Matches 156; Conservative 100; Mismatches 264; Indels 265; Gaps 36;
Qy 4 GCLLALTLTL-----FQSLIGSSSEPPPSAVTIKSWYDK--MOED--- 43
Db 10 GLLLVLPALLAVLOSTAHKNDINIYSLTVDKSSRFATHVTSRVNKGSAVOEATFQ 69
Qy 44 -----LVTLAKTAGVNLVDIYEK--YQDLYT-VEPNNAKQLVEIAARDIEKL--- 89
Db 70 MELPKAFITNFSMIIDGVTPYGNKAKAAEQYSAVARGESAGLVATGRTKTEQFOVA 129
Qy 90 LSNRSKALVSLALEAKVQAAHQWREDFASNEVYVYNAKDDLDPEKNDSEPGSQRIKPVF 149
Db 130 VSVAPAAKVTFELVYELLARH-----LGYIELLLKIQPQ-----QLVKHLQ 171
Qy 150 IEDANFGKQ-ISKY-QHAAVHIPTDIYEGSTIVLNE---LWNTSALDEVKKNREEDPSL 203
Db 172 MDIHFEFGISFLESTFTWELAEALTISQNKRAHIFKPTLSQ-OKSPQQQETV 230
Qy 204 L-----WQVFGSATG-----LARYYPASFWNDNRTPNKIDLYDVRRRPWYIQG 247
Db 231 LDGNFIVRYDNRVTGTGSIQIENGIFVHYFAPEW----- 266
Qy 248 AASPKDMLILVDVSSVSGLTSLKIRTSVSEMLETSLDDDFVNVASFNNAQDVSCFOHL 307
Db 267 SAIPKNVIFVDTSGMRGRKIQTREALIKILGDLGSRDQFNLSVFSGEAPR-----RRA 322
Qy 308 VQAVNRKVKLVKDAVNITAKGIDYKKGFSAFEPQLLNYNVSRANCNKI-----IM 359
Db 323 VAASAENVEEAKSYAAEIHAGGGTNINDMLMAVQLL-----ERANRELLPARSVTFII 377
Qy 360 LFTDG-----GEERAQEIFNKYNDKKVRV-----FRFSVGQHNHYERGPIONMA 403
Db 378 LLDGDPVTGETNPFSKI-----QKNVREADGQHSFLCLGFGFDVPVAFLEK-----MA 426
Qy 404 CENKG-----YY-----YEIPSGAIRINTQYLDVL--GR 432

Db 427 LENGGLARIYEDSDSALQLEDFYQEVANPLRLVAFEPSS-NAVEEVTQDNFRIFPKGS 485
Qy 433 PMVLAG---DKAKQYQWTVNVLDALELGLVITGTLFVFNITQGFENKTKLNQILG--- 486
Db 486 ELVWAGKLRDQSPDV-----LSAKVRGQLHMEVNTFVMSRVAEQEAEFLSPKY 534
Qy 487 -----VMGVVDSLEDI--KRLTPFTLCPNGYYPFADPNNGYVLLHPNL 527
Db 535 IFHSPMERLWAYLTIQQLLAQTVSASDAEKKALEARALSLSLNYSFVTLTSMVITKPEG 594
Qy 528 QPKNPKSQEPVTLDFLDAFLENDIKVEIRNMIDGESGEKTFRTLVKSQDERVIDKGNRT 587
Db 595 QEQSQVAERP-----VENGRNROGTHSGHSSF-----OFHSVGDR 630
Qy 588 YTWTPVNGTVDYSLALVLTPTSYFYIKAKLEETITQARSKKGMKDKSETLKPDPNFESGYT 647
Db 631 SRLTGGSSVD-----PVFS-----HRRGWKGQAQ-----GFEKMSY- 661
Qy 648 FIAPR 652
Db 662 -LPPR 665

Search completed: July 23, 2001, 07:47:59
Job time: 560 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 23, 2001, 07:37:14 ; Search time 125.88 Seconds
(without alignments)
1146.686 Million cell updates/sec

Title: US-09-397-548-14
Perfect score: 5748
Sequence: 1 MAAGCCLALTLTLFQSLIG.....IIGIQFLLMLVSGSTRLL 1091

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL.16.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_unclassified.*
13: sp_vertebrate.*
14: sp_virus.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5714.5	99.4	1110	4 Q9UIU0	Q9ui0 homo sapien
2	5635	98.0	1091	6 Q7773	Q7773 sus scrofa
3	5562	96.8	1091	11 Q9ERS3	Q9ers3 rattus norv
4	5498	95.7	1103	11 Q08532	Q08532 mus musculu
5	3972	69.1	745	4 Q9UDQ3	Q9udq3 homo sapien
6	3075	53.0	1150	4 Q9NY47	Q9ny47 homo sapien
7	3047.5	53.0	1143	4 Q9NY48	Q9ny48 homo sapien
8	3045.5	53.0	1156	11 Q9EGG2	Q9egg2 mus musculu
9	3034.5	52.8	1145	4 Q9Y268	Q9y268 homo sapien
10	3013.5	52.4	1076	4 Q9UEW0	Q9uew0 homo sapien
11	2844	49.5	975	4 Q9NSA6	Q9nsa6 homo sapien
12	1127.5	19.6	1091	11 Q921L5	Q9z1l5 mus musculu
13	1050.5	18.3	997	4 Q9NY16	Q9ny16 homo sapien
14	937	16.3	2190	5 Q9NK64	Q9nk64 drosophila
15	920	16.0	2172	5 Q9VJM0	Q9vjm0 drosophila
16	897.5	15.6	1191	5 Q9VJN7	Q9vjn7 drosophila
17	892.5	15.5	1255	5 Q9NK83	Q9nk83 drosophila
18	875	15.2	170	4 Q9UDL7	Q9udl7 homo sapien
19	851.5	14.8	1022	5 Q9V6T7	Q9v6t7 drosophila

20	738.5	12.8	519	4	Q9NY18	Q9ny18 homo sapien
21	580.5	10.1	1148	5	Q17517	Q17517 caenorhabdi
22	514.5	9.0	104	4	Q9UD81	Q9ud81 homo sapien
23	506	8.8	100	6	Q9GLH1	Q9glh1 bos taurus
24	498.5	8.7	121	4	Q9UD82	Q9ud82 homo sapien
25	492.5	8.6	223	11	Q9R142	Q9r142 mus musculu
26	482	8.4	98	4	Q9UDU5	Q9udu5 homo sapien
27	465	8.1	97	4	Q9UD80	Q9ud80 homo sapien
28	402	7.0	77	4	Q95026	Q95026 homo sapien
29	344	6.0	1185	4	Q9HCJ9	Q9hcj9 homo sapien
30	324	5.9	1449	5	Q9V917	Q9v917 drosophila
31	224.5	3.0	494	5	Q9U7P4	Q9u7p4 euliciculi
32	167	2.9	796	1	Q9HJRO	Q9hjr0 thermoplas
33	161	2.8	2706	5	O15870	O15870 plasmodium
34	156.5	2.7	903	6	Q9GLY5	Q9gly5 cryptotagus
35	155	2.7	1516	5	O96154	O96154 plasmodium
36	155	2.7	2364	2	O46342	O46342 clostridium
37	154.5	2.7	1315	2	O86488	O86488 staphylococ
38	153	2.7	932	11	O35802	O35802 rattus norv
39	152.5	2.7	789	2	O45793	O45793 bacillus th
40	152	2.6	1105	14	O9EM28	O9em28 ansacta moo
41	151.5	2.6	2867	5	Q9N2M3	Q9n2m3 plasmodium
42	150.5	2.6	2771	5	O26216	O26216 plasmodium
43	150	2.6	946	6	Q9GLY6	Q9gly6 cryptotagus
44	149	2.6	459	2	O25905	O25905 helicobacte
45	149	2.6	930	4	O9UQ54	O9uq54 homo sapien

ALIGNMENTS

RESULT 1

Q9UIU0 PRELIMINARY; PRT; 1110 AA.

AC Q9UIU0;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE DIHYDROPYRIDINE RECEPTOR ALPHA 2 SUBUNIT.
GN CACNA2D1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX .NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20003942; PubMed=10534405;

RA Schleithoff L., Mehrke G., Reutlinger B., Lehmann-Horn F.;

RT "Genomic structure and functional expression of a human alpha(2)/delta

RL Genomics 61:201-209(1999).

DR EMBL; AF083854; AAF03259.1; JOINED.

DR EMBL; AF083817; AAF03259.1; JOINED.

DR EMBL; AF083819; AAF03259.1; JOINED.

DR EMBL; AF083820; AAF03259.1; JOINED.

DR EMBL; AF083821; AAF03259.1; JOINED.

DR EMBL; AF083822; AAF03259.1; JOINED.

DR EMBL; AF083823; AAF03259.1; JOINED.

DR EMBL; AF083824; AAF03259.1; JOINED.

DR EMBL; AF083825; AAF03259.1; JOINED.

DR EMBL; AF083826; AAF03259.1; JOINED.

DR EMBL; AF083827; AAF03259.1; JOINED.

DR EMBL; AF083828; AAF03259.1; JOINED.

DR EMBL; AF083829; AAF03259.1; JOINED.

DR EMBL; AF083830; AAF03259.1; JOINED.

DR EMBL; AF083831; AAF03259.1; JOINED.

DR EMBL; AF083832; AAF03259.1; JOINED.

DR EMBL; AF083833; AAF03259.1; JOINED.

DR EMBL; AF083834; AAF03259.1; JOINED.

DR EMBL; AF083835; AAF03259.1; JOINED.

DR EMBL; AF083836; AAF03259.1; JOINED.

DR EMBL; AF083837; AAF03259.1; JOINED.

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DR EMBL; AF083838; AAF03259.1; JOINED.
DR EMBL; AF083839; AAF03259.1; JOINED.
DR EMBL; AF083840; AAF03259.1; JOINED.
DR EMBL; AF083841; AAF03259.1; JOINED.
DR EMBL; AF083842; AAF03259.1; JOINED.
DR EMBL; AF083843; AAF03259.1; JOINED.
DR EMBL; AF083844; AAF03259.1; JOINED.
DR EMBL; AF083845; AAF03259.1; JOINED.
DR EMBL; AF083846; AAF03259.1; JOINED.
DR EMBL; AF083847; AAF03259.1; JOINED.
DR EMBL; AF083848; AAF03259.1; JOINED.
DR EMBL; AF083849; AAF03259.1; JOINED.
DR EMBL; AF083850; AAF03259.1; JOINED.
DR EMBL; AF083851; AAF03259.1; JOINED.
DR EMBL; AF083852; AAF03259.1; JOINED.
DR EMBL; AF083853; AAF03259.1; JOINED.
DR EMBL; AF083854; AAF03259.1; JOINED.
DR InterPro; IPR000885; -.
DR InterPro; IPR002035; -.
DR Pfam; PF00092; vwa; 1.
DR ProDom; PD002078; -. 1.
KW Receptor.
SQ SEQUENCE 1110 AA; 125307 MW; 8358D6AD489C074 CRC64;

Query Match          99.4%; Score 5714.5; DB 4; Length 1110;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 1088; Conservative 1; Mismatches 2; Indels 19; Gaps 1;

QY 1 MAAGCLLALTFLFQSLIGPSSSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
DB 1 MAAGCLLALTFLFQSLIGPSSSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

QY 61 YEKYQDLYTVENPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVAQAAHQWREDFASN 120
DB 61 YEKYQDLYTVENPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVAQAAHQWREDFASN 120

QY 121 EYVYNAKDDLPEKNDSPGSGORIKPVIEDANFRQISYQAAVHIPTDIYEGSTIVL 180
DB 121 EYVYNAKDDLPEKNDSPGSGORIKPVIEDANFRQISYQAAVHIPTDIYEGSTIVL 180

QY 181 NELNWTSAIDVEFKKNEEDPSLLQVFGSAGTLARYYPASPDWNSRTPNKKIDLYDVR 240
DB 181 NELNWTSAIDVEFKKNEEDPSLLQVFGSAGTLARYYPASPDWNSRTPNKKIDLYDVR 240

QY 241 RPWYIOGAASPKDMLLVDVSGSVGLTKLRTSVSEMLETLSDDDFVNVASFNSNAQD 300
DB 241 RPWYIOGAASPKDMLLVDVSGSVGLTKLRTSVSEMLETLSDDDFVNVASFNSNAQD 300

QY 301 VSCFOHLVQANVRNKKVLKADAVNNITAKGIDYKKGFSFAFQOLLNYSRANCNKIIML 360
DB 301 VSCFOHLVQANVRNKKVLKADAVNNITAKGIDYKKGFSFAFQOLLNYSRANCNKIIML 360

QY 361 FTDGGEERAQEIFNKNDKKYRVFRFSVGOHNYBERGPTQWACENKGYIYIPISGAIR 420
DB 361 FTDGGEERAQEIFNKNDKKYRVFRFSVGOHNYBERGPTQWACENKGYIYIPISGAIR 420

QY 421 INTQEYLDVLRPMVLGAKAKOVQNTVYLDALGLVITGTLPVENITGOFENKTNLK 480
DB 421 INTQEYLDVLRPMVLGAKAKOVQNTVYLDALGLVITGTLPVENITGOFENKTNLK 480

QY 481 NQILGVMGVDVSLDKRLTRPFTLCPNGYFYAIDPNGYVLLHPNLQPK----- 530
DB 481 NQILGVMGVDVSLDKRLTRPFTLCPNGYFYAIDPNGYVLLHPNLQPKIGVGIGPTIN 540

QY 531 -----NPKSQEPVTLDFDALENDIKVEIRNKMIDGESGEKTFTLVKSQDERVI 581
DB 541 LKRRPNINQPKSQEPVTLDFDALENDIKVEIRNKMIDGESGEKTFTLVKSQDERVI 600

QY 582 DKGNRYYTTPVNGTDSLALVLPYTSFYIYAKLEETITQARSKKGKMKDSETLKPDPNF 641
DB 601 DKGNRYYTTPVNGTDSLALVLPYTSFYIYAKLEETITQARSKKGKMKDSETLKPDPNF 660

QY 642 EESGYFTIAPROYCNDLKISDNNTTEFLNFNEFIDRKTPNPNNSCNADLINRVLLDAGFTN 701
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DB 661 EESGYFTIAPROYCNDLKISDNNTTEFLNFNEFIDRKTPNPNNSCNADLINRVLLDAGFTN 720
QY 702 ELVQNYWSKQKNIKGVKARFVYTDGITRVYPKEAGENQENPETEYDSFYKRSLDNDNY 761
DB 721 ELVQNYWSKQKNIKGVKARFVYTDGITRVYPKEAGENQENPETEYDSFYKRSLDNDNY 780
QY 762 VFTAPYFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKTSIRDP 821
DB 781 VFTAPYFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKTSIRDP 840
QY 822 CAGPVCDCKRNSDMVDCVTLDDGFLMANHDDYTNQIGRFFGEIDPDSLMRHLVNSIYVA 881
DB 841 CAGPVCDCKRNSDMVDCVTLDDGFLMANHDDYTNQIGRFFGEIDPDSLMRHLVNSIYVA 900
QY 882 FNKSYDYQSVCEPGAAPKQAGHRSAYVPSVADIILQIGWATAAAWSILQOFLLSLTFFPR 941
DB 901 FNKSYDYQSVCEPGAAPKQAGHRSAYVPSVADIILQIGWATAAAWSILQOFLLSLTFFPR 960
QY 942 LLEAVEMEDDDFTASLSKQSCITEQTQYFFDNDKSKFSVGLDCGNCRIFFHGEKLMNTNL 1001
DB 961 LLEAVEMEDDDFTASLSKQSCITEQTQYFFDNDKSKFSVGLDCGNCRIFFHGEKLMNTNL 1020
QY 1002 IFIMVESKGTCPDTRLLIQAQTSQSDGNPCDMVQKQPRYKRGPDVCFDNNVLEDYDCGG 1061
DB 1021 IFIMVESKGTCPDTRLLIQAQTSQSDGNPCDMVQKQPRYKRGPDVCFDNNVLEDYDCGG 1080
QY 1062 VSGLNPSLWYIIIGIOFLLLMLVSGSTHRL 1091
DB 1081 VSGLNPSLWYIIIGIOFLLLMLVSGSTHRL 1110

RESULT 2
QY 077773 PRELIMINARY; PRT; 1091 AA.
ID 077773
AC 077773;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE VOLTAGE-DEPENDENT CALCIUM CHANNEL ALPHA-2 DELTA SUBUNIT PRECURSOR.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CEREBRAL CORTEX;
RX MEDLINE=98411353; PubMed=9738015;
RA Brown J.P., Gee N.S.;
RT "Cloning and deletion mutagenesis of the alpha2 delta calcium channel
RT subunit from porcine cerebral cortex. Expression of a soluble form of
RT the protein that retains [3H]gabapentin binding activity.";
RL J. Biol. Chem. 273:25458-25465(1998).
DR EMBL; AF077665; AAC36289.1; -.
DR InterPro; IPR002035; -.
DR Pfam; PF00092; vwa; 1.
KW SIGNAL.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 1091 VOLTAGE-DEPENDENT CALCIUM CHANNEL
FT ALPHA-2 DELTA SUBUNIT.
SQ SEQUENCE 1091 AA; 123150 MW; 293DDC7EBE9EE60E CRC64;

Query Match          98.0%; Score 5635; DB 6; Length 1091;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 1068; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MAAGCLLALTFLFQSLIGPSSSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
DB 1 MAAGCLLALTFLFQSLIGPSSSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

QY 61 YEKYQDLYTVENPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVAQAAHQWREDFASN 120
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Db 61 YEKYQDLTVTPNNARQVETAAARDIEKLLNSRKALVRLALEAEKVQAAHQWRDFASN 120
 Qy 121 EYVYNAKDDLDPEKNDSQSRQIKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180
 Db 121 EYVYNAKDDLDPEKNDSQSRQIKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180
 Qy 181 NELNWTSADEVEFKKREDESLWQVFGSATGLARYYPASPWVDSRTPNKIDLYDVR 240
 Db 181 NELNWTSADEVEFKKREDESLWQVFGSATGLARYYPASPWVDSRTPNKIDLYDVR 240
 Qy 241 RPWTIOGAASPKDMLILVDVSGVSGTLKLRISVSEMLETSLDDDFVNVASFNSNAQD 300
 Db 241 RPWTIOGAASPKDMLILVDVSGVSGTLKLRISVSEMLETSLDDDFVNVASFNSNAQD 300
 Qy 301 VSCFQHLVQVARNKVKVLDKAVNNITAKGIDYKKGFSFAFEQLLNNVSRANCNKIIML 360
 Db 301 VSCFQHLVQVARNKVKVLDKAVNNITAKGIDYKKGFSFAFEQLLNNVSRANCNKIIML 360
 Qy 361 FTDGGEERAQEIFNKYKNDKVRVFRFSGVGHYERGPQIOMACENKGYEYIPEISGAIR 420
 Db 361 FTDGGEERAQEIFNKYKNDKVRVFRFSGVGHYERGPQIOMACENKGYEYIPEISGAIR 420
 Qy 421 INTQBYLDVLRPMVLADGKAKQVQWTVNYLDALGLVITGTLPVFNITGOFENKTNLK 480
 Db 421 INTQBYLDVLRPMVLADGKAKQVQWTVNYLDALGLVITGTLPVFNITGOFENKTNLK 480
 Qy 481 NOLILGVMGVDSLEDKRLTPRTLCPCNGYFFAIDPNGYVLLHPNLPKPKSQEPVTL 540
 Db 481 NOLILGVMGVDSLEDKRLTPRTLCPCNGYFFAIDPNGYVLLHPNLPKPKSQEPVTL 540
 Qy 541 DFLDAELENDIKVEIRNKMDIDGESGKTRFLVKSQDERYIDKGNRTYTWTPVNGTDSL 600
 Db 541 DFLDAELENDIKVEIRNKMDIDGESGKTRFLVKSQDERYIDKGNRTYTWTPVNGTDSL 600
 Qy 601 ALVLPYTSFYIKAKLEETITQARSKKGMKDSKTLKPDNFEESGYTPIAPDYCNDLKI 660
 Db 601 ALVLPYTSFYIKAKLEETITQARSKKGMKDSKTLKPDNFEESGYTPIAPDYCNDLKI 660
 Qy 720 SDNNTFELNNEFIDRKTTPNPNCSNADLINRVLLDAGFTNVLVQYWSKOKNKGVRAR 720
 Db 720 SDNNTFELNNEFIDRKTTPNPNCSNADLINRVLLDAGFTNVLVQYWSKOKNKGVRAR 720
 Qy 780 FVVTGGITRYVTPKEAGENWQENPETEYDSFKRSLDNDVFTAPYFNKSGPGAYESGI 780
 Db 780 FVVTGGITRYVTPKEAGENWQENPETEYDSFKRSLDNDVFTAPYFNKSGPGAYESGI 780
 Qy 840 MYKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVPCDCRNSDVMDCVI 840
 Db 840 MYKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVPCDCRNSDVMDCVI 840
 Qy 900 LDDGGFLMANHDDYTNQIGRFFGIDPSLRHLVNIISVYAFNKSIDYQSCPEGAAPKQ 900
 Db 900 LDDGGFLMANHDDYTNQIGRFFGIDPSLRHLVNIISVYAFNKSIDYQSCPEGAAPKQ 900
 Qy 960 GAGHRSATVPVADTLOIGWATAAASILQOFLLSLTFPRLLAEVEMEDDDFTASLSKQ 960
 Db 960 GAGHRSATVPVADTLOIGWATAAASILQOFLLSLTFPRLLAEVEMEDDDFTASLSKQ 960
 Qy 1020 SCITEQTOYFFDNDKSKSGVLDGNCNCRIFHVEKLMNTNLIIFIMVESKGCPCDTRLLI 1020
 Db 1020 SCITEQTOYFFDNDKSKSGVLDGNCNCRIFHVEKLMNTNLIIFIMVESKGCPCDTRLLI 1020
 Qy 1080 QAEQTSQDPNCDVMKQPRYKRGDPDVCNDNVEDYTCGGVSGNLNPLSWYIIGIQFLL 1080
 Db 1080 QAEQTSQDPNCDVMKQPRYKRGDPDVCNDNVEDYTCGGVSGNLNPLSWYIIGIQFLL 1080
 Qy 1088 WLVSSTH 1088
 Db 1088 WLLSGSRH 1088

RESULT 3
 Q9ERS3

ID Q9ERS3 PRELIMINARY; PRT: 1091 AA.
 AC Q9ERS3;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE VOLTAGE-GATED CALCIUM CHANNEL ALPHA2/DELTA-1 SUBUNIT.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-SUPERIOR CERVICAL GANGLIA;
 RA Lin Y., Lipscombe D.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF284688; AAG28164.1;
 FT VARIANT 209 212 GSAT -> AADR.
 FT VARIANT 338 338 S -> T.
 FT VARIANT 599 600 SL -> RV.
 FT VARIANT 869 869 S -> R.
 SQ SEQUENCE 1091 AA; 123467 MW; C155088971628E19 CRC64;
 Query Match 96.8%; Score 5562; DB 11; Length 1091;
 Best Local Similarity 96.1%; Pred. No. 0;
 Matches 1047; Conservative 24; Mismatches 19; Indels 0; Gaps 0;
 Qy 1 MAAGCLLATLTLSQSLIGPSSEPPFSAVTIKSWDKMOEDLVTLAKTAGSVNQLVDI 60
 Db 1 MAAGCLLATLTLSQSLIGPSSEPPFSAVTIKSWDKMOEDLVTLAKTAGSVNQLADI 60
 Qy 61 YEKYQDLTVTPNNARQVETAAARDIEKLLNSRKALVRLALEAEKVQAAHQWRDFASN 120
 Db 61 YEKYQDLTVTPNNARQVETAAARDIEKLLNSRKALVRLALEAEKVQAAHQWRDFASN 120
 Qy 121 EYVYNAKDDLDPEKNDSQSRQIKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180
 Db 121 EYVYNAKDDLDPEKNDSQSRQIKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180
 Qy 181 NELNWTSADEVEFKKREDESLWQVFGSATGLARYYPASPWVDSRTPNKIDLYDVR 240
 Db 181 NELNWTSADEVEFKKREDESLWQVFGSATGLARYYPASPWVDSRTPNKIDLYDVR 240
 Qy 241 RPWTIOGAASPKDMLILVDVSGVSGTLKLRISVSEMLETSLDDDFVNVASFNSNAQD 300
 Db 241 RPWTIOGAASPKDMLILVDVSGVSGTLKLRISVSEMLETSLDDDFVNVASFNSNAQD 300
 Qy 301 VSCFQHLVQVARNKVKVLDKAVNNITAKGIDYKKGFSFAFEQLLNNVSRANCNKIIML 360
 Db 301 VSCFQHLVQVARNKVKVLDKAVNNITAKGIDYKKGFSFAFEQLLNNVSRANCNKIIML 360
 Qy 361 FTDGGEERAQEIFNKYKNDKVRVFRFSGVGHYERGPQIOMACENKGYEYIPEISGAIR 420
 Db 361 FTDGGEERAQEIFNKYKNDKVRVFRFSGVGHYERGPQIOMACENKGYEYIPEISGAIR 420
 Qy 421 INTQBYLDVLRPMVLADGKAKQVQWTVNYLDALGLVITGTLPVFNITGOFENKTNLK 480
 Db 421 INTQBYLDVLRPMVLADGKAKQVQWTVNYLDALGLVITGTLPVFNITGOFENKTNLK 480
 Qy 481 NOLILGVMGVDSLEDKRLTPRTLCPCNGYFFAIDPNGYVLLHPNLPKPKSQEPVTL 540
 Db 481 NOLILGVMGVDSLEDKRLTPRTLCPCNGYFFAIDPNGYVLLHPNLPKPKSQEPVTL 540
 Qy 541 DFLDAELENDIKVEIRNKMDIDGESGKTRFLVKSQDERYIDKGNRTYTWTPVNGTDSL 600
 Db 541 DFLDAELENDIKVEIRNKMDIDGESGKTRFLVKSQDERYIDKGNRTYTWTPVNGTDSL 600
 Qy 601 ALVLPYTSFYIKAKLEETITQARSKKGMKDSKTLKPDNFEESGYTPIAPDYCNDLKI 660
 Db 601 ALVLPYTSFYIKAKLEETITQARSKKGMKDSKTLKPDNFEESGYTPIAPDYCNDLKP 660
 Qy 661 SDNNTFELNNEFIDRKTTPNPNCSNADLINRVLLDAGFTNVLVQYWSKOKNKGVRAR 720
 Db 661 SDNNTFELNNEFIDRKTTPNPNCSNADLINRVLLDAGFTNVLVQYWSKOKNKGVRAR 720

Db 661 SONNTEFLNNEFIDRKTNPNSCNTDLINRILLDAGFTNELVQNSKQKNIGVKAR 720
QY 721 FVYTDGIGTRVYPKEAGENQWENPETYEDSFYKRSLDNDNDNYFTAPYFNKSPGAYESGI 780
Db 721 FVYTDGIGTRVYPKEAGENQWENPETYEDSFYKRSLDNDNDNYFTAPYFNKSPGAYESGI 780
QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWENFTKTSIRDPKAGVPCDCKRNSDVMDCVI 840
Db 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWENFTKTSIRDPKAGVPCDCKRNSDVMDCVI 840
QY 841 LDGGFLLMANHDDYTNQIGRFFGIDPSLHRLNYSVIAFNKSYDYOSVCEPGAAPKQ 900
Db 841 LDGGFLLMANHDDYTNQIGRFFGIDPSLHRLNYSVIAFNKSYDYOSVCEPGAAPKQ 900
QY 901 GAGHSAYVPSVADILQIGWATAAASLIQOFLSLSLFPRLLEAVEDEDDFTASLSKQ 960
Db 901 GAGHSAYVPSITDILQIGWATAAASLIQOFLSLSLFPRLLEAVEDEDDFTASLSKQ 960
QY 961 SCITEQYFFNDNSKFSGLDCGNCISRFHGEKLMNTNLFIMVESKGTCPDTRLLI 1020
Db 961 SCITEQYFFNDNSKFSGLDCGNCISRFHGEKLMNTNLFIMVESKGTCPDTRLLI 1020
QY 1021 QAEQTSQSDGPNCDVMKQPRYKRGPDVCFDNNVLEDYDCGGVSGNLNPLSMYIIGIOFLLL 1080
Db 1021 QAEQTSQSDGPNCDVMKQPRYKRGPDVCFDNNVLEDYDCGGVSGNLNPLSMYIIGIOFLLL 1080
QY 1081 WLVSQSTHRL 1090
Db 1081 WLVSQSTHRL 1090

RESULT 4
O08532 PRELIMINARY; PRT: 1103 AA.
ID O08532; O08533; O08534; O08535; O08536;
AC 01-JUN-1998 (TREMELrel. 06, Created)
DT 01-JUN-1998 (TREMELrel. 06, Last sequence update)
DT 01-JUN-2000 (TREMELrel. 14, Last annotation update)
DE DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-2/DELTA
DE SUBUNITS PRECURSOR.
GN CACNA2D1 OR CACNA2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97113514; PubMed=8955374;
RA Angelotti T.; Hofmann F.;
RL FEBS Lett. 397:331-337(1996).
CC -1- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN EXCITATION-CONTRACTION COUPLING.
CC -1- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS: ALPHA-1, ALPHA-2, BETA AND GAMMA.
CC -1- SUBUNIT: ALPHA-2 AND DELTA FORM HETERODIMERS THAT ARE DISULFIDE-LINKED.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: FIVE FORMS OF THE PROTEIN, ISOFORMS 2A-2E, ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THE SEQUENCE SHOWN HERE IS THAT OF ISOFORM 2A.
CC -1- TISSUE SPECIFICITY: ISOFORM 2A IS EXPRESSED IN SKELETAL MUSCLE AND AORTA, 2B IS EXPRESSED IN BRAIN, 2C IS EXPRESSED IN HEART, 2D IS EXPRESSED IN HEART AND SMOOTH MUSCLE, AND 2E IS EXPRESSED IN SMOOTH MUSCLE. ALL FIVE ISOFORMS ARE EXPRESSED IN THE CARDIOVASCULAR SYSTEM.
CC -1- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM A PRECURSOR FORM.
CC -1- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.
DR EMBL: U73484; AAB50139.1; -
DR EMBL: U73485; AAB50140.1; -
DR EMBL: U73483; AAB50138.1; -
DR EMBL: U73486; AAB50141.1; -

DR EMBL: U73487; AAB50142.1; -
DR MGD; MGI:88295; Caccna2d1.
DR InterPro: IPR002035; -
DR Pfam: PF00092; vwa; 1.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Calcium channel; Glycoprotein; Phosphorylation; Signal;
KW Alternative splicing.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 957 L-TYPE CALCIUM CHANNEL ALPHA-2 SUBUNIT.
FT CHAIN 958 1103 L-TYPE CALCIUM CHANNEL DELTA SUBUNIT.
FT TRANSMEM 446 469 POTENTIAL.
FT TRANSMEM 918 942 POTENTIAL.
FT TRANSMEM 1079 1098 POTENTIAL.
FT MOD_RES 501 501 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT MOD_RES 845 845 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 324 324 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 348 348 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 475 475 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 604 604 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 675 675 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 781 781 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 824 824 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 888 888 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 895 895 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 985 985 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 998 998 MISSING (IN ISOFORMS 2B AND 2E).
FT VARSPLIC 531 549 MISSING (IN ISOFORMS 2C AND 2D).
FT VARSPLIC 531 554 Y -> SKKGKKD (IN ISOFORMS 2A, 2D, AND 2E).
FT VARSPLIC 644 644
FT SEQUENCE 1103 AA; 124629 MW; 10377384735120D4 CRC64;
QY 121 EVVYVNAKDDLDPEKNDSEPGSQRKPVFIEDANFGROIYSQHAAVHIPTDIYEGSTIVL 180
Db 121 EVVYVNAKDDLDPEKNDSEPGSQRKPVFIEDANFGROIYSQHAAVHIPTDIYEGSTIVL 180
QY 181 NEELNWTSDALDEVFKKNEEDPSLLMQVFGSATGLARYYPASPVWDNSRTPNKIDLYDVR 240
Db 181 NEELNWTSDALDEVFKKNEEDPSLLMQVFGSATGLARYYPASPVWDNSRTPNKIDLYDVR 240
QY 241 RPWYIQGAASPKDMLILYDVSGVSGSLTLKLRTSVSEMLETSLDDDFVNVASFNSNAQD 300
Db 241 RPWYIQGAASPKDMLILYDVSGVSGSLTLKLRTSVSEMLETSLDDDFVNVASFNSNAQD 300
QY 301 VSCFQHLVQANRNKKVLKADAVNNITAKGTDYKKGFSFAFQOLLNYSRANCNKIIML 360
Db 301 VSCFQHLVQANRNKKVLKADAVNNITAKGTDYKKGFSFAFQOLLNYSRANCNKIIML 360
QY 361 FTDGGEERAQEIFAKYNDKVKRVFTFSVGQHNDRGPIQWACENKNGYIETPSIGAIR 420
Db 361 FTDGGEERAQEIFAKYNDKVKRVFTFSVGQHNDRGPIQWACENKNGYIETPSIGAIR 420
QY 421 INTQEYLDVLRPMVLGAKAKQVQWNTNYLDALGLVITGTLPVNITGQFENKTNLK 480
Db 421 INTQEYLDVLRPMVLGAKAKQVQWNTNYLDALGLVITGTLPVNITGQFENKTNLK 480

Query Match 95.7%; Score 5498; DB 11; Length 1103;
Best Local Similarity 93.9%; Pred No. 0;
Matches 1042; Conservative 24; Mismatches 18; Indels 26; Gaps 2;

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QY 481 NQILGVGMGVDSLEDIKRLTFRFTLCPNGYFAIDPNGYVLLHPNLPK-----530
Db 481 NQILGVGMGVDSLEDIKRLTFRFTLCPNGYFAIDPNGYVLLHPNLPKPIGVGPIPTIN 540
QY 531 -----NPKSQEPVTLDFDAELENDIKVEIRNMKIDGESGKTFRTLVKSQDERVI 581
Db 541 LRRKRRNVQPKSQEPVTLDFDAELENDIKVEIRNMKIDGESGKTFRTLVKSQDERVI 600
QY 582 DKGNYRTWTPVNGTDSLALVPTYSFYIYKAKLEETIQARSKKGMKDSKTLKPDNF 641
Db 601 DKGNYRTWTPVNGTDSLALVPTYSFYIYKAKLEETIQARSKKGMKDSKTLKPDNF 653
QY 642 EESGYTFIAPDYCNLDKISDNTEFLNFEIDRKTNNPNSCNADLINRVLLDAGFN 701
Db 654 EESGYTFIAPDYCNLDKISDNTEFLNFEIDRKTNNPNSCNADLINRVLLDAGFN 713
QY 702 ELVQNTWSQKNIKGVKARFVVTGGITRVYPKEAGENQENPETVEDSFYKRSNDNDY 761
Db 714 ELVQNTWSQKNIKGVKARFVVTGGITRVYPKEAGENQENPETVEDSFYKRSNDNDY 773
QY 762 VFTAPFNKSGPAGESGIMVSKAVEIYIQGLKLPVAVGIKIDVNSWIENFTKTSIRD 821
Db 774 VFTAPFNKSGPAGESGIMVSKAVEIYIQGLKLPVAVGIKIDVNSWIENFTKTSIRD 833
QY 822 CAGPVCDCRNSDMVDCVTLDDGGELLMANHDDYTNOIGRFFGEIDPSLMRHLNLSYA 881
Db 834 CAGPVCDCRNSDMVDCVTLDDGGELLMANHDDYTNOIGRFFGEIDPSLMRHLNLSYA 893
QY 882 FNKSYDQSVCPGAPKAGHRSAYVPSVADIQIGWATAAASIIQQLLSLTFPR 941
Db 894 FNKSYDQSVCPGAPKAGHRSAYVPSVADIQIGWATAAASIIQQLLSLTFPR 953
QY 942 LLEAVEMEDDDFTASLSKQSCITEQTFQFFDNDKSFSGVLDCGNCRIFHGEKLMNTNL 1001
Db 954 LLEAVEMEDDDFTASLSKQSCITEQTFQFFDNDKSFSGVLDCGNCRIFHGEKLMNTNL 1013
QY 1002 IFIMVESKTCPCDRLQLQAQSDTSDGNPCDMVKQPRYRKGPVDFDNNVLEDYDCGG 1061
Db 1014 IFIMVESKTCPCDRLQLQAQSDTSDGNPCDMVKQPRYRKGPVDFDNNVLEDYDCGG 1073
QY 1062 VSGLNPLSWIIQIOLFLMLVSGSSTRLL 1091
Db 1074 VSGLNPLSWIIQIOLFLMLVSGSSTRLL 1103

RESULT 5
Q9UDQ3 PRELIMINARY; PRT; 745 AA.
ID Q9UDQ3;
AC Q9UDQ3;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DE WUGSC:H.DJ0560014.1 PROTEIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99063792; PubMed=9847074;
RA Sulston J.E., Waterston R.;
RT "Toward a complete human genome sequence.";
RL Genome Res. 8:1097-1108(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX Mead K., Bauer C.;
RA "The sequence of Homo sapiens PAC clone RP4-560014.";
RT Submitted (DEC-1998) to the EMBL/GenBank/DBSJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX Waterston R.H.;
RA Submitted (DEC-1998) to the EMBL/GenBank/DBSJ databases.
RN [4]
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RP SEQUENCE FROM N.A.
RL Waterston R.;
DR EMBL; AC006145; RAD20938.1;
FT NON_TER 1
SQ SEQUENCE 745 AA; 84396 MW; BC07B53484B71EA4 CRC64;

Query Match 69.1%; Score 3972; DB 4; Length 745;
Best Local Similarity 99.7%; Pred. No. 3.4e-247;
Matches 743; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 347 YNVSRRANCKIIMLFTDGGEEAQAEIFNKYKDKKVVRFVSFGQHNQYRGPQIWMACEN 406
Db 1 YNVSRRANCKIIMLFTDGGEEAQAEIFNKYKDKKVVRFVSFGQHNQYRGPQIWMACEN 60
QY 407 KGYVEIPSIGAIRINTQEYLDVGRPMVLADGAKAKOVQWNTVYLDALGLGIVITGLPV 466
Db 61 KGYVEIPSIGAIRINTQEYLDVGRPMVLADGAKAKOVQWNTVYLDALGLGIVITGLPV 120
QY 467 FNITGOFENKTNLKNOLILGVMGVDVSLIEDIKRLTFRFTLCPNGYFAIDPNGYVLLHPN 526
Db 121 FNITGOFENKTNLKNOLILGVMGVDVSLIEDIKRLTFRFTLCPNGYFAIDPNGYVLLHPN 180
QY 527 LQPKNPKSQEPVTLDFDAELENDIKVEIRNMKIDGESGKTFRTLVKSQDERVIKGNR 586
Db 181 LQPKNPKSQEPVTLDFDAELENDIKVEIRNMKIDGESGKTFRTLVKSQDERVIKGNR 240
QY 587 TYTWPVNGTDSLALVPTYSFYIYKAKLEETIQARSKKGMKDSKTLKPDNFESY 646
Db 241 TYTWPVNGTDSLALVPTYSFYIYKAKLEETIQARSKKGMKDSKTLKPDNFESY 300
QY 647 TFIAPDYCNLDKISDNTEFLNFEIDRKTNNPNSCNADLINRVLLDAGFNELVQN 706
Db 301 TFIAPDYCNLDKISDNTEFLNFEIDRKTNNPNSCNADLINRVLLDAGFNELVQN 360
QY 707 YWSKQKNIKGVKARFVVTGGITRVYPKEAGENQENPETVEDSFYKRSNDNDNYVFTAP 766
Db 361 YWSKQKNIKGVKARFVVTGGITRVYPKEAGENQENPETVEDSFYKRSNDNDNYVFTAP 420
QY 767 YFNKSGPAGESGIMVSKAVEIYIQGLKLPVAVGIKIDVNSWIENFTKTSIRDPCAGPV 826
Db 421 YFNKSGPAGESGIMVSKAVEIYIQGLKLPVAVGIKIDVNSWIENFTKTSIRDPCAGPV 480
QY 827 CDCRNSDMVDCVTLDDGGELLMANHDDYTNOIGRFFGEIDPSLMRHLNLSYAFNKS 886
Db 481 CDCRNSDMVDCVTLDDGGELLMANHDDYTNOIGRFFGEIDPSLMRHLNLSYAFNKS 540
QY 887 DYQSVCEPGAAPKAGHRSAYVPSVADIQIGWATAAASIIQQLLSLTFPRLEAV 946
Db 541 DYQSVCEPGAAPKAGHRSAYVPSVADIQIGWATAAASIIQQLLSLTFPRLEAV 600
QY 947 EMEDDDDFTASLSKQSCITEQTFQFFDNDKSFSGVLDCGNCRIFHGEKLMNTNLIFMV 1006
Db 601 EMEDDDDFTASLSKQSCITEQTFQFFDNDKSFSGVLDCGNCRIFHGEKLMNTNLIFMV 560
QY 1007 ESKGTCPCDRLQLQAQSDTSDGNPCDMVKQPRYRKGPVDFDNNVLEDYDCGGVSGLN 1066
Db 661 ESKGTCPCDRLQLQAQSDTSDGNPCDMVKQPRYRKGPVDFDNNVLEDYDCGGVSGLN 720
QY 1067 PSLWYIIGIQLFLMLVSGSSTRLL 1091
Db 721 PSLWYIIGIQLFLMLVSGSSTRLL 745

RESULT 6
Q9NY47 PRELIMINARY; PRT; 1150 AA.
ID Q9NY47
AC Q9NY47;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
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DB GN CALCIUM CHANNEL, ALPHA 2/DELTA SUBUNIT 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYROID;
RA Klugbauer N.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=THYROID;
RA Hobom M., Dai S., Marais E., Lacinova L.;
RT "Neuronal distribution and functional characterization of the calcium
channel alpha2delta-2 subunit.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ251368; CAB86193.1; -
DR InterPro; IPR002035; -
SQ SEQUENCE 1150 AA; 129875 MW; 37875F687AF573C CRC64;

Query Match 53.5%; Score 3075; DB 4; Length 1150;
Best Local Similarity 54.3%; Pred. No. 3.5e-189;
Matches 595; Conservative 176; Mismatches 295; Indels 30; Gaps 13;

QY 7 LALTTLTFLQSLIGPSEEPFPSPAVTIKSWDKMQEDLVTLAKTASGVNQLDIYKYQD 66
DB 44 LWLLPLPLLAAPGASAYSPQOHTMOWARRLEQVGVGMFRFGVQQLREIYKDNRN 103
QY 67 LYTVEPNNAQLVEIAARDIEKLSNRSKALVSLALAEKVAQAHHQWREDFASNEVYYN 126
DB 104 LFEVQENEPQKLVKEVAGDIESLLDRKVAQLKRLADAENFQKAHRWQDNKEEDIVYD 163
QY 127 AKDDL--DPEKNDSPGSO--RIKPVFIEDANFGRIQSYQAAHVIPTDIYEGSTIVLN 181
DB 164 AKADAELEDPESEDERGSKASTLRDLDFIEDPNFKKNVSYAAQVPTDIYKGSTIVLN 223
QY 182 ELNWTLSALDEVFKNREDSLLWQVFGSATGLARYYPASPVDNSTPNKIDLYVRRR 241
DB 224 ELNWTALENVMENRQDPTLLWQVGSATGTVTRYYPATPW---RAPKKIDLYVRRR 279
QY 242 PWYTOGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSLDDDFVNVASFNQAQV 301
DB 280 PWYTOGASSPKDMLIIVDVSGSVGLTKLMLKTSVCEMLDTLSDDDIVNVASFNEKAQV 339
QY 302 SCFQRLVQANRKKVLKDAVNNTAKGITDYKKGFSAPEQLINYNVSRANCKIIMLF 361
DB 340 SCFTHLVQANRKKVFEAVQGVAKGTTGYKAGFEYAFDQLQNSNITRANCKIMMF 399
QY 362 TDGGEERAQEIFNKYN-KDKKRVRFRESVGOHNVYRGPIOWMACENKGYIYEIPSGAIR 420
DB 400 TDGGEDRVQVDFEYKNNPNRTRVTFESVGOHNVYDTPLOWMACANKGYIYEIPSGAIR 459
QY 421 INTOEYLDVLRPMVLADKAKQVQWNTVYLDALGLGLVITGLTPVNIYQCPENKTNLK 480
DB 460 INTOEYLDVLRPMVLADKAKQVQWNTVYLDALGLGLVITGLTPVNLQ--DGPGEKK 517
QY 481 NQLILGYMGVDVSLIEDIKRLTPRTFLCPNGYFAIDPNGYVLLHPNLPKPKSOEPTVL 540
DB 518 NQLILGYMGIDVALNDIKRLTPNVTGLANGYVFAIDLNGYVLLHPNLPKPTTFREPPTVL 577
QY 541 DFLDAELENDEKBEIRRMIDGESGEKFTFTLVKSQDERYDKGNRTYTPWNGTDYSL 600
DB 578 DFLDAELENDEKBEIRRMIDGNKGHKQIRTLVKSLSDERVIDEYTRNTWVPIRSTNYSL 637
QY 601 ALVLPYTSFYIKAKAETITQARSKGKMDSETLAPDNFEESGYTFIAPROYCNDLKI 660
DB 638 GLVLPYTSFYIQANLSDQILQVLRISKLDKDFEFLPSSFESEGHYFIAPREYCKDLNA 697
QY 661 SDNNTFELNFPNEIDRKTNNPCSNADLNRVLLDAGFTNELVQNTWSKQK-NIKGVKA 719

DB 698 SDNNTFELKNFIELMEKVTYPSDKQCNFLLHNLILDTGITQQLVERVWRDQDLNTYSLLA 757
QY 720 RFVVTGGITRVYVPEKAGENQWENPETYEDSFYKRSLDNDNVYVTFAPYFNK-SGPGAYES 778
DB 758 VFAATDGGITRVYVFNKAAEDWTENPEFFNPFNRSYRSLDNGHYVFKPHQDALLRPLELEN 817
QY 779 ---GIMVSKAVEIYIQGLKLPKPAVGVGKIDVNSWIENF-----TKTSIRD--CAGP--- 825
DB 818 DTGVLVSTAVELSLGRRTLRPAVGVKLEAWAEKFKVLASNRTHQDQPKC-GPNSH 876
QY 826 -VCDCKRNSDVMDCVILDDGGFLMLMANHDDYTQIGRFFGEIDPMSLRHLVNTSVAFNK 884
DB 877 CEMDCVNNEDLLCVLDDGGFLVLSNQNHQWDOVGFFSEVDANLMLALYNNNSFYTRKE 936
QY 885 SYDQSVCEPGAAPKAPKAGHRSVPSVADILQIGWATAAAWSILOQFLLSLTFFPRLLE 944
DB 937 SYDQACAPOPPGNIGAPRGVFTVADFLNLAWTSAANSLFQQLLYGLYHSHWFQ 996
QY 945 AVEMEDDDFTASLSKOSCITEQTYFFDNDKSFSGVLDGCGNSRIFPHGKMLNTNLI 1004
DB 997 ADPAEAG-SPETRESSCVMKQTYVYFGSVNAYNAIDCGNCSRLFHAQRLTNTNLLFV 1055
QY 1005 MWESKGTCPDTRLLIQAEQTSQPNPCDMVQPRYKRGPDVCFDNNVLEDYTDCCGVSG 1064
DB 1056 VAEKPLCSQCEAGRLQKETHSDGPEQCELVQRPYRRGPHICFDYNATEDSDCGRGAS 1115
QY 1065 LNPSLAVIIGIQFLL 1080
DB 1116 FPPSLGVLVSLQLLLL 1131

RESULT 7
Q9NY48 PRELIMINARY; PRT: 1143 AA.
AC Q9NY48;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE CALCIUM CHANNEL, ALPHA 2/DELTA SUBUNIT 2.
GN CACNA2D2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART;
RL Klugbauer N.;
RN Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RC TISSUE=HEART;
RA Hobom M., Dai S., Marais E., Lacinova L.;
RT "Neuronal distribution and functional characterization of the calcium
channel alpha2delta-2 subunit.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ251367; CAB86192.1; -
DR InterPro; IPR002035; -
SQ SEQUENCE 1143 AA; 129084 MW; 492556C9919A0CE5 CRC64;

Query Match 53.0%; Score 3047.5; DB 4; Length 1143;
Best Local Similarity 54.1%; Pred. No. 2.1e-187;
Matches 593; Conservative 174; Mismatches 292; Indels 37; Gaps 14;

QY 7 LALTTLTFLQSLIGPSEEPFPSPAVTIKSWDKMQEDLVTLAKTASGVNQLDIYKYQD 66
DB 44 LWLLPLPLLAAPGASAYSPQOHTMOWARRLEQVGVGMFRFGVQQLREIYKDNRN 103
QY 67 LYTVEPNNAQLVEIAARDIEKLSNRSKALVSLALAEKVAQAHHQWREDFASNEVYYN 126
DB 104 LFEVQENEPQKLVKEVAGDIESLLDRKVAQLKRLADAENFQKAHRWQDNKEEDIVYD 163

QY 1005 MYESKGTCPDTRLLIQARQ--TSDGNPCDMVKQPRYKRGPDVCFDNNVLEDYTDGCV 1062
DB 1049 VAEKPLCSQAGRLQKTHCPADGPEQCELVQPRYRGRPHICFDYNATEDSDCGRG 1108
QY 1063 SGLNPSLWIIIGIQFLL 1080
DB 1109 ASFPPLSGVLVSLQLLLL 1126

RESULT 10
Q9UEW0 PRELIMINARY; PRT; 1076 AA.
AC Q9UEW0;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TremBLrel. 14, Last annotation update)
DE ALPHA 2 DELTA CALCIUM CHANNEL SUBUNIT ISOFORM II.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wei M.-H., Latif F., Duh F.-M., Adreazoli-Angeloni D., Kashuba V.,
Zabarovsky E., Johnson B., Lerman M.I.;
RT "A new alpha 2 delta subunit of the L-type voltage gated calcium
channel resides in the lung cancer critical region on 3p21.3";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF042793; AAB96914.1; -
DR InterPro; IPR002035; -
SQ SEQUENCE 1076 AA; 122116 MW; EEC474836B7EDA85 CRC64;

Query Match 52.4%; Score 3013.5; DB 4; Length 1076;
Best Local Similarity 54.4%; Pred. No. 2.9e-185;
Matches 583; Conservative 174; Mismatches 276; Indels 39; Gaps 15;

QY 33 IKSVDKMQEDLVLTAKTASGVNQLVDIYKEYQDLTYTVPNNARQLVETAAIDIEKLSN 92
DB 1 MGHARRLEQGVDMRIFGGVQQLREIYKDNRLNFEVQENEPQKILVERVAGDIESLLDR 60
QY 93 RSKALVSLALEAKVQAAHOWEDFASNEVYNNAKDDL--DPEKNDSEPGSQ--RIKP 147
DB 61 KVQALKRLADAENQKARHWDNIKEEDIVYDADAELODDPESEVERGSKASTLRL 120
QY 148 VFIEDANFGQISYQAAHYHPTDIYEGSTIVLNELNMTSALDEVFKKNEEDPSLLWQV 207
DB 121 DRIEDPNFKKNYSYAAVQIPTDIYKGVSTVILNLTNLTNLTNLTNLTNLTNLTNLTNLT 180
QY 208 FGSATGLARYYPASPVWNSRTPNKLIDYVRRRPWYIQGAASPKDMLILVDVSGVSL 267
DB 181 FGSATGVTRYYPATPW---RAPKKIDLYVRRRPWYIQGASSPKDMWIIYDVSGVSL 236
QY 268 TLKLIPTSVSEMLTSLDDDFVNSFNSNAODVSCFQHLVQANVKNKVLKDVANNITA 327
DB 237 TLKLMKTSVCEMLTSLDDDFVNSFNSNAODVSCFQHLVQANVKNKVLKDVANNITA 296
QY 328 KGITDYKGFSAFEQOLLNYSRANCKNIIMLFTDGGEEAQEIFNKYN-KDKKVRFR 386
DB 297 KGITGYKAGFEAFDQLOLNSITRANCKNIMMFTDGGEDRVQDYFEKYNWPNTRVFT 356
QY 387 FSVGQHNYSRGIQWACENKGYEIPISGAIRINTQYLDVLRPMVLGAKQVQW 446
DB 357 FSVGQHNYSRGIQWACENKGYEIPISGAIRINTQYLDVLRPMVLGAKQVQW 416
QY 447 TNYVLDALGELVITGLTLEVFNTGOFENKTNLKNQILIGVGVDSLEDIKRLPRFTL 506
DB 417 TNYVLDALGELVITGLTLEVFNTGOFENKTNLKNQILIGVGVDSLEDIKRLPRFTL 474
QY 507 CPNGYFAIDPNGYLLHNPAPKPKSQEPVTLDFLDAELENDIKVETRNKMDGESGE 566
DB 475 GANGYFAIDPNGYLLHNPAPKPKSQEPVTLDFLDAELENDIKVETRNKMDGESGE 534

QY 567 KYFRLVKSQDERYIDKGNRTYTWTPVNGTDYSLALVLPYTFYFYIKAKLETITQARSK 526
DB 535 KOIRTLVSLDERYIDVTRNTYTWPIRSTNYSLGLVLPYTFYFYIQANLSQILQ---- 590
QY 627 KGMKMDSETLKPDPNEESGYTFIAPRDYCNLDKISDNNTNTEFLNFEFFDRKTPNPN 586
DB 591 ---VKYFEFLPSSFESEGHVFIAPREYKCDLNASDNNTNTEFLNFEFFDRKTPNPN 547
QY 687 ADLINRVLLDAGFTNELVQNYWSKQK-NIKGVKARFVVTDDGTRIVYVYKAEAGNMOENPE 745
DB 648 NELLHNLILDGTITQOLVERVNRDQDLNTYSLAVFAATDGGITRVFPNKAEDWTENPE 707
QY 746 TYEDSFYKRSILDNDNVFTAPYFNK-SGPGAYES---GIMWSKAVEIYIQGLLKRPVAVG 801
DB 708 PFNASFYRRSLDNHGVYFKPHQDALLRPLELENDVGVILVSTAVELSLGRTRLPVAVG 767
QY 802 IKIDVNSWIENF---TKTSIRDP--CAGP---VCDCKRNSDVMDCVILDDGGFLMA 850
DB 768 VKLDLEAWAEKVKVLASNRTHQDQOKC-GPNSHCEMCEVNNEDLLCVILDDGGFLVLS 826
QY 851 NHDDYTNQIGREFGEIDPSLMRHLVNIYAFNKSVDYOSVCEPCEPAAKQAGHRSAYVP 910
DB 827 NQNHQWDQVGRFESEVDANLMLALYNNSTYTRKESYDYQACAPQPPGNLGAAPRGVFP 886
QY 911 SVADILQIGWATAAAMSILQOFLSLTPRLEAVEMEDDDFTASLSKQSCITEQTQYF 970
DB 887 TVADEFLNLAWTSAASLSFLQQLLYGLYHSWFQDPAEAG-SPETRESSCVMKQOTY 945
QY 971 FNDKSFSGVLDGCGNSRIFHGEKLMNTLFIWVESKGTCPDTRLLIQARQ--TSDG 1028
DB 946 FGSVNASYNAIIDCGNSRIFHGEKLMNTLFIWVESKGTCPDTRLLIQARQ--TSDG 1005
QY 1029 NPCDMVKQPRYKRGPDVCFDNNVLEDYTDGCGVSGNLPSLWIIIGIQFLL 1080
DB 1006 PEQCELVQPRYRGRPHICFDYNATEDSDCGRGASFPSPSLGVLVSLQLLLL 1057

RESULT 11
Q9NSA6 PRELIMINARY; PRT; 975 AA.
AC Q9NSA6;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE LUAC11.1 (CALCIUM CHANNEL, VOLTAGE-DEPENDENT, L TYPE, ALPHA 2D SUBUNIT
DE (K1AA0558)) (FRAGMENT).
GN LUAC11.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Barlow K.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; 284492; CAB41767.2; -
DR InterPro; IPR002035; -
FT NON_TER 1 1
SQ SEQUENCE 975 AA; 110192 MW; C7874D46B88242BF CRC64;

Query Match 49.5%; Score 2844; DB 4; Length 975;
Best Local Similarity 56.5%; Pred. No. 2e-174;
Matches 548; Conservative 147; Mismatches 239; Indels 36; Gaps 14;

QY 132 DPEKNDSEPGSQ--RIKPVFIEDANFGRIYSQHAHVHPTDIYEGSTIVLNELNWTSL 189
DB 2 DPESEDEVERGSKASTLRLDIEDPNFKKNVNSYAAVQIPTDIYKGVSTVILNLTNLT 61
QY 190 DEVFKNREEDPSLLWQVFGSATGLARYYPASPVWNSRTPNKLIDYVRRRPWYIQGA 249
DB 62 ENVFNERRQDPTLLMQVFGSATGVTRYYPATPW---RAPKKIDLYVRRRPWYIQGAS 117

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QY 250 SPKDMILYDVSGVSGILKLIKRTSVSEMLETLSDDDFVNVTASNSNAQDYSCFQHLVQ 309
DB 118 SPKDMYIIYDVSGVSGILKLIKRTSVSEMLETLSDDDYVNVASFNKAQPVSCFTHLVQ 177
QY 310 ANVRNKKVLKDAVNNITAKGIDYKKGFFAFQEQLLNVNVRANCKIIMLTFTDGEERA 369
DB 178 ANVRNKKVKEAVOGVAKGTTGYKAGFEYFDQLNSNITRANCKIMIMFTDGEDRV 237
QY 370 QETFNKN-KOKKRVFRSVGOHNYERGIOWMACENKGYEYIPIPSIGAIRINTQEYLD 428
DB 238 QVFEKYNPNRTRVFTSVGOHNYDVTPLQWMAKACNGYFEIPIPSIGAIRINTQEYLD 297
QY 429 VLGRPMVLACDRAKQVQWNTNVLDALEGLVGTGTLPVENITQFENKTNLKNQILGVW 488
DB 298 VLGRPMVLAKKAQVQWNTNVLDALEGLVGTGTLPVENLTQ--DGPCKKNQILGVW 355
QY 489 GVDVSLDKRLTPRTTCLPNGYFAIDPNGVYLLHPNLPKNPKSQEPTVTFDLDAAELE 548
DB 356 GIDVALNDIKRLTPNTYTLGANGYVFAIDNGVYLLHPNLPKQPTTFREPVTDLFQDAELE 415
QY 549 NDIKVIRKNKIDGEGEKTFTFLYKSQDERIDKGNRTYTWTPVNGTDYSLALVLPYS 608
DB 416 DENKEIRSMIDGNKGHQIRTLVKSLEDERIDEVTRNTWPIRSTNYSGLVLPYS 475
QY 609 FYVIAKLEETITQARKKGMKDSLETKPDNFEESGYTFIAPRDYCNLKTSDNNTEFL 668
DB 476 TFLQANLSDQILQ-----VKYFELPSPFSESGHVFIAPREYCKDLNASDNNTEFL 528
QY 669 LNFNEIDRKTNPNSCNADLINRVLLDAGFNELQVNTWSKQK-NIKGVKARFVVTGG 727
DB 529 KNFELMEKVTDPKSCNCFLLHNLILDGTQQLVRYVRDQDLNTYSLLAFAATDGG 588
QY 728 ITRVYKKEAGENQWENPEYEDSFYKSLDNDNYVTAFNK-SGPGAYES---GIMVS 783
DB 589 ITRVFPNKAEDTENPEFNASFYRRSLDNHGYEKKPHQDALLRPLENDTVGILVS 648
QY 784 KAVEIYIOGKLLPAVVGKIDVNSWENF-----TKTSIRDP--CAGP---VCDCKN 832
DB 649 TAVELSIGRTLPAVGVVKLDLEAWAEKVLASRNRTHQDPQKC-GPNSCEMDCEVN 707
QY 833 SDVMCDVLDGGLFLMANHDDYTNIGRFFGEIDPSLMRHLNVISYAFNKSXYDQSV 892
DB 708 NEDLLCVLDGGLFLVSNONHWDQVGRFFSEVDANLMLALYNSFYTRKESYDQAA 767
QY 893 EPGAAKQAGHSAVPSVADILQGWATAAAWSILOQFLLSLTFPLLEAVEMEDD 952
DB 768 APQPPGNLGAAPRGVFPVTVADFLNLAWNTSAAAWSLFQOLLYGLIYHSWFQADPAE 827
QY 953 FTASLSKQSCITQOTQYFFDNDKSKFSGVLDGNCGRIFHGEKLMNTLIFIMVESK 1012
DB 828 -SPETRESSCMKQOTQYFGSVNASYNAIDGNCGRSLFHAQRLTNLLFVVAEPLCS 886
QY 1013 PCOTRLLIAEQ--TSDGNPCDMVKQPRYKGPVCFDNNVLEDYDCGGVSLNPSLW 1070
DB 887 QCEAGRLLOKETHCPADGPQCELVQPRYRGRPHICFDYNATEDSDCGRGASFPPLG 946
QY 1071 YIIGIQFLLL 1080
DB 947 VLVSQLLLL 956
RESULT 12
Q921L5 PRELIMINARY; PRT; 1091 AA.
AC Q921L5;
DT 01-MAY-1999 (TEMBLrel. 10, Created)
DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
DT 01-OCT-2000 (TEMBLrel. 15, Last annotation update)
DE CALCULUM CHANNEL ALPHA-2-DELTA-C SUBUNIT.
GN CACNA2D3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
TISUE=BRAIN;
RX MEDLINE=99098955; PubMed=9880589;
RA Klugbauer N., Lacinova L., Marais E., Hobom M., Hofmann F.;
RT "Molecular diversity of the calcium channel alpha2delta subunit.";
RL J. Neurosci. 19:648-691(1999).
DR EMBL; AJ010949; CAA09423.1; -.
DR MGD; MGI:1338890; Cacna2d3.
DR InterPro; IPR002035; -.
SQ SEQUENCE 1091 AA; 122777 MW; 7AEE2BDA10077A0A CRC64;
```

Query Match 19.6%; Score 1127.5; DB 11; Length 1091;
Best Local Similarity 28.6%; Pred. NO. 6.4e-64;

Matches 328; Conservative 230; Mismatches 451; Indels 137; Gaps 42;

```
QY 3 AGCLLALTTLTLOSLLIGPSSPEPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDIYE 62
DB 14 ASALLA-TALLYAALGDVVRSEQQIPLSV-VKLWASAFGEIKSAAYKSGSOLLQKKYK 71
QY 63 KYQDLYTEPNNAQOLVETIARDIEKLNSRKALVSLALEAEKVOAAHQWREDFASNEV 122
DB 72 EYEKDAVEIEIDGLQLVKKLAKIMEEMPHKKSEAVRRLVEAAEAHLKHEFDADL---QY 128
QY 123 VYNNAK--DDLPENDSEPGSQRIKPVIEDANRGR-QISYQHAAYHIPTDIYEGSTIV 179
DB 129 EYFNVLINERDKDGNFLGKEFI---LAPNDHFNNLPVNISLSVQVPTNMYNKDPAI 185
QY 180 LNELNWTSLDVEFKKKNREEDPSLLWQVFGSATGLARYYPASPFWVDSNRTPNKIDLYDV 239
DB 186 VNGVYWSLSLNVFVDNDRDPSLWQVFGSAKGFPRQYPGIKWEPDE---NGVIAFDOR 242
QY 240 RRPWTIQGAASPKDMLILVDVSGVSGELTKLIIRTSVSEMLETLSDDDFVNVTASNSNAQ 299
DB 243 NRKWTIQAATSPKVVILVDVSGSMKGLTIAKTQVSSILDTGLDGGDFNITTYNEELH 302
QY 300 DYS-CFO-HLVQANRNKVLKDAVNNITAKGIDYKKGFSFAFQEQLLNVNVRAN--CN 355
DB 303 YVEPLNGTLVQADRTNKEHFRHLDKLFAGKGMLDIALNEAFNLISDFNHTGQSGICS 362
QY 356 KIIMLTGDCGERAQBIFNKYN-KDKKRVFRSVSGOHNYERGIOWMACENKGYEYIPI 414
DB 363 QAIMLTIDGAVDTYTFIAKYNPDKRVIFTYLIGREAAAFADNLKWKMACANKGPTQIS 422
QY 415 SIGAIRINTQEYLDVLGRPMVLAKQVQWNTNVLDALEGLVGTGTLPVENITQFENK 463
DB 423 TLADVQENVMYELHLSRPKVI--DOEHVWVWTEAYIDSTLPQAQKLADDQGLVLTMTVA 480
QY 464 LPVFNITQFENKTNLKNQILGVNGVDVSLIEDIKRLTPRTCLPNGYFAIDPNGYVLL 523
DB 481 MPVFS---KQNETRSG--ILGVVGTQVVPVRELLKTIPIKYLGIHGYAFATNNGIIT 535
QY 524 HPNLOP---KNPKSREP--VTLDFLDALENDIKVIRKNKIDGEGEKTFTFLYKSQDE 578
DB 536 HPFLRPLIEEGKRRKPNYSVDLSEVEDRDDV-LRNAVNRKTKG--FSMEVK----588
QY 579 RYIDKGNRT-----YTWTVPVNGTDYSLALVLT-YSFYIIRAKLEETITQARKKGMK 631
DB 589 KGVDKGRVLVMTNDYYTDIKGTFPSLGVSLSRGHGKYFF-----RGNTV 634
QY 632 DSETLKPDNFEESGYTFIAPRDYCN-DLAISDNNTEFLNFEIDRKTNPNSCNADLI 690
DB 635 IEEGL--HDLEHPDVSADWESYCNITDLHPEHRHLSQLEAIKLYLKGKEP-LLOCKELI 691
QY 691 NRVLIDAGFTNELVQVWS-----KOKNIKGVKARFVVTGDTGTRVYP-----733
DB 692 QEVLFDA-VVSAPIEAYTWSLAINSENKSDKGVEAFGLGTRGLSRLNLFVGAELTNQD 750
QY 734 -KEAGENWOENPETYEDSFYKSLDN--DNYVFTAPY-----FNKSGPGAYESGIMVS 786
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Db 751 FLKAGKENIFNADHPFLWYRRAEAGIAGSVYIPFSTGTWNKS-----NVVTASTSI 804
QY 787 EYIYQKLLKPAVVGIGKIDVNSWENFTKTSIRDPCAGVCDCKRNSDVMDCVILDDGPF 846
Db 805 QLLDERKSPVAAGVIGKQMLEFQRFKFWTASRQASLDGCKSISCDDETVNCLYIDNNGF 864
QY 847 LLMAHDDYTNQIGRFGFIDPSLMRLHVNISVAFNPKSYDYOSVCEPAAQKQAGHRS 906
Db 865 ILVS--EDYT-QTGDFGVEGAVNKLITMGSKFRITLYDQAMCR---ANKESSDAH 918
QY 907 AVVPSVADILQIGWATAAASWTLQOFLSLTFLPRLEAVEMEDDDFTASLSK-----QS 961
Db 919 GLLDPKAEL-----SAKAWIMTELVLFLVEF-----NLCSWHSDMTAKAOKLKOTLEP 968
QY 962 CITEQYQYFFDNDKSFSGVLDGCGNSRIFHGEKLMNTNLIIFIMVSKGTCPCDTRLIIQ 1021
Db 969 CDEYPAFVSERTIKETTGNACEDCSKFSVIQIPSSNLFMVVDS--SCLESVAPIT 1026
QY 1022 AEGTSDGPN---PCDMVKQPRYKRGDPVCFDNNVLEDYDCCGVSGNLNLSWIIIGIQL 1078
Db 1027 MAPIEIRYNSLCKERLKAOKIRRRPESCHGFHPEENARECGGASLQAO-----AALL 1080
QY 1079 LLWLVS 1084
Db 1081 LLPLVS 1086

RESULT 13
Q9NK64 PRELIMINARY; PRT; 997 AA.
AC Q9NK64
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE CALCIUM CHANNEL ALPHA2-DELTA3 SUBUNIT.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Bugert P., Hanke S., Chudek J., Kovacs G.;
RT "Analysis of a putative tumor suppressor gene region of 100 kb at
RT chromosome 3p21.1 in conventional renal cell carcinoma.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ272268; CAB75962.1; -
DR InterPro; IPR002035; -
SQ SEQUENCE 997 AA; 112996 MW; B56D1313FD67B8D CRC64;

Query Match 18.3%; Score 1050.5; DB 4; Length 997;
Best Local Similarity 28.2%; Pred. No. 4.9e-59;
Matches 299; Conservative 216; Mismatches 420; Indels 125; Gaps 39;

QY 86 IEKLLNSRKALVSLALEKVAQAQHWREDPASNEVYNAK--DDLDPKNDSPGQS 143
Db 1 MEEMFHKKSEAVRLVEAAEAEHLKHEFDAL---QYEFNAVLIINERDKDGNFLELGE 57
QY 144 RIKPVIEDANFCR-QISYQHAHAVHPTDIYEGSTIVLNLNWTSLDDEVFKKNEEDPS 202
Db 58 FI---LAPDNHFNLPNLSLSQVPTNMNKDPAIVGVYVWSESLUNKVFDVDFNDPDS 114
QY 203 LMQVFGSATGLARYYPAGPVDVNSRTPNKKIDLYVRRRPWYIQGAASPKDMLILVDVSG 262
Db 115 LIWQFSGAKGFFRQYPIGWEPDE--NGVIAFDCKRNRKWIQAATSPKDVILVDVSG 171
QY 263 SVSGLILKIRTSVSEMLETSLDFFNVASFNNSQDVS-CFQ-HLVQANVNKKVLKD 320
Db 172 SMKGLRLTIKQVSSILDTGLDGDFFNIITAYNEELHYEPCNLGTLVQADRTNKEHFE 231
QY 321 AVNNITAKGTDYKKGFSFAFEGOLLNYSVRAN--CNKIIMLFTDGEERAEQIFNKYN- 377
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Db 232 HLDKFLPAKIGIMLDIALNEAFNLSDFNHTGSGISQAIMLITDGAVDYDTYFAKYNW 291
QY 378 KDKKRVFRFESVGOHNYERGPIQWMACENKYYEIPSTGAINRTOEYLDVIGRPMWLA 437
Db 292 PDKRVIRFYTLIGREAAAFADNLKMACANKGFFTOISTLADVOENYMLHLVLSRPKVI- 350
QY 438 GDKAKOVQNTNYLDAL-----ELG--LVITGTLFVENITGOFENKTNLKNOLLIG 486
Db 351 -DOEHVWVTEAYIDSTLPOAKLTDDQGPVLMVTVMVPFS-----KQNETRSGK-ILLG 404
QY 487 VMGVDSLEDIKRLTFRFTLPCNPGYFAIDPNCYVLLHPLNQ---PKNPKSQBP--VTLD 541
Db 405 VVGTDVPVRELLKTIKYKLGINGYAFATNNGYILTHPELRLLYBEGKKRRKRPSSVD 464
QY 542 FLDALENDIKVEIRKMKIDGESGKTFRTLYKSQDERYIDKGNRT-----YTWPVNG 595
Db 465 LSEVEDRDDV--LRNAMVNRKTK--FSMEVK---KTVDKGRVLMVTNDYYTIDIKG 517
QY 596 TQYSLALVLT-YSEYIIKAKLEETITQARSKKGKMKDSETLKPDPNFEEGSGYTFIAPRDY 654
Db 518 TPFSLGVALSRGHGKYFF-----RGNTVIEGL--HLEHPDVSADSEWSY 561
QY 655 CN-DLAKISDNNTFELNFEFIDRKTNNPNPSCNADLINRVLLDAGFTNELVQNYWS---- 709
Db 562 CNTDLHPEHRHLSQLEAIKLYLAKKEP-LLOCDKELIQEVLFDA-VVSAPIEAYWISLAL 619
QY 710 --KQKNIKGVKARFVYTDGTRVYP-----KEAGENWOENPETYEDSFYKRS 755
Db 620 NKSNSDKGVEVAFGLTGLSRINLFGAEQLTNODFLKAGDKENIFNADHPFLMYRRA 679
QY 756 LDN--DNYVFTAPYFNKSGPGAVESGIMYSKAVEIYIOGKLLKPAVVGIGKIDVNSWIENF 813
Db 680 AEGIPGSFYISIPF--STGVPKNSNVYVSTASTSOLIDERKSPVVAAGVIGKQMLEFQRF 737
QY 814 TKTSIRDPKAGPVCDCKRNSDVMDCVILDDGFLMANHDDYTNQIGRFGFIDPSLMRH 873
Db 738 WTASROCASLDGKCSISCDDETVCNVYLDNNGFILVS--EDYT-QTGDFGFEIGAVMKN 794
QY 874 LVNISVYAFNKSVDYOSVCEPAAQKGA--GHRSAVYPSVADILQIGWATAAASWILQ 932
Db 795 LLTMGSFKRITLYDQAMCRANKESSDGAHGLDIPY-----NAFLSAVKWIMTEL 844
QY 933 FLLSLTFPRLLEAVEMEDDDFTASLSK---OSCITEQYQYFFDNDKSFSGVLDGCGN 987
Db 845 VLFLVEF---NLCSWHSDMTAKAOKLKOTLEPCDTEYPAFVSERTIKETTGNACEDC 900
QY 988 SRIFHGEKLMNTNLIIFIMVSKGTCPCDTRLIIQAEQTSQGNP---PCDMVKQPRYKRP 1044
Db 901 SKSFVIQIIPSSNLFMVVDS--SCLESVAPITMAPIEIRYNSLCKERLKAOKIRRRP 958
QY 1045 DVCFDNNVLEDYDCCGVSGNLNLSWIIIGIQLLWLVS 1084
Db 959 ESCHGFHPEENARECGGASLQAO--VLLLLPILLMLFS 996

RESULT 14
Q9NK64 PRELIMINARY; PRT; 2190 AA.
AC Q9NK64;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE HYPOTHETICAL 249.8 KDA PROTEIN.
GN BG:DS07473.1 OR CG12455.
OC Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y, CN BW SP;
RC MEDLINE=99403001; PubMed=10471707;
RX
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RA Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T.,
RA Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,
RA Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
RA Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.,
RA Celnikier S., Rubin G.M.;
RT "An exploration of the sequence of a 2.9-Mb region of the genome of
RT Drosophila melanogaster: the adh region.";
RL Genetics 153:179-219(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Y, CN BW SP;
RA Celnikier S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,
RA Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
RA Ruten D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
RA Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
RA Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
RA Nixon K., Pacieb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
RA Sethi H., Snir E., Swirskas R.R., Wan K.H., Weinburg T., Zhang R.,
RA Zieran L.L., Rubin G.M.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE003415; RAP44988.1; -.
DR Flybase: FBgn0028859; BG:DS07473.1.
DR InterPro: IPR002035; -.
KW Hypothetical protein.
SQ SEQUENCE 2150 AA; 249754 MW; B8C657A2F80F236E CRC64;

Query Match 16.3%; Score 937; DB 5; Length 2190;
Best Local Similarity 24.9%; Pred. No. 3.5e-51;
Matches 289; Conservative 222; Mismatches 410; Indels 238; Gaps 47;

QY 29 SAYTIKSWDKQEDIVLAKTAGSNQVLDVIEKYQDLYTYEPNNAROLVETAIADIEK 88
DB 13 SKATVGNWATQFGDELFAQAQITKSOETKEKYEN--ARVELKNGTLEIKSITKNVGR 70
QY 89 LLSNRKALVSLALEAEKYQAAHQWREDFASNEVYVY-----NAKDDLDPEKNDSE 139
DB 71 MLARKWDVRCIOEAEYENEFNLTALQNTVYFSSKYSTFNNGSSELEP--NEAE 128
QY 140 PG-----SORIKPVIEDANF-GRIQSYQAHAHVPDIDYEGSTIVLNELNWTSLADEVPK 194
DB 129 FAWMYRNMELNP----DTHFYNPVPTDESHSVHVPSPNIWDRSERVLKTTMWEHLDEVER 184
QY 195 KNEEPPSLWQVGSATGLARYPASPWVDSNRTPNKDLDYDVRPVPYIOGAASPKDM 254
DB 185 QNTQSPALSWQVFGSDTGLRHYPAAQWTDTRPNRDDADTDYDCRKRKSWIETATCSKDI 244
QY 255 LILVDVSGVSGLTLLKRTSVSEMLTSLDSDDFVNVASFNSNAQD-VSCFQ-HLVQANV 312
DB 245 VILLDHSGMTGFRHHVAKFTIRSIDLTFSNDDFFILARYSEVNDIIPCFNGALVQATP 304
QY 313 RNKKVLKDAVNNI-TAKGTDYKGSFAFEQLLNTNVSF-----ANCNKIIMLFTDGE 366
DB 305 ENIEVFNQIEQLDDPEGANLTLAYETAFQLLRKYDYSRHCVTNCTCQAINMLVTDGVA 364
QY 367 ERAQELFNKNY-----KDKKRVFRSVOGHNYERGPIONWAKNGYVEIPSIGA 418
DB 365 GNTVEFQKTNWNGENGNGTSQMDTRFTVLLGKVTQVREIQWMACLNGYVSHVOTLDE 424
QY 419 IRTINQBYLDVLRPMVLAGDKAKAQVQWNTNVDLAL-----ELGLVITGTLPVFN 469
DB 425 VHEVLKYVDVIATPLVLQNEQHPTT-WTHAFTDKYDPKTSNEKRPRLMISVGVPAFDR 483
QY 470 TGFENKTNKQLIIGVMGVDSLEDKLTPRFLPCNPGYFAIDPDGCVLLHNLQP 529
DB 484 FYRANSTNPRAL-LGVAGTDVPEVIDKLTLPYLGNGYGVYVSNNGYVLLHDLRP 542
QY 530 -----KNPKSQEPVTLDFDAB-LENDIK-----VEIRKNMIDGSGE-KTFTLV 573
DB 543 IGNGKMNPNY---SIDFTEVHELDQSPREPGRGSILHIRNAMYHNEAFKSVKF 599
QY 574 KSQDERYIDKGRNTYWTVPNGYDYSIALVLPY-YSFYIKAKLEETITQARSKGMKD 632

DB 600 HYDKMRVRSEKQDYFFAPLPNTPTFTLGIVMSEYKGTWKVGEVD-----KNHKMKINI 655
QY 633 SETLKPNDNFEE-----SGYTIAP-----RDYK-----NDLKISDNTNTEFLFN 672
DB 656 SDFIGENKWKHPDWYKYHYHLEGHEFKTPEALREFLAKMNDKWKSEQYAEDESMD 715
QY 673 EFID-----RKTNNPNS--CNADLNRVLDDAGFTNELYQNYW-----SKQNKIKVKA-- 719
DB 716 DKDDLNCGRKTLGDDAYYCNKELVNLILFDKAVTNS-SYGVWRFSDEDEQLIERFADL 774
QY 720 RVVTDGGITRVYKEAGENQ-----ENPETYEDSYKRSL-----D 757
DB 775 RVFATMSGLTR-----WQIFGEVEVTDREFGDYHTAIDETWYKSAILQHHEDR 825
QY 758 NDNVVETAPYENKSPGAGVSESGIMYSKAVEIYIOGKLLKPAVVGKIDVNSWNIENFTKTS 817
DB 826 AESFYISVKYID-----DPMEDSE 844
QY 818 IRDPCAGPVCDCRNSDMOCVILDDGGFLLMANHDDYTNQIGRFFGIDPSLMRHLVNI 877
DB 845 VKCNHCLPIC-----TDDVDVCVVIDNNAYIVIGON---INTTGKFFGEFHGDVMTAMVER 897
QY 878 SVYAFNKSYDQSVQ--EPGAAPKPGAGHRSAYVPSVAD-ILQIGWATAAASLIQQLF 934
DB 898 GIFLSIEVDYQEQCKEKPAYME-----YTDEIEDEVYAVVAGDGGKSSA----- 941
QY 935 LSLTPRLLEAVEMEDDDFTASLSK-----QSCITEQTOYFFDNDKSFSGVLDC--G 985
DB 942 -----SKPKDSDSDENAMFDEPDPIYKACDKRSTLYAL--QPSALVGINDFVEA 990
QY 986 NCSRTIFHGEKLMNTNLIFIMVE---SKGTCPCDTRLLIQABOTS-DGPNPCDMYKQPRY 1040
DB 991 PSTREFLVKKIPNSNLVLYVNVNLPSPR-----SVRLTTEPQRMEDYKEFPCKYKLNMSFY 1045
QY 1041 -RKGPDPVCFDNNVLEDYTD 1058
DB 1046 ERRIIECY--TVHEDLSD 1062

RESULT 15
Q9VJMO PRELIMINARY; PRT: 2172 AA.
AC Q9VJMO;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE CG12455 PROTEIN.
GN BG:DS07473.1 OR CG12455.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RX MEDLINE-20196006; PubMed-10731132;
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Basley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Botchan P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Bouton M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lakso P., Lei V., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.M., Nelson K.A., Nixon K., Nusskern D.R., Pacled J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M.C., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhang M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
"The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000).
DR EMBL; AE003650; AAF53505.1; -
DR FlyBase; FBgn0028859; BG:DS07473.1.
DR InterPro; IPR002035; -
SQ SEQUENCE 2172 AA; 247574 MW; 39AA7BCB470D1A39 CRC64;

Query Match 16.0%; Score 920; DB 5; Length 2172;
Best Local Similarity 25.0%; Pred. No. 4.3e-50;
Matches 288; Conservative 216; Mismatches 406; Indels 242; Gaps 47;
QY 29 SAVTIKSWDKQEDLVILAKTAGVNLVDIYKQDLYTTPNARQOLVIAARDIEK 88
Db 13 SKATVKGATQGDLEFALAAQIKTSQETKEKYKN--ARVELKNGTELIKSITKNVGR 70
QY 89 LLSNRKALVSLALEAKYQAQHQWREDA--SNEVYVYNAKDDLDPEKNDSPEG---S 142
Db 71 ML-----ARKMDAVRCIOEHFTYFFSKYSFNGNSSELEPNEAEFAWYRN 117
QY 143 QRIKPVFTEDANF-QRQISYQHAHVHPTDYEGETVILNELNWTSDALDEFKKNEEDP 201
Db 118 MELNP---DTHFYNTPVDTESHVSPVSNIDRSERVLKTIWSEHLDEVERQNTQSDP 173
QY 202 SLLWQVFGSATGLARYYPASPHVDSRPNKIDLYDVRPRPHYIOGAASPKDMLILVDVS 261
Db 174 ALSWYIFGSDTOILRHYPAAQWTDTPRNRDDADTDYDKRRSWIETATCSKDIVILLDHS 233
QY 262 GSVGLTLKLIKRTSVSEMLETISDDDFVWASFNSNAQD-VSCFO-HLVQANVRNKKVLK 319
Db 234 GSWTGFRRHVAKFTIRSLDFTFSNDDFTILYRSEVNDIIFCFNGALVQATPENIEVEN 293
QY 320 DAVNNI-TAKGTTDYKGFSAFEOQLLYNVYSR-----ANCKNIIMLFTDGEERAQEIF 373
Db 294 QOIEQLDDPEGYANLTAYATAFQLRLKYDSRHCVNSTCQALMLVTDGVAGNTTEVF 353
QY 374 NKNY-----KDKKVRVRESVQHYVERGPIOWMACENKGYIYEIPSGAIRINTQE 425
Db 354 QKYNNGENGTSQMDTRFTYLLGKEVTKVREIQMAACLNAGYYSHVQTLDEVHEEVLK 413
QY 426 YLDVLRGPVWLAGKAKQVQNTNVYLDAL-----ELGLVITGLTPVFNITQGFENK 476
Db 414 YVDVATPLVLQNEQHPT-WTHATDXTYDPKTSNEKPRMISVGVPADFPRFHRANS 472
QY 477 TNLKNQILGVNGVDVSLIEDIKRLPRFTLCPNGYFAIDPNGYVLLHPNLQP-----K 530
Db 473 TNPRARL-LGVAGTDVPVEDIDKLPYKLVGVNGYSFVYSNNGYVLLHPDLRPIGTNGKM 531
QY 531 NPKSQEPVILDFDAE-LENDIK-----VEIKNMIDGESGE-KTFRTLVKSQDERY 580
Db 532 NPNNY---SIDFTEVEHLEFDQSPREGESILHIRNAMYRHEANEFKISVKFHYDKMR 588
QY 581 IDKGNRTVTWTPVNGTDYSLALVLPY-YSFYIKAKLEETITQARSKKMKDSETLKPD 639

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Job time: 574 sec

